

TGAATATTTT TTGTTTAACT CTTAAATTTT GGGTTTAACT TCCTCTATTT CTAACAGTTA 660
 TACTCCAGGA TTAGTTTCTT TAGAATCCGT ACCGATTAAAT TTAACAGTAT GGTTTTGCCA 720
 5 GTCAACTTCA TAAGTAGATG TAAACGTTAC TGTATTTTGA TnTTTGTAGT TATTTCCAAC 780
 CCAGTGTAGT CGATTCCATT GATTAGTATA TCTATCCATT TCTCTTTGGT AAGTTACTTT 840
 10 GATTTTAGAT TtTTTTGTAT CATTTTGTTC ATGAGAAAGT ACGCTTATAA ATTCTGGGTT 900
 AAAGTTACCA CGCGCCAATA AAGGCATTTC ATGTGTTGGC AAGAAATTTT GACCAGCATT 960
 TGAACTACTT TGTCTACCAC CTAAAAACAG TTCATTACCA TATGTTGGGT CATAACTATC 1020
 15 TCTACCATAT GGTCCCCAAC CATTATTCAT AATTTTGTGC GCCTCAACAC CCCAGCCAAT 1080
 TGATTTATGA TTTGTTTTTC TATCAATCGT AGTTCTGTAA CTTTCTTGTT TATAATTTAT 1140
 CGTTTCTGAA AATGATTTTG ATCCATTTAA TCCACCTGAT AAGCCATTAG ATATATTA 1198

(2) INFORMATION FOR SEQ ID NO: 742:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 818 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 742:

GTGGCATATn CAAACTAGTA CTGAAAGATC AATTACATAC GTACAGATTT TGCAAAATGA 60
 TCAAGATTAT CCAACAATTT TTAGATGAGa CAAAACGTAA ATCTGTAATT AATTcAGATG 120
 35 TTAATGTAAC GGTAAAAGAT AGAATAATGA CTTTATcAAC GTGCGAAGAT GCATATAGTG 180
 AAACGACGAA AAGAATTGtT GTTGTGCGAA AAATAATTAA GGTAAGTTAA ACAGAAAmGA 240
 GGATAATTAT GAAATTTATG GCAGAAAATA GGCTGACGTT AACaAAAGGA ACAGCAAAAG 300
 40 ATATTATAGA ACGATTTTAC ACGAGACATG GGATTGAAAC ATTAGAAGGC TTTGATGGCA 360
 TGTTTGTTAC ACAAACTTTA GAACAAGAAG ATTTTGATGA AGTGAAAATT TTAACAGTTT 420
 GGAAATCAAA GCAAGCTTTT ACGGATTGGT TAAAATCTGA TGTCTTTAAA GCAGCGCATA 480
 45 AACATGTTAG AAGTAAAAAT GAAGATGAAA GTAGCCCGAT TATAAATAAC AAAGTAATTA 540
 CATATGATAT AGGCTATAGT TACATGAAAT AATTGAATTT AAAGAGGTTG CAGTACTTGT 600
 50 TATGACAATT GGTATTGTTA GCTTTTGTAA CGACCATACA TGATACCGAT GATGGTCGTT 660
 TTTTAAATGa ACACAAACAT GCTAACAACA AATTGCTAAA ACATAGTTTG aTTTGAATGT 720
 GgCTTTGGAA AATAATCATC CAtTATATCa TTtTGGATTh TATTTTGGAA GAAGAAAAGA 780

(2) INFORMATION FOR SEQ ID NO: 743:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 743:

	TGCTGGTAAA TCTTCCCTTA TCAAGTCTTT AATTGGTGAA TTTAATGCTA CCGGTACTAA	60
15	ATTGTTATAT AACAAACCTA TACAACAACA ACTGCAACAT ATTACATATA TTCCACAAAA	120
	AGCACATATT GATTTAGATT TTCCTATAAG TGTGGAACAA GTGATTTTAT CAGGTTGCTA	180
	CAAGAAATT GGATGGTTTA GACGACCTAA TAAATCAGCA AGGGATAAAC TCAAACAGTT	240
20	ATTAAGCGAT TTAGAATTAG AATCTTTACG TCATCGACAA ATTTCAGAAT TAAGTGGTGG	300
	ACAATTACAA CGTGTGCTAG TAGCAAGAGC ATTGATGTCC G _n AAGTGAAG TTTATTTTCT	360
	AGATGAGCCG TTTGTCGGAA TTGATTTTAG TAGCGAAAAA tTAATCATGA CAAAAATcGA	420
25	GAACTTAAaA CAACAAGGAA AACTTATTcT TATCATCCAC CATGATCTAT CAAAAGCAAA	480
	GCAATACTTT GATCGCATTa TTCTATTAAA TCAAACATTA CGATACTTTG GTGATAGTGA	540
30	AGAGGCTATG AGTGTCACTC GCTTAAACGA AACATTTATG AGTAGCACTG ACTGTAGTGA	600
	CCCTAGTCAA AGGAGCAATA TAACATGTTA GAGTTTGTCG AACATTTATT TACATATCAA	660
	TTCTTGAATC GAGCATTGAT AACTTCAATT ATTGTAGGGA TAGTTTGTGG TACAGTTGGT	720
35	AGTTTAATTG TATTACGTGG TCTTTCATTA ATGGGAGATG CAATGAGTCA CGCAGTATTA	780
	CCTGGTGTTG CCCTATCATT CTTATTTGGT ATTCCAATGT TTGTAGGCGC ACTTATAACT	840
	GGTATGATCG CAAGTATTTT TATCGGTTAT ATCACATCTA GTAGTAAAAC GAAACCTGAC	900
40	GCCGCTATTG GAATTAGTTT TACCGCTTTC TTAGCTTCGG GGATTATTAT TATTAGCTTA	960
	ATAAACACTA CGACAGATTT GTACCATATT CTGTTTGGTA ATTTACTGGC AATCACAAAT	1020
45	AGTGCATTTT TAACAACATAT TGTGATTGGT TCAATCGTCC TTATTCTAAT CATTATTTTC	1080
	TATCGTCCAT TAATGATTTT TACATTCGAT CCAACGTTTA GTAGAATGAG TGGTCTAAAT	1140
	ACGACGTTAT TACATTACTT TGTGATGTTG tTACTCTCAT TAG _n AACAGT AGCAAGTatT	1200
50	C _m AACGGTA	1209

(2) INFORMATION FOR SEQ ID NO: 744:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 744:

CCGCCTTTTCG TAAACCTAAT ATAATACGAA ATTTTCGTAT TGTCAACATT AAATACGTTT 60
 10 TTTTCGTAAA AAACCTTACT ATGATATGAA AATTTTCGTAT AATAAGAAAA AAGGAGGTAA 120
 GTAATATGAA CAAAGAmAGm AATATTATTA TAGCCAAAAm CATTAGAAAA TTTCTCAACG 180
 ATTCAAATAT GTCTCAAAAG AAACCTTGCTG AaCTCATTAA CATAAAACCA TCTACTTTAA 240
 15 GCGATTATTT AAATTTACGT TCCAACCCCT CTCACGGCGT TATACAAAGG ATAGCTGATG 300
 TTTTCGAGGT TGGTAAAGC GACATAGATA CTACATACAA AGACGATAAC GACATCACTT 360
 CCATATACAA CAAACTCACA CCTCCCCGCC AAGAAAACGT ACTTAACTAT GCAAATGAAC 420
 20 AATTGGAAGA ACAGAATTCT AAAGGAGATA ACGTTGTAGA TATTAATTCA TATAAACAGG 480
 AGAAAACCTCC AGTTAACGTC AATGGTTGCG TCTCTGCTGG TGTAGGAGAA CGTTTACACG 540
 ATGAAACGCT ATTTACTGAA ATGGTTAAAG GACCTATCCC CACACACGAT TTAGCGTTAA 600
 25 AAGTAAATGG TGATTCTATG GrACCTATGT TTAAAGATGG CGAAATCATA TTTGTGGAGA 660
 AAACCTCACAA TnTGA 675

30 (2) INFORMATION FOR SEQ ID NO: 745:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 924 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 745:

CAGGTGTCAT AGTTGAACTT GGtGGTTTTG GACTAATCGT TAAATCATCA ATTTGTGTCA 60
 TCCAAGGTTG GAATTTACTG CTTGTGTCT CCAGTGCCT GAAAATACCT TTATCTTGAA 120
 45 ATAAGTCAAC TAACTCTTGG ATACCTTTAA TTAATGCTGG GTTACCACCA GAAATTGTAA 180
 CGTGGTTAAA TAAATCGCCA CCAATTCGTT TTAATTCATC ATAAATTTCT TCAGCGGTCA 240
 TGAGTTTTAT ATCGCCTTTA GCACTACCAT CCCAAGTAAA TGCAGAATCA CACCAGCTAC 300
 50 AGgATaATCA CATCCAGCTG TTCTCACAAA CATCGTTTTT CTACCGATTA CTCGACCTTC 360
 ACCCTGAATG GTTGGACCGA ATATTTGAG TACAGGAATT TTAGCCATTA GTTACACCTG 420
 55 TTCCTTTGGT CTAAATACGA CATAACTTGT TGGTGTCTCT CTTACAAATA CTTGAATACA 480

TACGATTTCA GTTGAAGGGA TTTTGTITTTT AAAAGCAGGT AAGTTATTTA ACAGTTGATG 600
 GTCAAATTTA CCGTGTATCA TCTTTTTCAT ATGGCTAAAG TTCACTAAGA AGCCAGTGTC 660
 5 ATCTAGTTTA TCACCGACAA TTGTTAAaya CAAAGTAAGT ATGACCATGG ACATTTTGAC 720
 AAATACCTGC TTCTTCACAT GGAATGTGAT GTGCAGCCGA AAAATTAAAA TCTTTATTTA 780
 10 ATTCGAATTG ATATGGATGC GTTGTACTAG GATAGATTTG TTGTAACATT TTAAAGCGCT 840
 CCTTTACTTT CAAGATATTG ATTTAGTCCA CGTTGACGTA AATGACAAGC TGGACATTCA 900
 CCACAGCCAT CCCCAATGAT ACCG 924

15 (2) INFORMATION FOR SEQ ID NO: 746:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 971 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 746:

25 ATCTTTTGGG TATTTTCTAT ATTAGCTGTT GTTTTCTTAG TATTATTTAG TTTTGCTGTT 60
 GGTGCATCAA ATGTACCAAT GATGATTTTA ACATTTATAT TACTCGTTGC AACCTTTGGA 120
 30 ATTGGATTTA CTACAAAGAA AAAATATCGA GAAAACGATT GGCTATAAGT TATATCGACA 180
 ATAACACGCG TTGATTTAAG ACCACACATG TTCATGATGA ACATTTAACT GGTTTTATAT 240
 TGGCGCGTGT TTTTATTATT TAAGGTATAA AAGCGTAATA TGTTACCTAA TTGTTAGGAC 300
 35 TACATATTAC GCTTTTGGTA ATTATTTTGA TTTTCTTTTA AATCGTTGTT CATGTAATTG 360
 TATTAACGCA TCATGGTGGG GCTCTAAaTA ATCATtGCTA ATTcTTGATG GAGACCMCGA 420
 TTtCCAAC TA rGATkGAATT kGGACCMCTA ATkGTTAATG GTcctCCTAG TAAATTGGAA 480
 40 GCTTGTCAT TaCTTCCaTA TAAAtAACCA ATCCGCCAGC AAAtCCCcAT GGTKGAAGTC 540
 TTGGCGTCAT ATATGCTTCT AAaTTACCTG TAGCAACTGA AACGATTTCA AGCGCTGCAC 600
 TACCATATGC CCTTGCACTT CTAGAATCAT TAACAATTTT TTTAAAGATT TCTCCTAAAA 660
 45 TTGGTTTAGT TAACCAGTTC GGATTGATCC CAATAATGCT TTGTCTTAGA TTAGAATCAT 720
 TCAATGGTTT CAAGGGTTGG CTACCACGAT ATGCACCTTC CCCTACTTTA GCATGATATA 780
 50 AGACATCAGC CATAACATCA TATACAAAAC CTGCATAAGG TTTACCATCG ATATAAATAC 840
 CAATTGAAAT TGCGAAATTT TCTTGTTGAT GAACAAAATT CAATGTACCG TCTATTGGGT 900
 CAACAATCCA TACCGTACCT TTGGAAGTAT CGATGTCATG ACCATGCCCT TCTTCACCTA 960

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(2) INFORMATION FOR SEQ ID NO: 747:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 865 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 747:

TTCTCGTCAC TGTACGTTGT ATTGCGGCAT CATCCATTAT GATACGTTCA GACATATTCT 60
 CACCCTTTCA AAATTTAGAA ACAAAAAACC TCATGTCTTT AATATCGACA TGAGGTTTAG 120
 TATATACAAT CAGCCTATTT ACATAGAAGA ATCGTAGTAT TACTACTTAT TCTTGCATAT 180
 GTGAAAGTGT TATGATCATT TTAGTATATA TCTATATTTT CATGTCTTTG ACGTCTCTCT 240
 GGACGCTCAA TTAAAGACTC TTTATGTTGT ACTTAAACTG TTATAAGGAT AATACTAATC 300
 AGGCGCTTTG TCAATCTATA TTGAAAAATT AACCATACTC AGTAAAAATG TTAACCTTAA 360
 TCTATTTTAT AATGTGTTTT CATTTAAAAA AAACGAAAAC GATAAACACT TATAGTTTAC 420
 ATAATAATGT TATCGTAATT ATAGCAGCAC ACAATTATGC ATCTCTTTTT CGAATTGTAT 480
 CTAATAAATC TTCAAAGTCT TGTGGTAATT CAGCATGTCT TTCAATATAT TCACCTGTTA 540
 CTGGATGTTT GAATCCAATA AGTCCAGCAT GTAGAGCTTG ACCACCAATA TCCAATGTCT 600
 TTTTCGGTCC ATACTTTGGA TCACCAACTA ATGGGAAGCC AATATATTTT ATGTGAACAC 660
 GGATTTGaTG CGTACGTCCT GTTTCAGTT GACATTCAAC AAGCGTATAA TCTTTAAAT 720
 GTTCTAGTAC GTTAAATGT GTCAGTCTT CCTTACCATC ATCAACAACA GCCATAGATT 780
 GACGATCATT TTTGTTTCTA CCAATTGGCG CATCGATTGT ACCGTAATCA TGAGGAATAT 840
 TCCCGTGGAA CTAAACGAT ATAGT 865

(2) INFORMATION FOR SEQ ID NO: 748:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 818 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 748:

ATAACATTGT GGAGCCTATG ACATTGATTT ATGTCTCGGT CTCAAATGTT CTGTGAAAAA 60
 AACTAAGTAT AGTTGAATTT TAAGTTAAAA AAATTGTTTT TGCAAAAATA AAATAATCCA 120

TTTTAGGTC TTCGCCTCTA AAAATCCTTG CGaTATTAGA GCGATGTCTA ATTATCAATA 240
 TGATTGAAAC TAAGAAACTA ACGACTAATA AAATATAGTC TTGAATGATA AGCGAGCCAA 300
 5 TCACACAGCA AATTGCTGCA ACGATACTTG CTAAAGAAAC ATATTTAAAA ATCTTCAATA 360
 CAATAAAGAA GATAATTGCA AGTATTAGTA AAAGTATCGG ATTGACTCCC AAGACGACAC 420
 CTGCACTAGT TGCAACAGCT TTGCCACCTT GGAATTTTAA ATAAACAGGA TAAACGTGTC 480
 10 CAAGTATAGC GAATAAGCCA ACAATTAAAC CATTTGTAAA AAAAGTACTA ATAGGGCCAT 540
 CTGCGTGAAC TTGTAACCAT AAAGGGAAGA AAACAGTTAT GAACCCTTTG AAAATATCTA 600
 15 GAAATGTTAC CAAGAATCCT GCAGGACGAC CTAATACTCT AAAGCTATTA GTAGCGCCAG 660
 TATTACCACT ACCAAATTGT CTAATATCTT TTTTGAAAAA TAATTTTCCA ATTACGAATC 720
 CACTTGGGAA AGCGCCGATA AGATAACTTA GTAGTAACAT GACGATTATC ATCATAAATA 780
 20 TTACACATCC TTTAATATCT TAGGACTATT TTATCATA 818

(2) INFORMATION FOR SEQ ID NO: 749:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 971 base pairs
 25 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 749:

ATATCCAATa ACTGTTcATT GTCTTGATAT TCCTTAAATG TTTcATAATG CTCATTAGAA 60
 ATGACAATTt CAAGCAACCA ACCCGTGCCA CTTTcCTCTT TATTaATTAT TACGCCATCT 120
 35 TCTaATTcAT ATTCTATAAT TCTGCCGTGT TCATTcACAA TTTGAAACCT TACTGCTTTA 180
 AAAGTTTTCA TATTCCcACA TCCcATTAGT TTAATATTTA TGATTTTTGA ATTATTTAGA 240
 40 AGATTTAAGG TCATTTcATG ACTaATTTCT TTAAATATAA CAAATAACGA GATGCTATAG 300
 CTATTAATTA TATAAAATTT GcCATTTTgA CCATTTTTAA GCTAGTAATT AAGATATAGG 360
 cATAGGAGGT GAATCACACA CTACATGCTA AATAAAATCG TAATTGTcGG GAGcTGACGA 420
 45 AAGACGCACA AATATTTGAA AAGGAGGATA GAAAAATTGC AACGTTTTGT GTTGCAACGC 480
 ACCGAAATTA TAAAGATGAA AATGGAGAAA TCGTCTGTGA TTACTTATTC TGTAAGCAT 540
 TTGGCAAGTT AGCTTCTAAT ATAGAAAAAT ATACTAATCA AGGTACATTG GTTGGTATAA 600
 50 CTGGTCAAAT GAGATCAAGA AAGTATGATA AAGACGGACA AACACACTTT GTCACTGAAT 660
 TATATGTTGA AACAAATAAAA TTTATGTCCC CTAAATCCCA AAATAATGAA ATTCTCTCAG 720

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TCCAATTATC CTAAACATCC TTAATATACA TTTAATCCAT CCTAAATTTT TTATAGATCT 840
 AATTAACTTG AAATATACTC ACTTAAAAAC GACTTACATG ACCTAGTACT GTTGGTAAGG 900
 5 TCGnCTTTTG GTGTAGTTTT CCTAATAGAn AATAGACnTA GGTGCCCCAA CCGATTACAT 960
 AAAAAATTGC C 971

(2) INFORMATION FOR SEQ ID NO: 750:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 832 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 750:

20 ATAGATTACT CTTTGTATCT GTAGATCCTA CTGTAACGAC ATTGTCCATA GATGCAGGAA 60
 CATCTTTCAC TTCGCCATTA CCTTGATATT CACGCTGTAA TTTTAGTTTC TGTTTGTTCAT 120
 TGACATCAAT ACCATCATT A CCAGCTGCAG CAACAACGAT AGATTTTTTC TTCTTGGCGT 180
 25 AATTGATTGC TTTCTGTAAC GCATCGTATT CTACTTTTTC ATCTTTTCTA AATGTTTGAT 240
 GGTCATTTTT GTCCAAAATA ATATAACTAC CAACACTAAT ATTAATGACT TGAATTCCAT 300
 CATTTCGAGC TTGAACAATC GCTTTTGATA CCCAAAGCAG TTCTGTTTTT TTACTIONACAA 360
 30 ACACGCGATA CATTGTAAAT TTGTTATTCTG GTGCAACACC TATTAACTTA CCATTAGCAC 420
 TCGTTTGACC CGACACCATC GTGCCATGTC CTTTCCTATC ATTGACATCG TGAACATCAC 480
 CTGTTTCCTC CGGTTTCAGTA CCTCTAAAAC CGTTTAAAGG TACTAAATTT TTAGAATCAG 540
 35 TCGAGAAATT ATTTTTCAAA TCGTCATGGT TTTTCATCAC ACCTGTATCT ATGATTGCTA 600
 TTTTGGTGTT AGCATGTTTT GGCAAATCAT CATACGATGC ACCATTATTG GTTATTTTAT 660
 40 TCATATCCCA TTGTCTTGAA AATAATGACT CATTGTATGT TCTGTCTATT GTTTTCTCGC 720
 TAGTAATACA AGTTGAACAT GTGGCATTGA TATATTTAat ATCATTMTTA TAGTTTGCTA 780
 AAGCATTAGC ATGCATTTTC GTCATTTTAA TCTGTGCCAC ATGGAATTCC GG 832

(2) INFORMATION FOR SEQ ID NO: 751:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 475 base pairs
 - (B) TYPE: nucleic acid
 - 50 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

GTAATATCAA TCTCTTCATA AGCTGAATTA TTTTCATGCA CTTCTTGATG TGATGATTTG 60
 TCACGAACCG CTACAACTAA CATTTTATCG TCTAAAATAA GTTGTTTATA TTTTCTAAT 120
 5 TCATCAGGCG CTAAGTTGTA GCGTGATAAA ACTGCATGTT CACCATCTTC TCCTGTTAAC 180
 AGTTTAGTCA TTCTATCACT AAATGTTCCA CTTGTTGAGA TAAGGGAGAT TTCAGAGTCG 240
 TGTAAGTCAT TTAGGTGTAA TTTACTTTTA CTAATAATTG TTAGCTCTGA TTCTAAATAA 300
 10 CCTTCAGATT TCTTTTGATT GATTACGTTG TATAATTCGC CAGTGTCAAT TACTACAGTA 360
 ATATCTGCCA TAGTTGTCGC CCCTTTAAAA ATTGTTTAT tTAATCTTTT ACCCTTCTTA 420
 15 TnATAAAGTA AAACCCTTAC ATTATTAAGT nATAAGTCTT CATTGCGATT AAACG 475

(2) INFORMATION FOR SEQ ID NO: 752:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1019 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 752:

GCGACACTTG TGAGTTCTCC AGCAGCAAAC GCGTTATCTT CAAAGGCTAT GGACAATCAT 60
 CCACAACAAA CGCAGTCAAG CAAACAGCAA ACACCTAAGA TTCAAAAAGG CGGTAACCTT 120
 30 AAACCATTAG AACACGTGA ACACGCAAAT GTTATATTAC CAAATAACGA TCGTCACCAA 180
 ATCACAGATA CAACGAATGG TyATTATGCA CCCGTAACCT ATATTCAAGT TGAAGCACCT 240
 ACTGGTACAT TTATTGCTTC CGGTGTAGTT GTAGGTAAAG ATACTCTTTT AACAAATAAA 300
 35 CACGTGCTAG ATGCTACGCA CGGTGATCCT CATGCTTTAA AAGCATTCCC TTCTGCAATT 360
 AACCAAGACA ATTATCCAAA TGGTGGTTTC ACTGCTGAAC AAATCACTAA ATATTCAGGC 420
 40 GAAGGTGATT TAGCAATAGT TAAATTCTCC CCTAATGAGC AAAACAAACA TATTGGTGAA 480
 GTAGTTAAAC CAGCAACAAT GAGTAATAAT GCTGAAACAC AAGTTAACCA AAATATTACT 540
 GTAACAGGAT ATCCTGGTGA TAAACCTGTA GCAACAATGT GGGAAAGTAA AGGAAAAATC 600
 45 ACTTACCTCA AAGGCGAACT ATGCAATATG ATTTAAGTAC AACTGGTGGT AATTCAGGTT 660
 CACCTGTATT TAATGAAAAA AATGAAGTGA TCGGaATTCA TTGGGGCGGT GTACCAAATG 720
 AATTTaATGG TGCGGTATTt ATTAATGAAA ATGTACGCAA CTtCTTAAAA CAAAATATTG 780
 50 AAGATATCCA TTTTGCCAAC GATGACCAAC CTAATAACCC AGATAATCCT GATAACCCTA 840
 ACAATCCTGA TAACCCTAAC AACCCAGATG AACCAAATAA CCCnGACAAC CCTAACAACC 900

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CAATTAAGTT CGTCTAGATA AAATAGGAAG CAAAGTCTTA GCAACGTAAA ATATTTTGA 1019

(2) INFORMATION FOR SEQ ID NO: 753:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 533 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 753:

ATTCTTATCC CAGGTAGGTG nTTTACTTCT TATATTAGGT GCAATAACTC ATGCCACTCA 60
 TCTTGTGGCA CAACATGAaT CGCATTtTTCA AAAATTGCAT GTCCTGCTTG ATCAGTCAAA 120
 CCGGCAGCAT GATCAAAATG CATATGTGTC ATTAGCACAT AATCAATATC CTTTGGCGtT 180
 AAATTATAAT TTGCCAAATC AGCAATTATA TGACTTTCTT CATCTACTCC AAAATTACGT 240
 AATTGCTTTT CAGATAATTT ACCATTACCA ATACCTGCAT CTATAATCAA ATTATATTGA 300
 GCCGTTTGAA TCAAAATTGG ATGTGTCGGT AAATTGATTt GATTTCGtTC ATTtGCATTG 360
 TATTGCTTTG ACCACAACGG CTTCGGAACA ACACCAACA TTGCACCGCC ATCCATTTTT 420
 GTATTGCCAC CATTTAGaTA ATGAATAGaT ATATCCCCGA TTTTCATAAC ATCACCTATT 480
 CTTTCTGTAT TCGTTATTAC AATTAGCATG TGTTTATTAC ATCATATCAC TAT 533

(2) INFORMATION FOR SEQ ID NO: 754:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 754:

ATCCCCTGCA AGTGATAAAA TTATTGAAAA AGGCGACATG ATTACATTAG ATTTTGGCGC 60
 GTATTATAAC GGCTATTGTT CAGATATTAC TAGAACATTT GCTATTGGAG AACCAGATCC 120
 TAAACTGAAA GAnATATATC AnATAGTACT TGAATCTCAA ATGAAAGCAA TTAATGAGAt 180
 TAGACCTGGC ATGACTGGTG CAGAAGCTGA TGCCATTtCA AGAACTATt TAGAGTCAAA 240
 AGGGTATGGA AAAGAATTTG GACATTCACT AGGACATGGT ATTGGTTTAG AAATCCATGA 300
 AGGGCCAATG CTGGCTCGTA CGATACaAGA TAACTTCaA GTTAACAACT GTGTTACAGT 360
 AGAACCTGGT GTTTATATAG AAGGTTTGGG CGGTATAAGA ATAGAAGATG ATATTTTAAT 420

AGCGTGTAAG ATGAGGAGGA AACTGAATGA TTTCGGTTAA TGATTTTAAA ACAGGTTTAA 540
 CAATTTCTGT TGATAACGCT ATTTGGAAAG TTATAGACTT CCAACATGTA AAGCCTGGTA 600
 5 AAGGTTTCAGC ATTCGTTTCGT TCAAAATTAC GTAATTTAAG AACTGGTGCA ATTCAAGAGA 660
 AAACGTTTATG AGCTGGTGAA AAAGTTGAAC CAGCAATGaT TGaAAATCGT cGCATGCAAT 720
 ATTTATATGC TGACGGAGAT AATCATGTAT TTATGGATAA TGAAAGCTTT GAACAAACAG 780
 10 AACTTTCAAG TGATTACTTA AAAGAAGAAT TGAATTACTT AAAAGAAGGT ATGGAAGTAC 840
 AAATTCAAAC ATACGAAGGT GaAACTATCG GTGTTGAATT ACCTAAAACT GTTGAATTAA 900
 15 CAGTAACTGA AACAGAACCT GGTATTAAAG GTGATACTGC AACTGGTGCC ACTaAATCGG 960
 CAACTGTTGA AACTGGTTAT ACATTAAATG TACCTTTTATT TGTAACGAA GGTGACGTTT 1020
 TAATTATCAA CACTGGTGAT GGAAGCTACA TTTCAAGAGG ATAATCTCTA ATTTGTTAAC 1080
 20 AAATAGCTTG TATTCATAT ACTGATTTAA CGTAAGAnAT TCTAAATAAG TCTCATAAAG 1140
 CTATTGCCIA AAATGATTAT AGGTTATATG CTGATATGAG GCTTTTATT TTTAAATAA 1200
 TTTTAAAT ATAAACGAA TCGTC 1225
 25 (2) INFORMATION FOR SEQ ID NO: 755:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 755:
 35 ACAAACAAAT CACTTAGTTA AAATTGACAG TGCATTATAT TCCGATAAAT TATTCAACAT 60
 TGTAGAAAnn AGAATTGATA CACCAGATAT TGGCTATAAT ACAGTGGTTT TATCAGAAAA 120
 40 ATGAGTGTAG AAATTAAAGG GATACCTGAn GTGTTGAATA AATTAGAATC GGTATACGGT 180
 AAACAAGCAA TGCAGGCTAA GAGTGATAAA GCTTTAAATG AAGCATCTGA ATTTTTTATA 240
 AAGGCTTTAA AGAAAGAGTT CGAGAGCTTT AAAGATACGG GTGCCAGTAT AGAAGAAATG 300
 45 ACTAAATCTA AGCCTTATAC AAAAGTTGGT AGTCAAGAAA GGGCTGTTTT AATTGAATGG 360
 GTAGGTCCCTA TGAATCGCAA AAACATTATT CACTTGAATG AACATGGTTA TACAAGAGAT 420
 GGAAAAAAT ATACACCAAG AGGTTTTGGA GTTATTGCAA AAACATTAGC TGCTAGCGAA 480
 50 CGTAAGTATA GAGAAATTAT AAAAAAGGAG TTGGCCAGAT AAATGAATAT ATTAAACACC 540
 ATAAAAGGAA TTTTATTATC TGATGCAGAG CTCAAAACAC ATATAAATTC TAGAATATAC 600
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TATGATTTGC CTTCAGACTT TATGTCTGAT AAATATCTCA GTGAAGAATA CTTAATTCAA 720
 ATAGATGTAG AATCTTCAAA TAATCAGAAA ACAATTGATA TAACAAAACG AATAAGATAC 780
 5 CTGTTATATC AACAAAATTT AATTCAAGCA TCTAGTCAGT TAGATGCTTA TTTTGAAGAA 840
 ACTAAACGTT ATGTGATGTC GAGACGATAT CAAGGCATAC CCAAAAATAT ATATTATAAA 900
 AATCAGCGCA TCGAATAGGT GTGCTTTTAA ATTTTAAAGG AGGAAATAAG CAATGGCAGA 960
 10 AGGACAAGGT TCTTATAAAG TAGGTTTAA AAGATTATAC GTTGGAGTTT TTAACCCAGA 1020
 AGCAACAAA GTAGTTAAAC GCATGACATG GGAAGATGAA AAAGGTGGTA CAGTTGACCT 1080
 15 AAATATCACA GGTTTAGCAC CAGATTTAGT AGATATGTTT GCATCTAACA AACGTGTATG 1140
 GATGaAAAA CAAGGTACTA ATGAAaGTTA AGTCcTGaCA TGaGTaTTTT CaATATTCCa 1200
 AGTGaTGaTT TAAaCAGaGT TaTTGGaCGT ACTAAAGATA AAAATGGGTA CATCTTGGGT 1260
 20 AGGAG 1265

(2) INFORMATION FOR SEQ ID NO: 756:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1111 base pairs
 25 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 756:

CATATACCCG GGTTCGAAGA ATCCTCTATC CATATGGTCC CCCAATTTTG ATTCCACCAT 60
 ATTGTTAAAT ATCACTTTCC CAGCCTACTT TTTTATnCAG TTGGGCTCTC TAAATTTGTT 120
 35 TTGAAATCCA GGTGGAACAT ATTTCCAGTG TATGACCAAT CGAAACATTT GCACCAATAA 180
 GGCCGCCAAT TTTTCCTGTA TCATCACCAG TAACATTACC GTTGAATCCA TAAGTTAAAG 240
 40 TACTCATATA CTCTTTTGTA TCAATCGAAT TTCTTGGATA GTAATCAGAT ATTTGAGCTA 300
 CTTCAATTATC AGGTAGTTGC AACTGTACCT TAAAGGCTGA AGGCCAGGCT AAACCACTTT 360
 TGTTAGCACC TTCTTCGCTA TAACTCTAT ATTGACCAGC AATGGTACCT TTCGTTCTAA 420
 45 TAACTAGCAG TTTTTTATTA TGATTTTAT CATCGATAAA ACTATAAAAT ACTTTTTTGT 480
 GCATGCCATT TTCTTTATCA TAAGTACTA AATCACCTGT TTTTACTGTA GTATTGCTTC 540
 CAATATCTGT AGTACCGGT TTAATATTAA TATCAGAATC TGCGGCATTA GCGACAGGAT 600
 50 TCATTAATAT GGAACCTAGC AATAGTGTG TTGTTACTGA GCTGACTATA CGTGTTTTCA 660
 TTTTCATCAT CCTTCTATTT TTTAAAACGA TTTGAGGAAA CAATAATCAA TATGTCAATT 720

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GTAGCAACTG ATAAATTACT GAGTGATGAT GAGTGATTAT TTTAAGAATA TGTTTTTAAC 840
 TTTTATTTAA AATTTGAAAG GAAGCATTTTC AATTTTCGAGG GTTAGTCAAA GTTGAATAAA 900
 5 TTCTTTATGA AACAAGGAAA AGACATAGCT AATTTtATTG ATTAATTTCT TTAAACTAA 960
 TGATTTGTTT GATTTAAAAA TGAATCGAT TACAATATAA AAATACAAAT ATCTTAGAAT 1020
 TAAATCAATT AATTAACAT TAAATAAAAA TTAACATAT ATTAACATAGT GTAAATTAAT 1080
 10 AAATAGAAAT AGAGAAAAAG GGTATTAATT A 1111

(2) INFORMATION FOR SEQ ID NO: 757:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 466 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 757:

TATCTAITGT ATGTAACAAT AGGTACATAA TATTTTTAGG GTGGGTTATA TGAGCATAAT 60
 25 TACAAGATTG TTTAATAACA GTGATTTTGA AAAATTAAAT CAACTATGTA AATTATATGA 120
 TGATCTAGGT TATCCAACAA ATGAGAATGA TTTAAAAAAG AGACTAAAGA AAATAACGAA 180
 TCATGATGAT TACTTCCTAC TGCTTTTGAT AAAAGAAAAT AAAATAATTG GTTTAAGTGG 240
 30 TATGTGTAAG ATGATGTTTT ACGAAAwAAA TGCAGAGTAT ATGAGAATCC TTGCGTTTGT 300
 TATACATTCT GAATTTAGGA AAAAAGGTTA TGGAAAGAGA TTATTAGCTG ATTCTGAAGA 360
 ATTTTCTAAA CGGTTGAATT GTAAAGCMAT AaCACTAAAT AGTGGTAATA GAGATGanAG 420
 35 ACATCTGCAC ATAAACTATA TAGTGATant GGGTATGTTA GCAATA 466

(2) INFORMATION FOR SEQ ID NO: 758:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 402 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 758:

CGTACAGCAT AACCAAATAC ATATCTGCCA AAATCGCCAT ATGCCCCAGT TCCTCTTCCA 60
 50 TATTCGGTTG TCATTGAGTT TTTAATTTTA TCGATAGAAA AATGTAAATG GCTATCTAAT 120
 TTGTTTTTTA AAGATTTTAT GTAATCtCTA TATTTAAATT CGAATATTCT TTTTATACC 180

55

AACTAATATA TwCAATTGTA TGCCTAGCAT AATCTCTCAT TAAAATATGA GGATATACCA 300
 TTTCTTTATC AAATATtTCT TCATAAATAT AATTAGCAAT CTCTATATGT ATTTcACAAA 360
 5 TGTCGATTcG AAGTGTcGCC CCTAAAACAG rAGCATATAA TC 402

(2) INFORMATION FOR SEQ ID NO: 759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 759:

AAGTTACTCA ACAGCCATTT GACACGTCTC GATTAGAGCG ATTAGGTATA ACCGAGCGCC 60
 20 AAATAAAGA CATGTATCGT TTATTAGGAC TAGCCAAATA TGAAGATCGA TTTGTTATTC 120
 CAACATCACA CAAAGAAACC TATTTAGATA CGTATCACGC ACAAGGTAGT ACAGGATACA 180
 ATTACGGCGG CGAGCATTTT GGAGATAACT GTGAAGGCTG TGGCGTTGCA GTAGGTTcAG 240
 25 GGAAACTGG TCAAGAAATT TATAATGGAG AATTCTATGG AGGGATTTC GTGGTTAATT 300
 TCGATAATTT AAAAAATATC CAAGAAAGTT TGGGTnnn 338

(2) INFORMATION FOR SEQ ID NO: 760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 760:

CTCTATTATA TTTAGAGTTA TAGCTATTGC aGTTGTTTAT TTATTGAAAA TAAATGTACT 60
 40 ATCATTAGtT TTAGCAAGTG TATTAGGCAG TTTgGTATCt AGGCTACTAT TATCTATTAT 120
 TTTAAATTTA CCTGTGTGGG TAGTGTGTGTT AAaCGCGATT CCAGGCGTAA TATTCACTTT 180
 45 AATTGTAGcT ATTCCTTTAT ATCTCACATT GAGAAAAAGA ATGGCAGTAT TACTAAGATA 240
 ATAAATCAAA ACACGGTCGT CACAATTACT GTTGGCGACC GTGTTTTACT AGCTATTTAT 300
 TGTTTTcAGT TTTTTTGTA TCTAACAAAT TCACTTTGTG ATTTTCCCA TCAATTTcAT 360
 50 ATGTTGaTTT AAATGTTCTA GTTTTAAAGT TTTTATAAT 399

(2) INFORMATION FOR SEQ ID NO: 761:

(A) LENGTH: 639 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 761:

10 GCATATnCAA AACAAATAGCT GCTTTAGGTG CGGGGGCTAT TAGCGTTATT TCTGCACTAA 60
 CAGGAGGTTT AGTTGGCGCA GGTGTTGGTG GTTTCCTTGG ATCTATAGCT GCATCGAATA 120
 TTGATACTAG TAAGGGAATA TATATAAAAT TAAAACTAA AAAGTATGCA GCCGGGGAAT 180
 15 ACGTTCTGAC AGGAGAAAAA TGGGGATATC AGTAAGGGTG ATTTTATGGA TAGATTAAAA 240
 TATTCACCTA AAGTTGGAAT TTTAGCATT TATTATTTT GTACTTTAAA TTATTTAGTT 300
 CCAATGCAAA GCAATGCTTT TTCAATAATT ATATATTCGG CAATTTTTTGC TGTGTTACTT 360
 20 ATGCTTTTAG TTTATATATT TTTAGGAATT TTAAAGAAAT GACATGAAAC AAATTAGCAT 420
 TGGCTATGAA GAAATCTATG GGGATAGAAT TTTTCATAGC CATTTTTTAA AAGAGCATGA 480
 25 AGTAAAAAAT TGGAAAACCG TCAATCAAAT AATTGAAAAA GAACACTTGG ACAAAAATGA 540
 ATATGnAAGC GGAACCGCCG TTATTTTTCT TTTGCAGGAT CGTTAGATTA GATTnCGGTT 600
 GTATAGTATA ATGAAAAATA TTATAATAAA TTTATAAAA 639

(2) INFORMATION FOR SEQ ID NO: 762:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 852 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 762:

40 nTGTTCTGTTG TCTGGATCCA ACGTAAACAG TCGCTTCATC TAATACAATG ATAGGCCGCAT 60
 CTTTTAATAT CATTCTTGCA ATAGTGAATC GTTGTTTTTC ACCACCAGAC AATTTATCTC 120
 45 CCACTGTACC AACATTGCTA TCATATCCAT CTGGCAACTT TTCAATAAAT TCATGACATT 180
 GTGCTAACTT GGCAGCTTTT TCAACTGCCT CATCCGTAGC TTCTGGATTG CCAAGTTTAA 240
 TATTTTCTTT AAAAGTAAGA TTTAATAAAA AGTTATCTTG TCCAACAAAA CCAACTAAAT 300
 50 CGTTAAGTTG TTTCGATTCA ATATCTTTTA TATTTATACC GCCAATCGTA ATTTACCTG 360
 AAGTCACATC CCAGTATCGT GATATAAGCT TGGCAATGGT TGACTTACCG CTACCAGaTG 420
 CCCCAGCGAT AGCTGTGAAA TTATTTTTCTG GTACTGTAAA TGATAAATGC TTAAAGACCA 480

55

GAGGCTTCTT AAATTTTGTT GACAATACTA ACTCTTCTAG ACTTAATATT TGATTCACCTT 600
 CAGTTAATGC GTATTGTATA GACTTTAAAT GATTTACATA ATTAGTAAAA TTCTTAATCG 660
 5 GTGCTACTAC ACCTAAAGAT AATACGATGC ATAGGAAAAA TTCCGCATAG TTTAATTGGT 720
 TGATAGATAT CAAATACATG CCGACCGGTA AAATCCCTAA AAATGTTGAA GGTAATACAC 780
 TAGCTCCTAA ATTCATATAC CCCCATGTAT TTTTAAACCA ATTCAAAGTG TGAATCTTAT 840
 10 AATTATCTAC TG 852

(2) INFORMATION FOR SEQ ID NO: 763:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 852 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 763:

CTCTTCATGC GTCATACGTT GTGTCGATTG ATCAGTTGTT TTGTCTAAAT CACTAGCTTT 60
 25 AAATTTAGAT TGATTTGATT GACGTGTCGT AAATnGTTGT TCCTTTTGTT GGC GTTGGCC 120
 TTTTTTCTT GATCTTATTA AAAATAAATT GATAACCCCA ACAATAATGA GCGCTAAAAT 180
 30 AATGTAGCTA ATAATGAAGG TCGTAGTCAT TTAATGACCC CCTTAATTTT TATGGATTTT 240
 TACTTCAGCG TTCaTTCCaG GAACAACTTG TTTAGACGGT TcTGATTCTA GAGTGATTTT 300
 AACAGGTATT ACTTGAGAAA CTTTAGTGTA GTTACCATCA CTATTTGATG ATGGCATTA 360
 35 TGAAAgtTG CAGCAGTTGC TTTTCCAATA CTATCAACTT TACCTTTAAT AGAAGCTTTT 420
 TGACCGTCAA TAGTCACATC AACATCTTTA CCTACTTCAA CATCTTTAAT ATCTTTTTCG 480
 TCAATATTTG CTGTTACATA TAAATCATCT AAATTGTATG CATAAGCGAT TGGGTTACCA 540
 40 GCTTGACCA TTGAACCTTC CATACCATCT AATTGGCAA TTGTACCTTT TTGAGGCATT 600
 TTAAGATCCA TATCTTTTCGT TTCGCCATCT TGACCTTGTA CAGTAACAAT TGCTACTTTG 660
 TCACCTTTAT CGAGTTTGTC ACCTTGTTTA ACATTAAGTG ATTTAATTTG TCCAGATGCA 720
 45 GGACTTGCTA TTTTAATTTG ATCGCCATTT ACTTTTGCAT TATCAGTTGT TACATAGCTT 780
 GTTGTTTTAT TCCAAAATA AAAGCCAGCA ATCCCAATGG CTAACnGTAC AACAAACCGTA 840
 50 ATGACATTnA AT 852

(2) INFORMATION FOR SEQ ID NO: 764:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 747 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 764:

	ACATATTCGA CATTCAATTT AAATTGCATA TAACTACATT AACCATTTCAT TGTGCAGCGC	60
10	CTGTTGTTTA GATGATCATT TATTGACTTT TTGCTCTTAT nCCAnGCAAT TTTTGGATTT	120
	ATTGCTTATA ATACATTTTA AGACAAATGT TTGTTTCAAC ATCGCATGCG ACATCATTA	180
	YTATTCATTT AAATTTATCC AGTTTCTATT TGTCTGCAAT TGCTGAAAAT TAAAGGAGCT	240
15	TATTTTTAAT AATGGAACAA ATTATCACTG AATTTATTAG CCGTTTTGGG TATGCAGCCA	300
	TTTTTATATT AATTTkATka GAAAATGTAC TACCTaTCGT aCCATCGGga AATTATTCTG	360
	ACATTTGCTG GTCTTATGTC TGTAAATCA CATTATCAA TTTAACTTT ATTTATTATT	420
20	GCAACTATCG CATCGTTTAT AGGGCTGTTA ATTTTATATT ATATCTGCCG TTGATTTCA	480
	GAAGAACGTC TATATCGTTT TATTGATCGA CACGGTAAGT GGATTAAATT GAAAAGTAAG	540
25	GATTTAAAGC GAGCAAATGA TTGGTTTAAA AAGTATGGCG TATGGGCTGT ATTkATCTGT	600
	CGTTTCATAC CTGTATTACG TGTATgGATT ACCATTCCAG CTGGTGkaAA CCGCATGAAT	660
	GTGTGACaT TtACCGTTAT TTCATTAAATA GGTACTACAA TCTGGAATTT CGGTTTAATT	720
30	TTACTAGGAC GCACTTTGAG CGATAGC	747

(2) INFORMATION FOR SEQ ID NO: 765:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 820 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 765:

	TTTACCTTTT AACCAATCAT GCATTAATGC AATGTGTAAT GTCTTAACAA ATGTTGCATA	60
45	TtCATCTTCT GCACTCCACT TTTCAATTC CTGTTGATTA ATGGCATGTT TTTCTCCATT	120
	TTCCAACATA TTGACATACA ATTTATAATG TTTTCAACT GCCTGAATAA AAGCGAGTTG	180
	ATTTTATTTT AAATGTGATT TTAACTTTTC TAAATCTGAA TTAATAAAGT CTTCTATAGT	240
50	CGAATAAGAC ATATCTTGGT ATTCAACTAC TGCATTAATT TCATCTAATA ATTGCGATTG	300
	TGATTTTAGC GTTATATAAC TCTCGTCTCC ATAAGATATT TCTGTAGTAG CTGCTGTAGT	360
55	AGGATTTGGA GAACTGACTA AAATATGCTC GCCTAATAAT GCATTTATCa AACTACTTTT	420

TGTTCGTGG ATATCTTGCT TTGTACGCTT GAACAAAGGC ACATCCGAAA TTATATCAAG 540
 CGCTTTTGA ATATCTATAG ACATATTTGT TGTAGCTGTA TTTTGATTTA GCTGCTGATT 600
 5 ATCACGATTA TCCTGAGCAT TATCAGTAGC CACTTGATAT GTTGTCTCTT GTCGACCTAT 660
 TAATTTATCT AGAGATTCAT CTAAATGAAT ATAGTAGTGA CGATAATTCT TAGTCGTCAA 720
 TGACTGACGC AGCTCATTTA ATTCTGTATA ACGTTGATAT TCTTTTAAAT CATCACTTTC 780
 10 TTCTGTTGGn AATTCATCTG CCTGCACATT TTCTATnATT 820

(2) INFORMATION FOR SEQ ID NO: 766:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 672 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 766:

TCAACATGAC ATTAATTTAA TAGCGATGCA TACAAATTTA GATGTAAATC CGTATGGTGT 60
 25 CAATATGATG TTGGCGAAGG CGATGGGTTT GAAGAACATT TCAATAATAA ATAATCAACA 120
 AGATGTATAC TATAAAGTTC AAACATATAT ACCTAAGGAT AATGTTGGAC CATTTAAAGA 180
 30 TAAGCTTAGT GAAAATGGAT TAGCGCAAGA AGGTAATTAT GAATATTGTT TCTTTGAAAG 240
 TGAAGGAAGA GGGCAATTCA AACCAGTTGG TGAAGCTAAT CCAACAATAG GACAAATTGA 300
 TAAAAATGAA TATGTAGATG AAGTTAAAAT TGAATTTATG ATAGATGCAT ATCAAAAGTC 360
 35 AAGGGcTGAG CaATTAATTA AACAATACCA TCCATATGAA ACACCGGTAT TTGATTTTAT 420
 TGAGATAAAA CAAACATCCC TTTATGGACT TGGCGTTATG GCAGAAGTGG ATAATCAAAT 480
 GACATTGGAA GATTTCGCAG CTGATATTAA ATCTAAATTA AATATCCCAA GTGTCCGTTT 540
 40 TGTTGGTGak TCTAATCAGA AAATTAAACG TATTGCaATT ATTGGTgGTT CAGGTATTGG 600
 ATATGAAKAT CAAGCtGTCC AACAAGGcGC AGATGTCTgT TACGGTGATA TTAAACATCA 660
 GATGCCTAGA TG 672

45

(2) INFORMATION FOR SEQ ID NO: 767:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 403 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

5 GAAAAAGTTA AACCTACTGT AACTACAACA AGcmaAGTTG AAGACmATCa CTCTACTAAA 60
 GTTGTmAGTA CTGaCACAAC AAAAGATCAA ACTAAAACaC AAAGTGTCTA TACAGTTAAA 120
 ACAGCACAAA CTGCTCAAGA ACAAATAAAA GTTCAAACAC CTGTTAAAGA TGTGCAACA 180
 GCGAAATCTG AAAGCAACAA TCAAGCTGTA AGTGATAATA AATCACAACA AACTAACAAA 240
 10 GTTACAAAAC ATAACGAAAC GCCTAAACAA GCATCTAAAG CTAAAGAATT ACCAAAAACT 300
 GGTTTAACTT CAGTTGATAA CTTTATTAGC AcAGTtGCcT TCGCAACACT TGCCCTTTTA 360
 GGTTCATTAT CTTTATTACT TTTCAAAAGg AAGaaTCTAA ATA 403

15 (2) INFORMATION FOR SEQ ID NO: 768:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 483 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 768:

25 TTCAATGCTC GTTTGCTTG CGTTAGTAAT TTCTAACATA TTCATTCACT TTTGGAGCC 60
 TAAACTATCA ATCACCCTC AAATCATCAT CGTTTGATT TTAATTGAAG CACTAATTGG 120
 30 ACTGCGTTTC TTGAAAGCGT ACGATGTTAA GCGTGGCAAA GATAAAGAAA ATAAGAAAAA 180
 TAGTAAGGAT TTCGTTAAAC TAAATCAAT TTTAGTAGCA ATTTTATTTA CATCATTTGGC 240
 GCTGACAGCA GGTACTGTAG CTGATATATA CGGTTTCACT GACTTAGGAA ATACTAGAAG 300
 35 TGATTTAATC GTTTGGAGCA TAGGTGGTAT TATATTTGGC CTCGTATGTT ACACAATGGA 360
 AGATAAAAGA TAACGATAAG GAGCTGGCGA TTATAAAGCT AGCTCCTTTT TTAACCTaTA 420
 TATGTAAAGA aCTaTCCTAA GGGkTTTTAA TCATATGTCA ATAATTCTA TAATACATTA 480
 40 TTA 483

(2) INFORMATION FOR SEQ ID NO: 769:

- (i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 769:

ATTATATGTC TGATGTATTT CATGTCGTTA AAAATAAAGG TACGGAAGAT TTAAAGAAG 60

GGATGATGCT TGAAGGTGAA AAAATCAAAG CTTTTTATGA AGATATGCCA CCGTATCAGA 180
 CTGTCAAAAA AGGAACGATA CAAATTAAGC GTGATGGCAC ACCTATTATC CTATTAAATG 240
 5 TCATTATACG CTnGTAGCTA CCCGCAAATC GGTACAATCG CAGTTATCAT TTACGAATTA 300
 GCACAAAACC GCAGGATCAC GTTGAATTCC ATTATAGTAT TTACGGCTGA AGACTGTAAG 360
 nTAnACTGGT AACCATATCA TGGATGATTG ATCATAGATG 400

(2) INFORMATION FOR SEQ ID NO: 770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 770:

ATCTCTTCTA CTTCTTTTAC AAATTGAGAA CGTCTTAAAA TGGCTTTCAC ACGGGCAACA 60
 ACTTCTCTAG GTkAAAAAGG CTTAGTCATA TAGTCATCGG CACCTAATTC TAAACCTAAT 120
 25 ACCCGATCAA ATTCATCATT TTTCGCCGTT AACATTAATA TAGGGACTAA ATTTTATTTT 180
 GTTCTTACAG TCTTACATAC GTCAATGCCA TCTTTTTTATG GTAGCATAAC ATCTAAAATA 240
 ATTAAATCTG GCTGTTCACT TTCTACCTTT TCTAAAGCCT CATCACCATC AAATGCGACA 300
 ACAACTTCaT AACCAGCTGk TTCTArGyTA TATTTAAGTA ATGgTTaCGa TTGaATGtTC 360
 GTCATCTACT wCCaACACTT TTTGCGACAT GGtATGCCTC CCTAACTtAk AATTATATTT 420
 35 cATTATAACC GAACTATTTA TAAAAATAmC ATCCTACACA TTATCTTTAC ACATTTTTTA 480
 CATTACTTTA CATATAAATA AAATACTTCT TATATTTCCT TCTmTCATTT GCATGACTTA 540
 CTCTGGGACA ACGAAATAAA TTTTGTAATA ATAGCATTTT TATCCCACTA CCTATGCATG 600
 40 AGTTTTACTC ATTTATTCCT AAGCTTATGT ACATATTCGC TTTGTCTAAT GTGTAAGAAA 660
 CACTACATAA TCAATCATTG GTGACTCTTT ATTATTTCTA TCCTGTTGCC AaCTTCAATT 720
 CATTTAAAAA GGCGAACCTA GCAATTAAAG 750

(2) INFORMATION FOR SEQ ID NO: 771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1462 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

	ATTTAATTAT TATTTTTC	AATCAATACG ATATAATTTT	ATGTTTTTAT CTTTGGTGC	60
	TGAGGCAAAT TGATAAGtCG	TTTTGCCTTT TTCAATATAT	CCAAAATTAC CAGCAACTTT	120
5	GCTATATTCC GTATGTGTTA	CTGCTTTGCC AACATAATTT	TTAACAGCTT GATATGTTGG	180
	ACCATTAGCA TCATTATACA	TCATTGAAAT ATGAGTTACT	TTACCATTGT TTTTCTTACC	240
	ATCAGTAGTT ACTAATAACA	TACCTTTTTT AGTATGGAAT	TCGTAATAAT GTTCAGTTCC	300
10	ATCTTCATTG TAAGAATACA	TCGGATTTTT GTACTTAGTT	AAAACATCTT TAATAGATTC	360
	GCCAAATTTTC ACATTTTCTA	ATGACTGATC ACCCTTAATT	AATTGTTTAA CAGTATCAAT	420
15	AGAGTTGCCA CTTGCTGCTT	CGGCAC TAGT GTTCACTAAG	CCTACTCCCA TTACAACAGA	480
	ACATGCAATT ATACTTGCCG	TTAGTAGCTT TTCATAAGC	ACTCTCTCCT TTTATTTATA	540
	TCGTCTTGTC CTCACAACCA	TTATACAACA ATCATTCTA	AAACAACAGT CATATTACAA	600
20	TTATATTACA AATAATAATT	ACTACTTTTA TATTTCACTT	ATCACTAAAA ATTAAACATG	660
	CTTTTCATCG TGATGTTTGT	TGATAAATGC AGCTGTATCT	TCGACGAATC TTTCTTGCTC	720
	TTcAACAAAT GGAATGCAC	TTGATTCTTG ATATACTTCA	AAGTCCGCAT TTTGGATTAA	780
25	ATCAGCTACT TCTTTAGCTT	CTAATCTTGT TGTTCTTTCA	CCGAATTCTC CTGCAATAAT	840
	TTTTGTGGT ACTACGACAT	TTCTATAAGT TTGAGAAATA	TCAGCGTTTT TGAATACCTC	900
30	TTTAACTGCT TGAATTTCTT	CTTTAGTTGA TATTTCAATT	GTATCTACGA CATGTTTGAG	960
	GAATCGATT C ATTTTCTCG	GACGATAATA CTTACGCTTA	TTTAAAAATT TAwCyTgTtT	1020
	TTCaGGATCC CaGTTtCGAA	TAATATGGGC ATaTTTTCTA	AATAAACGTT CTTCCGGTAA	1080
35	TTACCTTCA ATAGATGTTG	GATTTACCAA CGTAAGTGAT	GATGTAAATT CAGGATAACG	1140
	TACTGAAATA TCCGCACCAA	TGATTCCACC CATTkCATGG	cATACAAATG CAACTTCTTC	1200
	AATATATAAA TATTTAAGTA	ATTCAACAAT GTCATCAGAA	AAATCTTTTA TTTCAATGTG	1260
40	ACGAGGTTTA TCAGAATAGC	CATGTCCACG TAAATCAATT	AACACAAC TT GAAATGATTT	1320
	TGCTAATTCT GCTGCTAATT	TATTAAACAC AGAATAATTA	TCAAGTACAG TATGAATCAA	1380
	TACGATAGGA TAGCCTTCAC	CTAAngTACT GTAATGTATC	GATGTTCCAT CTTTCTAGT	1440
45	AAATAGATCC ATAATTTTCT	CC		1462

(2) INFORMATION FOR SEQ ID NO: 772:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 704 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 772:

ATTATTATAA GGAGTTATCT TACATGTTAA ATCTTGAAAA CAAAACATAT GTCATCATGG 60
 5 GAATCGCTAA TAAGCGTAGT ATTGCTTTTG GTGTCGCTAA AGTTTITAGAT CAATTmGGTG 120
 CTAAATTAGT ATTTACTTAC CGTAAAGAAC GTAGCCGTAA AGAGCTTGAA AAATTATTAG 180
 10 AACAATTAAA TCAACCAGAA GCGCACTTAT ATCAAATTGA TGTTCAAAGC GATGAAGAGG 240
 TTATTAATGG TTTTGAGCAA ATTGGTAAAG ATGTTGGCAA TATTGATGGT GTATATCATT 300
 CAATCGCATT TGCTAATATG GAAGACTTAC GCGGACGCTT TTCTGAAACT TCACGTGAAG 360
 15 GCTTCTTGTT AGCTCAAGAC ATTAGTTCTT ACTCATTAAC AATTGTGGCT CATGAAGCTA 420
 AAAAATTAAT GCCAGAAGGT GGTAGCATTG TTGCAACAAC ATATTTAGGT GGCGAATTCG 480
 CAGTTCAAAA CTATAATGTG ATGGGTGTTG CTAAAGCGAG CTTAGAAGCA AATGTTAAAT 540
 20 ATTTAGCATT AGACTTAGGT CCAGATAATA TTCGCGTTAA TGCAATTTCA GCTAGTCCAA 600
 TCCGTACATT AAGTGCAAAA GGTGTGGGTG GTTTCATAC AATTCTTAAA AGAAATCGAA 660
 GAGCGTGCAC CTTTTAAAAC CGTAATGTTG ATCCAGTAGA AGTA 704
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(2) INFORMATION FOR SEQ ID NO: 773:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 427 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 773:

GACCACGACA CCACAAGCTA TGAAGAATGC CyTTGTTAAG CCGCcTTTGa ATTGCATAGA 60
 GATGAAAATA CCAATATTAA TAAAGAAGTT ACAGAAAATA CCTTTTGTA AAATATTCAA 120
 40 CCATGTTGAA TCAACAGTCT TTTTCTGAAC TAAAGCTGTT AAAGCTTG TG TCATTTCAGG 180
 TGTCATGACA TGCGCAAATT TCATTAAGAA AAATAACACA AACCACCTA AAATATTTC 240
 TAAGAAACAA TATAATAAAA TCCAAGTCAT CTTCTTAACA GAAACGACTT TATAATACCA 300
 45 GCCTACTGTA AAGTACATGA AGTTACTTGT TAATAATTCA GAGTTAGTTA ATACAACTAA 360
 AATCAAACCT AAATAAAG CAATGGCTCC CATTAAATTG ATAAGTCCAT CTACGTGAGT 420
 50 ACTCGCA 427

(2) INFORMATION FOR SEQ ID NO: 774:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 774:

	AGGTGAGCAT TATTAAATAT TGCCAAGAAA TCAAACTAA AACTATGCA AAAGATGTAG	60
10	ATATATTATT TATTCTTGGC GGTGATGGCA CGGTTAACGA ACTTATAAC GGTGTTATGA	120
	CACATGACCT TCAACTCCCT ATTGGCATT TACCAGGCGG TACTTTTAAT GATTTTACAA	180
	AAACGCTAAA TATAGCACCT GAATCATAAA CAAGCTAGTG AACAAATGGA TTTCTGCACA	240
15	AGTTGGTACA TACGATGTAA TTGAAAATGA AATGAATCAA TATGCACTCA ACTTTGTGGG	300
	CTTAGGTCTC ATGTTCAAAA CGCGGAAAAC GTACAAGAGG TTCAAAAGAT GTATTGGGTA	360
	AATGGAGTTA TATTGGGTCC ACCGTCCAAA ACnCGGCnAA	400

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(2) INFORMATION FOR SEQ ID NO: 775:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 484 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 775:

	AATTATTCCT CAATAGGAGC ATTACCCGCT CTCTACCAA TCCCCAAAA TGTAAGTTTCT	60
	ATTTGCTTTG CACCATTTAA AATTGCAGCT AATGTATTTG CAGTAGCCAA CCCTAGATCG	120
35	TTATGACAAT GAGCAGAAAa AATTATGTGA GAATATTTTT TTACAAAGTA ATTAAAAATA	180
	TCTCCGTATT CTAATGGTGT CGAACATCCT ACAGTGTCG CAAATGTAAC TGTTCCTACT	240
	TGATATTTTG AAATAATTTT CATGTATTCT TTCAATTTTT CTCTAGAAGT CCTTGTTCCA	300
40	TCTTCAAAAC AAATATCTAC TCCTTTTTTA TCTTCTTTA ATATATCCAA GCAGTCTTTG	360
	ATTTTCTGAA TATAATATTT ATTTGAAAAA TTAAGCTTTT CTTTATATG CAAGTCAGAT	420
45	ATTGGCAATA GTATTTtTAC CACTAAATTA TGAATTTtCA ATtTGACTAT TTTTgGTATG	480
	TCnT	484

(2) INFORMATION FOR SEQ ID NO: 776:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 788 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 776:

5 CGCAAGATGA AGTTAAAGAA CTTAATCGCT TATTAGGTAA AGTCATTCAT GCATTTGATG 60
 AAACAAAGGA AAAATAATTA ACTTTTGTCA TGACAATTAA AGTAATGTTT AGAATTTATT 120
 AAGAATAGAA AAACAATTAG CACGCGTAAC TTGTTAGTAA AAAAAGTCTG TGAAAGGTTT 180
 CTTAGCCTAT CAAGCAGTTT TTTTATGCAT TATATTGAAT CATATTCCAT AAAGCACCTT 240
 10 GATTAGCTAG TAATTGTTGA TAGTTTCCCT TTTCAACTAT TTTACCATT TATCATCACA 300
 TGATGGTCTC AAAACGTGAC AATAAAGTTA AATCGTGTGT AGCAACAATT AATGTTTCTG 360
 CATGTGCTTC AATTAAATCC ATAACTTTAA AACTATTTTG TTTATCTAAT GCAGTTGTTG 420
 15 GTTCATCTAA AATCCATGTT GATGCAGTAT CTTTAAATAA CATCCTCGTA ATCGCTAAAC 480
 GCTGAATTTT TCCGCCAGAT AATGTATGAC CATCTAAGTC AATTGACGT CTAGTGCCA 540
 20 AATGTTCTAA ATCTAATTGC TTAAATATTG CTTGCACCGC TTCATCTTTT TCATCGGTAA 600
 ATAAATTTTG ACGTATTGTA CCATCAAATA ATTGTTGAGA TTGTAGCAAG ACATTTAACG 660
 ATTCAAACCT ATCTTTGTCA TCTATTTCAA ACATATCCAT ATTTTCGAAA CGAACAGAGC 720
 25 CACTATCTAA TTGATATAAC CCTGCCATAA TTTGTAGTAA TGTACTTTTT CCTGAACCAG 780
 AAGGACCC 788

(2) INFORMATION FOR SEQ ID NO: 777:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 777:

40 TTACAAAAGA AATGCAACAA AATTTTGTAA TCATTACATT TTTTATAAA AATTTCACTT 60
 TAGATTCACA ATAATTACTT ATTTTGTCAA TTTATTTAAT GTCAATATGT TGATTAATTA 120
 ATAGTGTGTT CTAATGTATA TAATATTTAG GTCATCGTTA TAGTCAACAA TAATAAGGTA 180
 45 TTTCGAGTTG AAATTTATCT TATTATTTT CCACTTTAC GTGCTATCCC ATTACACAAA 240
 AACAAATAAG TAAAGATATT AAGTACAAA AAGTGAACA CCTTGTAGAT GCTCCACCTC 300
 AATTATATTA AGTTATATTA TTTTGCTGCT TGGTATAATT CATCAACTTT TTTCCAGTTA 360
 50 ACAATGTTCC AAAATGCAGT CATATAGTCT GGACGTTTAT TTTGATATTT CAGATAGTAG 420
 GCATGCTCCC AAACATCAA TAGTAAGATT GGTGTTTTC CTTCTGTAA TGGATTATCT 480

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GATCCAAATA ATGTTGTTGC TTTATTTGCA AATTCATTTT TAAATTCATC TAAAGTGCCC 600
 CACTGCGcTT TGATGTCATC TATTACGCCA CCTTTTCTT CAGAATTAGG TGATAGTATT 660
 5 TCCCAGAATA ATGAATGGTT AAAATGACCA CCGCCATTAT TACGGACTGA CATCCTCATC 720
 GCTTCCGGTA CCTTGTCTAA GTnAGCAATC ATATCCGCTA GTGATTGATG CTCTAACTCT 780
 GTTCCTTCAA CTGTTGCGTT TAATTTCTGTC ACGTACGTAT TGTGATGTTT GTCGTGATGA 840
 10 AACTCCATTG TTCTTTGATC TATATATGGT TCCAATGCAT CATATGCATA TGGTAAATTT 900
 GGTAATTTAA ATGCCATAAG TATATTCCTC CTTTTATGAA TATACTTTTA TAATAATTTA 960
 TTTTGGGTGT GTTTTGCAAT AATTATTATT TATTTGTTAT ATCCAATTAT ATAAAATTTA 1020
 15 AATATTCGAA ATTGATATAA TATTTAATAT TGAATGCAA AAGGCATTTA ACTGCTTTTG 1080
 TTTCCCGCTT TTAAAGAGAA TTAAAAAGA CAACTTCCAT TTTTCAATAA GAAATTGCCT 1140
 20 TTCT 1145

(2) INFORMATION FOR SEQ ID NO: 778:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 902 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 778:

AAAAGAGGnC CAATATTATC AATATACGGC CGGAAGATT CTTTTTCTT CTCCACTTAC 60
 TAAGCCCATC AATGGTGTAT GTTATCaATT GGTGCTATCC GCATTAAATA ATTATCTTCA 120
 35 ATTGTGGTAT CAAAGCTATT CGCTTTTCT CCAATAATGT CTTTACCATA TTTATTGAAT 180
 GCACCTACTA AAATCAACAT AAATGGAATT AACAAGGTTA CTACAATTGC CATTCTTATA 240
 40 AATTGTGGTA TATAAGAAGG TCGCCAATTT AAAGCTTTAA TACCTTCTTw TCTAAATGGA 300
 GTTCTATAA AGCGATATGA TAGCTCTGCA AATATAATTG TTAAACTTAT ATCTATAAAG 360
 TACACATATA CAGGTATCTG TCCGTCTACA TAGTAACTAT GTACGAACT AATTACTGCA 420
 45 AAATGCCATA AATATAAACT ATAAGACCTT TTCCCGATAA ATACTAACAC TGGATTTGAA 480
 AATATCTTCG CtATCCATGT AGATGGATGA ACGACACTAG CAATAATAAA TAACGTTAAT 540
 ATGGATATTA AATAGAAACC ACCATCATAT ATCCAATTCG TCTCATCATT AATAATGAAA 600
 50 AATAATAATA TAAGTACTAT AAATGATAAA CTACCTATGC TATCAATAAC ATATTTTACA 660
 ACTTTAGGTG GATCATTTTT CAATTTAAAC GGTGGCCATA AAAAAGCTAA AATAACACCC 720

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ATACTATAGA TAAACATCAT TAACCCTAAA GAAATTATTG ATACTCCCCA AAAAATAAAT 840
 CCTATTTTGT ATCGCTTTTT AATTGTTAAC AATAATGTAA CCAAATAAC TGGGAAAAAT 900
 5 AT 902

(2) INFORMATION FOR SEQ ID NO: 779:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 779:

GGAATTAGTT TCCTAATGAT CAAACCATAA CCATTAGCTT TTAATGATGT TACGCCTTTA 60
 AAGATTAGAG GATGATGACT AATAATAGTA TTATAACCTT TTTTCGATTGC TTCATTTACT 120
 ACTTCCAACG TACAGTCTAA TGCTGTTAAA ACACCAGTAA CTTCAACATC TTCATCACCT 180
 ATTAACAATC CTACATTATC CCAAGATTCA GCAGTACTAA ATGGCACATG ATGATCTAAC 240
 AATGTCATTA AATCAGCTAT TTTCACTaTA TAACACCCTT TCAATTACaG CAATTTCGTC 300
 aTTAATTTGa GCTAAAcGTT GakGakGTTG TTCAGTawTG AGtTTCGaTT TAAtATGATA 360
 AAgTGCyTct AACTctCTTT GcCATTTtTT TATAAAATAT 400

(2) INFORMATION FOR SEQ ID NO: 780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 780:

GTTCTGTTT TAACATCAAT ATCTATCTTT TTAATATCTT GAACATAAAG CAGATTCAGT 60
 TGGCTAATAT TTGAATTTAT GTTAATCACT TTTTTCGTTT CATTTTAAA ATGTACTGTG 120
 TAAGTnGCTT TTTTTCATA TTTTAATTCA CGTTCCCCGA TACCTCTATC ATGCTTCAAT 180
 ACTGaTTTAA CTTTTTTAGA GATATCTTTG TAGCCTACAC GTGGGTCACC TGTAAATTTT 240
 AAATCTGaTA AAATTGGTGT TGATGTGCCA TTTACTGCAA TTGTGTATGG TACATATCTG 300
 TCTGCTTTTCG CTTAGTTCC TGTTTTAACA GTAATTTCAA TTCTCTAAC ATCTTTCGCA 360
 TGAACtaAGT TTGCTGTGTA ATTTTTTGAA TTCAACTGTA AGATTCTTTT ACCACCATT 420

CTATCATGCT TCAGTACTGA TTTTATTTGA CTAGTTAAAT TTTTGTAATT TGTCCAAGGT 540

TTATnTGAAA ATGAAAAG 557

5 (2) INFORMATION FOR SEQ ID NO: 781:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 781:

TTCTGATAAC ACAACTTTCT TGGACCAAGT GACAAATGGTA AAGTTGATAT TCTCAAAAAA 60
 TATATTTTAT TGAAAAGGTA ACTATATCGA CCGCTCTGTG CGACTTGCTG TGTAGAAACA 120
 TCAAGCCCAG CTTGAAACTT CATATAAACT AATAACTTTT GATAAATGCT ATTCCCAATT 180
 TGTTCACTACT GCTCCAAGTT ATCATTAAAT CTAAATTTAA TACTTACTTC ATTTTTAACT 240
 GGAATAAAAT GTACATCACT CGCTTTCATT TCTATCGCTT TATTAATTAT TTCTTGAAAT 300
 AGAATCTTCA AAAAAACACC TCCTACATAT AATCACGTAG GAGGTGTTTT TATTACTTCA 360
 ATTTAACCGT GTAAAAATGG ATTTAATTGT TCATCATCAA CCGTCGTATA TGGACCATGT 420
 CCAGGGAATA AAGGTAAATC GCCTTCTAAT TCAAATATTT TATCTTGAAT AGAAT 475

30 (2) INFORMATION FOR SEQ ID NO: 782:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 782:

ATGAATATCG GTGCAGGACG TATCGTTTAT CAAAGTTTAA CTCGAATCAA TAAATCAATT 60
 GAAGACGGTG ATTTCTTTGA AAATGATGTT TTAAATAATG CAATTGCACA CGTGAATTCA 120
 CATGATTGAG CGTTACACAT CTTTGGTTTA TTGTCTGACG GTGGTGTACA CAGTCATTAC 180
 AAACATTTAT TTGCTTTGTT AGAACTTGCT AAAAAACAAG GnGTTGAAAA AGTTTACGTA 240
 CACGCATTTT TAGATGGCCG TGACGTAGAT CAAAAATCCG CTTTGAAATA CATCGAAGAG 300
 ACTGAAGCTA AATCCATGAA TnAGGGCAtn GGCCATTTGC ACCGGGGCCT GGCCGTAATA 360
 AGCCAAngGA CCGGGCCAAC CGTTGGGACC GGGAAGAAAA 400

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 810 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 783:

10 GATTAATGTA CTCGTGTACA TAACGTTTGA AGTATGATAA ATAGATATAG AAATAAAGTC 60
 ATATGTGACA TCAATTAAAT GATGTTCAAA TGACAAGATA CAATAGAGGA ATGTTTGTA 120
 15 TAAAAACGCT TCATATAAAG GTCGAGTCAA TATATGATAC GACTTTATAT GAAGCGTTTT 180
 ATTTGCTATG AGCTAGTATA TTTTATAATA ATTTTCTAT TTCTCTTTCG ATTTGAACAG 240
 GTTTTTTTTG AGGTGCAAAT CGTTTAAACAA CGTTACCyTC GCGATCCACT AAAAACTTAG 300
 20 TGAAATTCCA TTTGATTTTC TCATTAAAGA ATCCGTGTTG TGCCGCAGTC AAATATCTAA 360
 ATAAAGGTAA TTGATGTTCC CCTTTTACGT CTATTTTTTG ATGCATAGGG AAGGTAACAC 420
 CATAGTTTAA TTTACAGTTT TGAGCTGCTT CTTGCGCTGA ACCAGGTTCT TGGCCACCAA 480
 25 ATTGATTACA AGGGAAACCT AGAATTACAA ACCCTTGATC TTTGTATTTT TCGTATAATG 540
 ATTGCAAACC TTCAAATTGT GAAGTAAAGC CACATTCGCT AGCTGTATTA ACAATTAGCA 600
 30 TAACGTCACC CTTATATGCA TCTAATTTGT AAGTAACACC TTTATTTGTT TCTACTACAA 660
 AATCATAAAT TGTCTCCATT GTATCATCCT TTCGATTTAC TTAAaATGTA CCaCAAAATC 720
 GTGTAAtAGT CTkTACTAxA ACTCTATGAT AGAATACTTT GAGTAGGATT TTATTAAGGA 780
 35 GATGTATAAC ATGGnTCAGC AACAAATTCA 810

(2) INFORMATION FOR SEQ ID NO: 784:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 788 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 784:

AAATTCATTG CAGAAAACAT AGATAAATAA ACAAATTGAC TTAAACGAG CGTTGCAACA 60
 50 TATCTCGAAT TGTAAGGAG CTTGAAAATG AATAAAAATA TAGTCATTAA AAGCATGGCA 120
 GCATTAGCCA TTCTAACCTC AGTAACTGGA ATAAATGCTG CAGTCGTTGA AGAGACACAA 180
 CAAATAGCAA ATGCAGAGAA GAATGTTACG CAAGTTAAAG ATACAAATAT TTTCCATAT 240
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ACCAATAAAC ATGTATCAAA AGATTATAAA GTTGGCGATA GAATTACTGC CCATCCAAAC 360
 GGTGACAAAG GAAATGGTGG TATATATAAA ATTTAAAGCA TTTCTGATTA TCCGGGTGAT 420
 5 GAAGACATCT CTGTCATGAA TATTGAAGAA CAAGCAGTCG AACGTGGACC AAAAGGCTTT 480
 AATTTTAATG AAAATGTCCA AGCATTCAAT TTTGCGAAAG ATGCTAAAGT TGATGACAAA 540
 ATTAAAGTTA TTGGTTACCC ATTACCTGCT CAAAATAGTT TTAAACAGTT TGAATCTACA 600
 10 GGAECTATAA AAAGAATsAA AGACAATATT TTAAATTTTG GATGCCATAC ATTGGAACCC 660
 GGGGAATTCA GGGATCACCA GTTCTAAATT CTAACAATGA GGTCTAGGT GTGGTGGTAT 720
 15 GGGCGGTAT TGGGAAAAAT TGGGTTCTGG AATAATAATG GGTGGCCGTA TACTTTACGC 780
 CTCCAnAT 788

(2) INFORMATION FOR SEQ ID NO: 785:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1023 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 785:

30 CAATATTTTA GAAACAaTAA TTAAGTTGCG ATGAACAAAC TATTAACAAT AATCTTGAGT 60
 ATTATATTTA TCTTAATTAA TAATATATTT ATTAAAGATT ATGTTACTTC CAACTTTCAA 120
 AGTAGAAAAA CGGTATAATT TGTGATGGG TGTATTATGA TAACTGCAA AAAATACAGC 180
 35 CTACAACCAC ATAGATTGTA GACTATATTT AAAATAATAG GTATTTATCA TATCTCGTAA 240
 ACTTAGTGCC AATTTTTATA CTCGTGGTGC TGGTAAGCTA CCCTTAAATT CAGGAACGTA 300
 GTGTGTaGGG CTATAAGTTG GAACAGCATA TTGATAATTT ACATTTTGA TATTTAATGA 360
 40 TGGTTTCCCA ATTTTATAAC CATTGATTG TGAAATGAG AAATAKTTCT TCACACCTTT 420
 AACTACTTTA TAAGAATAGA AGTATTTATA GTCATATGCT TTATTTACTT TAGCATTTTG 480
 45 ATGTGTTGCT GTTGTGTTAT TTTGGAACT TGGTACATGC ATACGATGTG AATTGTGACC 540
 ATATGGTGGA ATTACCTTGA AACTATTTAT TTGTGGCACA ACACAAAAGT GATTAATTTT 600
 AATGCTAGCA TGCCCTGGTG TAACAAATTT ATGCGCGTGA TATCCAGGAA CTGCAAAATG 660
 50 ATGCTTGATA ATTAAAGATT gAGATGGATG TGTATATCTA GCGATTCTG ATGGTTTAAC 720
 AATAAAGTGT TTATTAATAG AATCCTTTGC ATGATTTACA TGTTTATGTA CATGTGTTGA 780
 TTTGTATGAA GTAATAACTT TCTGTAGTG GGTTCGCGTA GTAATGAAGT GGTGGTTTAC 840
 55

TTGTTGTGAA GCTGGATTGT TTGTTGCTAC ATTCACGCGA TTATTGATTT CTTTGTACTC 960
 TGGCACAATG TTTCCTAACT TTGATTCTGG nACGACAAAG TTTTATCTA CAATTTTACT 1020
 5 AGC 1023

(2) INFORMATION FOR SEQ ID NO: 786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 786:

TCAAGTTTAT TCGCTTGTG GAAAGCTTTA ACTTGATTTT CTAAAGCTTT ATCAAATTGC 60
 GTTGATTCAT TATCAACTTT ATAACCTAAA GCTGATAAAC CAATTTTAAT AGTTTAAATA 120
 TTTTATCAT CGTCTCCAAC TTTAAATGTT TTCGTATTAG GAATGACATT TAAAGATTGA 180
 TATTTAGGTG TGTCAATAGT AACGTCTGGT TTAATGCCTT TACCGTGAAT ATAATGACCA 240
 TCTGGCGTTA ACCATTTTAT TTCAGTATAT TTTAACAATG AACCATCCTT AAACCTCTCTT 300
 GTAGTTTGTA CGACACCTTT GCCGAATGTT TTTGACCCAT AAACCTTTAGC TTTATTATAG 360
 TCTTTTAGCG CACCAGTAAA CACTTCAGAA GCGCTAGcTG AACCTTCATT CACTAAGATG 420
 GATATATCCA TGTCTTTTCGC TTCTTTTAAAC GCATCATTAG AAGTtGAATT GCTCAGTACT 480
 TTACCTT 487

(2) INFORMATION FOR SEQ ID NO: 787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 787:

GnAAACnATA TTTAnAATTA AGTGTTCGAT TTGCAGTAAA TTCATACAGA AAAGCTAAAA 60
 TTAAAATGAT ACaGTGGAAT AATGTCACAT TCTCCATAAA TAATTGACCG AAGAAGCATA 120
 AAACATAGAA TAGTACAGTA ACACTTACCG GCTGCTTTTC TTTATATATA ATTGCATTAA 180
 TACAATAATA AATAATAAAG AGTGAAATTA GTGTTGATGT CGCATAATTA TAAAATCCTG 240
 CAAACCAGCC ATATGTATCT GCATAAATAG CACTTGGTAA AATTAACATT AAAGAAAATG 300

TCCCCATACT AATGAGGCCA TATGAAAGCC AACGTAACCA GCTTACATGT ACAGCTATAA 420
 TTTCAAAGAT ATTTCCGATA TAGCGACCAT TAAGTGATGC AAATCCTACT TTTAAAATAT 480
 5 CAGTATTATA ATTGCTAAAC CATTGTAAAT CATCGTGCAT GAGTGGTAGT AAGATACCCA 540
 TAAAAGTATA AAACAATAAT ATCGCAATTA ATATCAAAGT TGTCTTGTGT AATTGAAITG 600
 TTTTCACTTT GCTAATCCTC AAATCTAGTT AAATTTTCCT CAACTTGTAG GTCGAAAAAT 660
 10 TAATTCAATA TTTTAAATGT ATTTCTAATT TTCACCTATG CATGTTTCCT CAATCAAATT 720
 AGATAAACAA GGTATTTAAT ATTACTTTCA ACAATTTATC TAAATCGCCC CTCGTCTTTT 780
 TCTATGaCGA ATGATTACAC TTG 803
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(2) INFORMATION FOR SEQ ID NO: 788:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 788:

GAAAAGTTGT ATTATGAATA AAGTTAATCA AGGTGCTCAG GAAGAGGCCA TGGAAGAGTT 60
 ATTAGTGA CT TTTCAAAAAT TGATTAAAGA CTAAAGGAGT TTAAGATGAT ACATCAAAAT 120
 30 ACGATTTACA CAGCGGGAAT TGAAACAGAA GAACAAGTAA GTCAATTGAC AGAACGCATT 180
 TCAAATATGA TAGGTGTTCA TCAAGTGAAT ATTAATATAA TAGATGGTCA AGTAACTGTA 240
 TCGTATGAGA CACCAGCAAA TTTGAATAGT ATTGAAAAAG AAATCTATGA TGAAGGATAC 300
 35 AAAATTGTAT TTTAGGGTAT AATGTAGAGT GCGCTATAGA TTTTAATTTT GAAAATAAAT 360
 TAAAAATTTT GTAAATGATG TAGTAAAGGT ATGTGCAATA 400

40 (2) INFORMATION FOR SEQ ID NO: 789:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 762 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 789:

GTTTAAAGAT GGAGAGATTA TTGATTTTTT AGCTGGAAAA GGTGAAGCGG TATTGAAAGA 60
 TTTAATCAAT ACTGATGAAG GTTCAAGAAG ATTAGGTGAA GTAGCATTAG TACCTGATGA 120

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ATGTCATTTA GCGATTGGAT CTGCTTACGC CTTTAATATT CAAGGTGGAA CGGAAATGAC 240
 TGTGAGGAA AAGATTGCAA GCGGATTAAA TGATTCAAAT GTACATGTCG ATTTTCATGAT 300
 5 TGGTAGTAGT GATTGACTA TTTATGGCAT ATTCTGAAGAT GGTTCAAAAG AACTAGTATT 360
 TGAAAATGGA AATTGGGCAT CAACATTTTA ATAAATGTTA TTTTGAGGTG CTGAGTAGGA 420
 AATGAAACAT GTATTTAAAG GTCAAATACG TGATTAAAGT ATAGATTGGG AGATAAAATA 480
 10 ATGACAAATC AGGACAGACC AATGAAATCT ATGTCAGAAT CAAAATGTTA TAAAAATAGA 540
 CAAGTTTTCC CTCAAGATAC GAATCACCAT CATACAATGT TTGGTGGTAC ATTGATGGCT 600
 15 AATATTGATG AAATGTCAGC AATCACAGCT ATGAAACATG CTGGTGCACA AGTAGTTACC 660
 GCATCTACAG ACTCAGTAGA TTTCTTAAAG CCGATTAAAA CAGGGGACAT ATTACAATAC 720
 GTAGCGATGG TTTCATACGC TGGGACTAGT TCAATGGAAG TG 762

20 (2) INFORMATION FOR SEQ ID NO: 790:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 790:

TTTAATTTTA TCTTTTGAT ATCACATAGA TGCTACTTTT CTATACTGTT CTAAATCTAT 60
 TATTTTCGTCATTGATTG CAATAGCCAT ATCATGTGTT GCTAAAATCA GCACTTTATT 120
 35 TTCATCGACC AAACCAAATA ATGATTGAAT AATCATCTGT CCTGTTTTAG GATCTAACGC 180
 ACCCGTTGGT TCATCAGCTA ACATAACAAT CGGATCTTTT AACATCATTC TAATTAAAGC 240
 GACACGTTGT TGTTACCTC CACTTAGCGT ATGAACTTTT CTTTTTAAAC TGTTTGACAG 300
 40 ACCAACTGT TcATATAAC GtATCTtAT TTGTnCTTTT TCTTTCTTAC TTATTTTTTT 360
 ATATGCTAAT CCAATATCTA AATTTTCATT TACTGnCAAA 400

45 (2) INFORMATION FOR SEQ ID NO: 791:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 791:

AACGTAAAGC GGAAGTTGGG ATGGTTGAAG ATGCTGAATT TCATGCGCAA CTACATCGTT 120
 ATAATGCTTT TCTAGAGCAA CATCAAGATG ATAAAGTGTT GTATTTnGAA ATTGGAATTG 180
 5 GTTATACTAC ACCACAATTT GTGAAGCATC CTTTTCAGCG TTGACACGTA AAAATGAAAA 240
 TGCCCTTTTAT ATGACGATGA ATAAAAAGGC TTCGCATTCC GAATTCAATT CAGGACGTAC 300
 CATACTTTAA CTGAGATTCT CAACTTGTTT AGCAGACTCC GGACGCAGCA CACGAAATAC 360
 10 ACATGGGGGC AGAGTnACTT ATGGACCGTT GAATGnGATA 400

(2) INFORMATION FOR SEQ ID NO: 792:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 678 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 792:

GTTCCGTTTG ATACAGAGAA GCGAATGTAA GCATAATCTT TAACAGTATC GTATGATATA 60
 25 AtTTAATTGG CAACTTTTTG TCACCTTCAT AAACCTCAAA TTTTCTCCAA AATTGACCTG 120
 AATTGAATCC TAATTCAATT TCTGGTTTTG AATCAGTGAA AATAACTCTA GCAGGTTTAA 180
 30 CAGAACTTGC ATAATGATAA AACTGTTGAG TTCCATCTTT CTTTTTCATT TCAAAATCAA 240
 TTGGACGAGA GTTTGGTGCG CTATGATCTT TGTCTTTTAT TGCAGGGTTT TTAATCGCTT 300
 CTCTAAGTTC CTGaTTCAAA ATAGGATATG TATTGTTagT GGCyTTTGCT GCTGGTTTAA 360
 35 CTTCTTTTGT TTCCTTAGGG GcTTTAACTT CTTTAACTTC TTTAGCTTCT TTTGTTTCAG 420
 AAGTAGGGGC CTCAACTTCT TTATTAGATA CTGAGACAGC ATTAGCTACT GGTTTAGTTT 480
 CTGGAGCTTT TTCAGATGTT GTTGTGGGAC TTGCAACTGC TTCAGTTTTT GGTTGTGCTT 540
 40 CTGTATTTGT ACCACCTGTT TCTTCAGCTG CTGCTTGTGT TCGCCATTG ACATTAAATAA 600
 TAAAAGTGTA CTAATTGCTA CAGATGCAAC GCCTAGTGAT GACTTTCTAA TTGAATAAAA 660
 TGATTTAAAT TCTTTTTG 678

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(2) INFORMATION FOR SEQ ID NO: 793:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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ACTGGCGGAT CCACGATGGC ATGTGTTAGT GAAGCAATTC ATTTATTACC ATATAATGTA 60
 TTCTTCGTAC CAGCCAGAGG TGGACTAGGC GAAAnTGTTG TCTTTCAGGC AAACACAATT 120
 5 GCAGCCAGTA TGGCACAACA AGCTGGCGGT TATTATACGA CGATGTATGT ACCTGGATAA 180
 TGTCAGTGAA ACAACATATA ATACATTGTT GTTAnGAGCC ATCAGTCATT AAACACTTTA 240
 GGACAAAATT AAACCAAGCA AACGTTAATA TTACACGGGC CTTTGGTGAT GCGCTGGAAG 300
 10 ATnGGCGCCT CGGACGTCCA ATCACCTGGA AAAGGTCTT GGAACCACTT C 351

(2) INFORMATION FOR SEQ ID NO: 794:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 794:

GGGCGAGGCG TTCGCGCACC GGCCGAGCAG CAAATAGGCC GGGATGTCGC GTCTTGCTGC 60
 25 AGGTCCGAAA AATATCAACT TGAAGAGGTA ACACCGnTAG ATATGTTTCC ACAAACAACA 120
 CATGTTGAGA CAGTGGCATT ATTCAATTTG AAATAGCGCA CATGATTTGA GATAAAATTT 180
 30 CGCCTTAATA AGTGAAGAAA GAAGTCGTAT ATTAAAATTT TATTACAGCC AATTTACTTT 240
 CTTGATATGA ACTTTTAA TTAATGTGA CATTGTATAC TATATTTAAA GAAGAATAAG 300
 AATGTCATGA TCGGGAGGGT TGGTAATGCA TAAATTGAT TTAACGACAA ATAATTTTCA 360
 35 AATGCGAGGT TTATTATCCT GGCAACCTGG TTATTGCGTT 400

(2) INFORMATION FOR SEQ ID NO: 795:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 407 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 795:

ATGTTCCAGG AACGTATTTT TACAACCGAC AATTAGCATA TGTCATAATG AGTTTTATAA 60
 50 TTGTATTTT TATTGCATTT TTAATGAATG TTAAATTACT GAGTAATATT AAAGTGCAAA 120
 AAGGTATGAT TATAACTATC GTCTCACTAT TATTACTGAC GTTAGTAATA GGTAAAGATA 180
 TTAATGGTTC TAAAAGTTGG ATAACTTAG GATTTATGAA CTTACAGGCA TCTGAGTTAT 240

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TAAGTAAACC AAAATTAATc TTAAGTCCTA TTGTATTAGC ATTAGGTTGT ACGTTTTTAG 360
 TTTTCCTACA AAAAGACGTG GGCAACATTA CTAATATTAA TnATnTT 407

(2) INFORMATION FOR SEQ ID NO: 796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1053 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 796:

CAGTAGGTAC ACTTGCAGCA TTTGTTGGAT ACTTAGAGTT ATTGTTCCGG CCTTTACGTC 60
 GTTTAGTCGC ATCATTTACA ACTTTAACGC AAAGTTTTGC TTCAATGGAC CGTGTATTCC 120
 AATTAATTGA TGAAGATTAT GACATCAAAA ATGGTGTGG TGCTCAACCT ATTGAAATTA 180
 AACAAAGGTCG TATTGATATT GATCATGTTA GTTTTCAATA TAACGATAAC GAAGCTCCAA 240
 TTTTAAAAGA TATTAATTTG AGTATTGAAA AAGGAGAAAAC AGTTGCTTTC GTAGGTATGA 300
 GTGGTGGTGG TAAATCAACA TTAATTAACT TAATACCGAG ATTTTACGAT GTAACCTCTG 360
 GGCAAATTTT AATAGaTGGT CACAACmTTA AAGaTTTTTT AACGGGAAGT TTAAGAAATC 420
 AAATAGGATT GGTGCAaCAG GATAATATTT TATTCTCTGA TACAGTTAAG GAAAATATTT 480
 TaCTTGGTCg TCCaACAGCa ACAGATGAAG AAGTAGTTGA AGCGGCgAAA ATGGCTAATG 540
 CACATGACTT TATTATGAAC TTGCCACAGG GATATGACAC TGAAGTAGGT GAACGAGGTG 600
 TTAAATTATC AGGTGGTCAA AAACAAAGAT TATCGATTGC TAGAATATTT TTAAATAATC 660
 CGCCAATTCT TATCTTGGAT GAAGCAACAA GTGCACTTGA TTTAGAAAGT GAATCCATTA 720
 TTCAAGAAGC ATTAGATGTG TTGAGTAAAG ATCGAACGAC ACTTATCGTA GCGCATCGCT 780
 TGTCCACTAT TACACATGCT GACAAAATTG TCGTAATTGA AAATGGACAT ATTGTTGAAA 840
 CAGGTACGCA TCGTGAATTG ATTGCAAAAC AAGGTGCTTA CGAGCATTTA TATAGCATTC 900
 AAAACTTATA AAGTATTAGT TGTTTGACTT CAGTACAATC TTGAAGAGAA AATTTGTAAC 960
 AGGATGGTGG GGTcATAACA TAGAAAAAGC AGTAAGAGAT TTTCTTAGTT GAAAATAATC 1020
 TtnCTGCTTT TTTAAATTTA ATTTcGnGAT TCA 1053

(2) INFORMATION FOR SEQ ID NO: 797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 544 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 797:

5 AAGAGTGA CTGAAGTGA AAGAAGGGGA CCGTGTCGTG TTCCAACAAT ATGCTGGTAC 60
 AGAAGTTAAA CGAGATAATG AAACATATCT GGTATTAAAT GAAGAAGATA TTTTAGCAGT 120
 TATTGAATAA TACAGAACTT AATTCATAAA TAAATTAAAT AGAACGAAAA TGAAACACAA 180
 10 CTAAACAAAT GGAGGTTTAT CATTTATGGT TAAACAATTG AAATTCTCTG AAGATGCACG 240
 TCAAGCAATG TTACGTGGTG TTGACCAACT TGCAAATGCA GTTAAAGTAA CGATTGGTCC 300
 TAAAGGACGT AATGTTGTAT TAGATAAAGA GTTTACAGCA CCTTTAATTA CGAATGATGG 360
 15 TGTGACGATT GCyAAAGAAA TCGAATTAGA AGATCCATAT GAAAATATGG GGGCTAAACT 420
 AGTTCAAGAA GTCGCAaATA AGACAAATGA AATTGCTGGT GACGGTACGA CAACTGCAAC 480
 AGTATTAGCT CAAGCAATGA TTCAAGAAGG CTTGAAAAAT GTTACAAGTG GTGCGAACCC 540
 20 AGTT 544

(2) INFORMATION FOR SEQ ID NO: 798:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 372 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 798:

CAATTGCATA GATATTGCTG ATAGACGTAC GGCTTTGTTT ATCAACTTCT AATAATCCAC 60
 35 GGTCAGCGAA TTTAACACCT AATTTCGTCT GTGTTTGGAC GACGACCTAC AGTTACTAAT 120
 ACATAATCAG CTTGATTGT TTTCTCTTCG CCTTTAGCTT CATAAGTAAC TTTAACTCCG 180
 TTATCTGTTT CTTAGCTGA TTTAGCCATA GCTTCAGTAA CGATTTC AAC ACCTTTTTTCT 240
 40 TTCATACCTT TTTTAACAGG TTGTGTGCAT TTGnTTTTTC GAGGCCACCT AAGATATCTT 300
 TAGCACCTTC AAGGGATGGG GTACTTTCTG nAACCAAAGT TAGCAAATGC TGTACCTAAT 360
 45 nCTGGTCCAA TG 372

(2) INFORMATION FOR SEQ ID NO: 799:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 799:

5 AAACGACATT TGTTTAATTG GAAGAATTaG CACCATTTTT TGAGGCGGGT ATAGatTCAT 60
 TTAAAATCGA TGGTATTCTA CAAACGGAAG AATATATTAA TGTGGTAACG GAACAGTATC 120
 GTCAAGCGAT AGATTTGTAC AATGAAGATC CTGAAATCTA TGAAGATGAG AAATTTATGT 180
 10 TGATGGATCC AATTGAAGAA ATTCAACCTg ATCATCGACC ATTTGACGAA GGTTTCTTAT 240
 ATAAACAAAC AGTATATTAA GGAGGTTAAT CATGAAGACA ATAGAAGAGA TTAAATCAAC 300
 TCCTAAACA GTTATGAAGA AACCAGAATT ATTAGCACCT GCTGGAAACT TAGAAAAGTT 360
 15 AAAAATAGCA GTACATTATG GCGCTGATGC CGTATTTTTA GGTGGTCAAG AATATGGATT 420
 ACgTTCaAT GCTGaTaATT TCaCGATGGA AGAAATAGCT GAAGGTGTTG AATTTGCGAA 480
 CCGTTACGGT GCCAAAATTT ATGTTACGAC AAATATTATT GCACATGATG AGAATATTGA 540
 20 AGGTCTAGAA TCATATTTGC GTAATTTGGA AAAGACTGGT GCGACAGGTA TCATTGTTGC 600
 AGATCCTTTA ATTATCGAAA CATGTAAAGA AGTTGCGCCA AAAGTTGAAA TTCATTTATC 660
 TACTCAACAA TCACTTTCTA ATTACAAAGC TGTAGAATAT TGGAAAGAAG AAGGATTGGA 720
 25 TCGTGTGTA TTAGCACGTG AGACCGGCGC GATGGAAATG CGTGAAATGA AGGAAAAAGT 780
 AGATATTGAA ATCGAAGCAT TTATTCATGG TGCTATGTGT ATCGCCTATT CAGGTAGATG 840
 30 TACATTAAGT AATCATATGA CTGCAAGGGA TTCCAACAGA GGCGGTGCT GTCAAAGTTG 900
 CCGTTGGGAT TATGAATTAT TAGAAGTTGA TGATAATGGT GAACTTGATG TTTTTTATAA 960
 TCAAgGTGAA GTTACACCGT TTGCGATGAG TCCTAAAGAT TTAAAATTAA TCGAATCAAT 1020
 35 TCCTCAAATG ATGGATATTG GTGTGGACTC ATTAAAAATT GAAGGACGTA TGAAGTCAAT 1080
 TCATTATATT GCAACAGTTG TCTCAGTATA TCGTAAAGTC ATTGATGCGT ATGCGGCAGA 1140
 TCCTGACACT TTAAGATTAA TCCGGAATGG TTAATAGAGT TA 1182

(2) INFORMATION FOR SEQ ID NO: 800:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 989 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 800:

50 GTATTCTTCC AATAACACCT TTCATTGGA AACCGTTTAG AAAGAATACA GTTACTTCAG 60
 TTTGGTTTGC TTTAAAATTC TCTaGTGCTT TGTCTTGGAT GTTTTCGtTG cAATCATCTG 120

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TTTTCTTTAT CTAACCAATG AACACTCATT TTATTCCTGA ACCATGTCAT TTGTCGTTTT 240
 GCATATTGGC GTGAATGTTG CTTTAAATCA TTGACAGCAT CTTCATAAAT CATTTGTCCG 300
 5 TTAATCACAG GTATTAATTC TTTATATCCA ATAGCTTGCA TACTTTGGCA AGATTCATAG 360
 CCTTGTTCAA CAAGTTGTTG CACTTCTCTA AATAATCCGT GATCCAACAT AATATCAACA 420
 CGTTTATTTA TTCTTGAATA TAATGTTTTA CGCGACATTT CAATCCCTAA TAATAATGTA 480
 10 TCATAATTTT CAGTAAATTG TTGCACTTTC TTGCGATTAC TCAAAAGTTT TTTTGTTTTT 540
 AAATAATATT CAATAGCGCG CAACACTCTT TGGcGGTTGT TAGGGTGAAT ATTTTCTGaC 600
 15 AGAAACCGaC ATCAAATTGA GCTAAATAAT CGTGTAGTTG CTGATTATCT AAATGTTCTA 660
 ATGCAGATAA CTTTTGTTTA ACTATGGATA ATTGTGCAGG TGTAcTGTtT CATCTTCTAA 720
 TTCATAATTA TATATTAATG ATTGAATATA TAAGCCTGTT CCACCTGCTA TGATTGGaAC 780
 20 TTTACCTCTA TTCGtATAT CAGTAATTAA ATCTTCTGCT AATCGCTTGA ATTCAATATGC 840
 TGAAATGTA TCATCAGGAT TCAAGATATC AATTAAATGA TGTGGAATAC CATCCATTTc 900
 TTCAGGTGTh ACTTTTGcAG TTCCAATATT CATATGTCTG TAGACTTGCA TAGAGTCACC 960
 25 GCTTATGATT TCACCATTGA TACGCTTCG 989

(2) INFORMATION FOR SEQ ID NO: 801:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 543 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 801:

CGTTAGATAT AGAATTAAAA GATAATATTA AATTTCAAAA CGGTCAAAAA TTGACTGCAG 60
 40 AAAAAAGTGAA ATCTAGCCTT GAAAATAGCA TGAAAAAAG CGACTTGGTC AAATATTCAT 120
 TACCAATATC ATCAATTACC GCTAAAGGTC AAAAAGTAC AATTAAAACC AACTCCGCTT 180
 ACCCTGgACT TGTATCTGAA TTAGCTAATC CTTTTATGGC AATTTATGAT ACAGATGCTA 240
 45 AATCAGATGT TAATCAAACCT CCTGTTGGTA CAGGCCCTTA CCAAATAAAA GATTATAAGC 300
 AATCTCGAAA AATATCATTG TCGAATTTTA AGGACTATTG GCAAGGTAAA CCGAAACTTG 360
 ATCATATTAC TGTGACGTAC CAAGAAGACG GCAATAATCG CGTCAGAAAT TTAGAATCTC 420
 50 AAAAAAGATGA TTTAATAACT GATGTCCCAG TTAATAAAGT TCAAGACATA GAAAATAATC 480
 AAAATTTAAA AGTGTCAAAA GAATCTGGAT TTAGAACTTC TTTACTTATG TATAATCATA 540

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(2) INFORMATION FOR SEQ ID NO: 802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 802:

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GCGAATTCGT ACACACATAT ACACAAAGAT AATCATAGTT TTACATTGAA GCACATGAAA      60
GATAATTCAT TTAAAGGAAG GTATTATCAA TGAATAAAAA AATGGGATTA TTAGTTATGG      120
CTTATGGCAC ACCTTATAAA GAAAGTGACA TAGAGCCATA TTATACAGAT ATTAGACATG      180
GTAAACGTCC ATCTGAAGAA GAACTTCAAG ATTTGAAAGA TAGATATGAA TTTATAGGTG      240
GTTTATCACC ATTAGCAGGT ACAACAGATG ACCAGGCTGA TCGCTAGTT TCAGCATTAA      300
ATAAAGCATA TGCAGATGTT GAAITTTAAAC TATACTTAGG ATTAAAACAC ATTTCACCAT      360
TTATCGAAGA TCGGGTTGAA CAAATGCACA ATGATGGCAT TACTGAAGCA ATCACGGTAG      420
TACTAGCACC ACATTATTCT TCATTTTCAG TAGGATCATA TGACAAACGT GCTGATGAAG      480
AAGCTGCAAA ATATGGTATT CAACTTACAC ATGTGAAACA TTATTATGAA CAACCTAAAT      540
TTATTGAATA TTGGACGAAT AAAGTCAACG AAACATTAGC TCAAATACCG GAAGAGGAAC      600
ATAAAGACAC GGTATTAGTT GTTTCGGCAC ATAGTTTGCC AAAAGGTTTA ATCGAAAAGA      660
ATAATGATCC ATATCCACAA GAACTAGAAC ATACTGCGCT TTTAATTAAA GAACAATCTA      720
ATATTGAACA TATCGCGATT GGTTGGCAAT CTGAAGGTAA TACAGGTACA CCTTGGTTAG      780
GGCCAGATGT ACAAGATTTA ACACGTGATT TATATGAAAA ACATCAGTAT AAAAAGTTTA      840
TATATACGCC AGTAGGTTTT GTATGTGAGC ATTTAGAGGT GCTTTATGAC AATGATTATG      900
AATGTAAAGT AGTTTGCGAT GATATTGGTG CGAATTATTA TCGTCCAAAA ATGCCGAATA      960
CACATCCATT ATTTATCGGT GCAATTATTG ATGAAATCAA GTCTATATTT TAATGACGAA     1020
AGAAGCGTGA AACGTTGTGA CTAAATCAGT GGCTATTATA GGAGCGGGGA TAACAGGTTT     1080
ATCAAGTGCA TATTTTTTAA AACAGCAAGA TCCTAATATT GATGTAACCA TCTTTGAAG     1139

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(2) INFORMATION FOR SEQ ID NO: 803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 989 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 803:

5 TATCCnAAAT AnAAATGTGC GCATTTATCA AAACCTTACA TACAATAGAG TTTTCCCTAA 60
 CAGTAAATTA GATATTATTA CACCTGTTGA TATGTCTTCT AATGCCAAAC TGCCAGTTAT 120
 TTTTGGATG CACGGTGGTG GTTATATTGC GGGTGATAAG CAGTATAAAA ACCCATTATT 180
 10 AGCGAAAATT GCTGAACAAG GGTACATTGT TGTGAATGTA AATTATGCAT TGGcGCCACA 240
 ATATAAATAT CCCACACCAT TAATTCAAAT GAATCAAGcA ACTCAATTCA TTAAAGAAAA 300
 TAAATGAAT TTACCTATTG ATTTTAATCA AGTAATTATT GGCGGTGAYT CTGCAGGTGC 360
 15 TCAATTAGCT AGCCAATTTA CGGCAATACA GACGAATGAT CGCTTAAGAG AAGCCATGAA 420
 ATTTGATCAG TCATTCAAAC CATCGCAAAT TAAAGGTGCT ATACTATTTG GTGGTTTTTA 480
 TAATATGCAA ACAGTTAGAG AACTGAGTT TCCAAGAATA CAGTTATTTA TGAAAAGTTA 540
 20 TACTGGCGAA GAAGATTGGG AAAAGAGTTT TAAAAACATT TCACAAATGT CGACAGTAAA 600
 ACAATCGACA AAAAATTATC CaCCAACATT TTTATCTGTT GGAGATAGCG ATCCATTCTGA 660
 AAGTCAAAAT ATAGAATTCA GTAAGAAATT ACAAGAATTG AATGTACCAG TAGATACTTT 720
 25 GTTTTATGAT GGTACGCATC ATTTACATCA TCAGTATCAA TTTCACCTTA ATAAACCTGA 780
 ATCGATAGAT AATATCAAAA AAGTGTTACT TTTCTTAAGT CGTAATACAT CCTCTAGTGG 840
 30 TATTCAAACCT GAAGAGAAAC CACAAATAGA AAATCCGAGT AATGAATTAC CGTTAAATCC 900
 TTTAAACTAA TGATAAACAG TAGTAATTTA TTAATAAGC AACATTTAAG ATTTTCAAAT 960
 TAAAAACGAG AATTTAAAAC ATGTGGTGC 989

(2) INFORMATION FOR SEQ ID NO: 804:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 711 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 804:

45 TAAcCCCTGG TTTAATGATT TTGATTACGT GTTTTTATAA TAAAAACATA TCGAACATTG 60
 ACTACGTTAT TAAGCTGCTT TTTGTACAC TTTATAACCA ATAGCTTAAG ATTTAAACT 120
 50 AATCGGAAAG AACAATGATT CACCAcAAAA ATATTTATGT TGCTATTAAA AATCAGTTAA 180
 TACGAATGTT AAAATACGTT TGATTTTCAT TAATAATGAT TCAAGTTTAT TTAAATGAGC 240
 GTTAATGTCA GTCTGTTTTG ATGCACCTTA TAATAAGAC AGATAGTTCA AATTACGTAA 300
 55

AAAGCAACAT TAGCATTAGG AATATTA ACT ACAGGTGTGT TTACAGCAGA AAGTCAA ACT 420
 GGTACGCGA AAGTAGAACT TGATGAGACA CAACGCAAAT ATTATATCAA TATGCTACAT 480
 5 CAATACTATT CTGAAGAAAG TTTTGAACCA ACAAACATTA GTGTAAAAAG TGAAGATTAC 540
 TATGGCTCTA ACGTTTTAAA CTTTAAACAA CGAAATAAAG CTTTTAAAGT ATTTTTACTT 600
 GGTGACGATA AAAATAAATA TAAAGAAAAA ACACATGGCC TTGATGTCTT TGCAGTACCT 660
 10 GAATTAATAG ATATAAAAGG TGGCATATAT AGCGTTGGCG GTATAACAAA G 711

(2) INFORMATION FOR SEQ ID NO: 805:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 680 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 805:

ATCAGGAAAA ACAGaATAAT GTAAATCAAG CTGTTCAGCC TCAAAATAAT ACTAATGAAA 60
 25 CATCAAAAGT ACCGGCTAAT TTTGTCAAAT TGAATGATAT TAAACCAGGT GATACTTCTA 120
 TACAAGGAAC AACTTTACCA AATCAATTTA TACTATTAAC TATTGATAAA AAAGATGTGA 180
 GCTCAGTTGA AGATTCTGAC AGCAGCTTTG TTATGTCTGA TAAAGATGGG AATTTTAAGT 240
 30 ATGACTTAAA TGGTCGCAAA ATTGTTTATA ATCAAGAAAT TGAAGTGTCT TCATCAGATC 300
 CCTATTTAGG TGACGATGAA GAAGATGAAG AAGTAGAAGA AACTTCAACT GAAGAAGTTG 360
 GTGCTGAGGA AGAAAGTACA GAAGCTAAAG CTACATATAC AACACCGCGA TATGAAAAAG 420
 35 CGTATGAAAT ACCGAAAGAA CAGCTAAAAG AAAAAGATGG ACATCACCAA GTTTTTATCG 480
 AACCTATTAC TGAAGGTTCA GGTATTATTA AAGGCCATAC CTCTGTAAAA GGTAAAGTTG 540
 40 CTCTATCTAT TAATaATAAA TTWATTA ACT TTGAGaCAAA TGCTatGGTG GtCCaAATaA 600
 AGAAGaAGCG AAATCTGGAT CAGAAGGAAT CTGGATGCCT ATTGATGACC AAGGATACTT 660
 TAATTTTGAC TTCCAACGA 680

45 (2) INFORMATION FOR SEQ ID NO: 806:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 950 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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GTATTTTCATT AGCCATTGGC AATTGACATC TGACAATGAG GAATGGCTTT TGCATTGGAA 60
 TTCACAGTTG GAGTGCATTT ACTGGTTATT TTGGAGGTCA TTGTTGATAC ATTATTAATG 120
 5 GAGAATAACC GAATTTGTGA TGTIATTTCC ATTTTAAATA TTTGCAATTG TATTAAATGC 180
 TGCACCTTGA GATAAAATTA AAAATCCTTA TGGATCTGCC ATAATTCCTG TTCTAGTTAT 240
 TATCGTATTA AGTTGGGGAG GTATTGACAA GACTTGTTTCG TGGTAAAGTA CTTCAAGAAA 300
 10 AAGAAAATGA ATACTTTTTG GCAGCAAAAT CAATTGGTAC ACCCACATAT AAAATTATTT 360
 TGAAACATCT TTTGCCGAAT ATATTAAGTG TAGTTATCGT ACAAGCAACA TTGTTATTTG 420
 CCGGTATGAT TGTAGTGGAA TCAGGrTTGA GCTTTTTAGG ATTCGGAATT AGTAAAGCAA 480
 15 TACCATCTTG GGGTAATATG TTGAGTGATG CTCAAGAAGG GGATGTTATA AGTGGTAAAC 540
 CGTGGATATG GATGCCACCT GCTATAATGA TTACATTAAC TATATTAAGT ATAAACTTTG 600
 TAGGGGAAGG GATTAAAGAT GCTTTTAATC CTAGAGGTAG ACGTTAAATA ATAAAAGAGG 660
 20 CACTAGTTAA TTCTAGTACC TCTTTATTTT ATCTCTTACG TCCTAAACCC ATCGCTTTTT 720
 CCATTTTTTT GACAGTTTTA AATGAACTT TGTGTGCTyT ATCTCTACCT TGATCTAAAA 780
 25 TATCAyCAAG TTTATcTGAG TTATAGAAAC TTTCGTATTT TTCTTGGAAT TCTACTAAAA 840
 ATGCTTTAAC TATTTcAGCA AGGTCACCTT TAAATTTACC ATAACCTTCG CCCTCATATT 900
 TTGCCTCAAT ATCTTTAATT GGCATGTCTG TTAATCCAGC GTATATTGAA 950

30 (2) INFORMATION FOR SEQ ID NO: 807:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 418 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 807:

GTTACCAGTC GAAGCTTTAC GACCTGTTAC GAAACATTGT TTACCCATAT GAGTACCTCC 60
 TTTAATAAAT ATAAATACAC ATAACTACTT ATATACTTAA TTAAGATAGC ATAGTTTCAT 120
 45 TTGAAAAACA ATGAATAATT TTCACATAAA AGTCAAAAAT ACTGAGTTTT GTGATATAAT 180
 TGTAGACTGT GAAGTTATGT AGTATGATAT TTTAGAGAAA TAAGTGAATG AAACATTTAA 240
 AATTTTTTATT TrATGATACT ACATCTATTA AAAGAAAACG CCTATAGATA ATCGTCaTGA 300
 50 GTGTAAATTC AGTTtACTCa AcAtATAaTA GGkGaTTTAA gCgTAAGtCa TTCTGATAAG 360
 TTGTACCATT GATATTTTAT GAAATAnTCh ATGAACTTAA AGCGTTTATG CTACACTA 418

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 842 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 808:

10	AATGGCnATT AATCTTTAAT ACGATGCTTG AGGATTTTTC CTAATAAAAC CTTGATTTCm	60
	AAAAGGGTTT AAATCmATG AAACAATAAT AAaAAATGw CGCAATATAA TAATAAGTAC	120
	AAATTTAATT AAGAAATTAA ATTGATTGTA TATGTATATT TTGGTAACGT AAAAGAGAnA	180
15	TATACAAAAT AATTAATTAT TTATATGAAA AGAGAATATA AATGAAGTAT AAAACAGAGA	240
	GACGTGAAGC GATGGGATAT TTAAmAAGGT TTGCATTGTA CATAAGCGTT ATGAyTTTAA	300
20	TATTTGCGAT AGCAGGTTGT GGCAAGGTA ATGAACAAA AGAAGATTCA AAGGAAGAAC	360
	AAATCAAAAA GAGCTTTGCG AAAACATTAG ATATGTATCC AATTAAGAAT CTCGAGGACT	420
	TATACGACAA AGAAGGATAC CGAGATGGCG AATTTAAAAA GGGTGATAAA GGGATGTGGA	480
25	CGATATATAC AGATTTCGCC AAAAGTAATA AACAAAGGTGG ATTGAGTAAT GAAGGTATGG	540
	TCTTATACTT AGATAGAAAT ACACGGACTG CAAAGGGACA TTATTTTGTT AAGACATTCT	600
	ATAATAAGGG CAAATCCCA GATAGAAAAA ATTATAAAGT TGAAATGAAA AATAATAAAA	660
30	TTATCTTATT AGATAAAGTA GAAGATACAA ATCTAAAAA GAGAATAGAA AACTTTAAAT	720
	TTTTTGGACA ATATGCAAAC CTTAAGAAT TGAAAACTA CAACAATGGT GaTGTCyCAA	780
	TTAATGAGAA TGTCCAAGT TATGACGCAA AATTTAAAT GAGCAATAAA GATGAAAATG	840
35	TT	842

(2) INFORMATION FOR SEQ ID NO: 809:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 451 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 809:

	TAAGACTATG CCATCTTGGC AACGCGTTGT CGCATATTCA TTATTAGTAA GTATATGCAA	60
50	GCATGATTTT GCCATAACTt TACctCtTTC TATATTTAAG TACCACTTTT ATCATTCCCT	120
	ATAATATTTA ACTTATTTAA TTAAACGTAA ATTTAACACA ATACGAATAC CAAATCAAAA	180

AAAAATAGAT GTAGTCAGTT TAATTAAACT ATCCAATTGA AAACACACTA CTTTTTAGTA 300
 TTTTCAAAT AATTTTAAAT GACCACATCT ACAACGTATT ACTATTATCT TTTGTTAGTT 360
 5 ATATATTTCAT TTTCAATTTA TAAATAAACA CTTAcTTAA TCACATTCTA CTTTTGAGAT 420
 GAGCTCAAAC TAACATTAAA TTGTTTATAT T 451

(2) INFORMATION FOR SEQ ID NO: 810:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1499 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 810:

ACATTTTGTTG CTTGTTGTCC AATCCAATTT CTACTTTGTT GAACAGTATG AGTTGCTTGA 60
 CCACGCATGT TACTCAGCAT TTGTCCAACA TGAGTATTTT GAGCAAAGTT ACGAGATTGA 120
 TTCAACACAC TGTTTTTTCAT CATThCCATT TTAGGTGAAA TACGACTAAC TGCTTGTTGC 180
 25 ATTGTCTTTT GCAATCCTGT TTTAACTGCA AATTTTCTC CGCCTTTGAA GCCTAATTTT 240
 ATTAACTTT TCCCAGCACC TTTGAGGAAG CCCATACCTG GCAATGGAAT AAGCGAAAGT 300
 CCTCCATGA TTCGTTCTTC TTTAGATAGC TTTCTTCCAG TTACAATATT TTTTCCTGTG 360
 30 GCTGCATTTG CTGCTGAATA AGCGGAATAA GCACCAATAG CTACTGCTCC AGCAACAGGA 420
 TTAATACAAG ATAAACTAC CATACCAGCT AGTGCTGCAA TCTCTATAGC TTCTTCTTTT 480
 TTCTTTTGCT CCTCTAGcTC TTCCGCTTCA GCTACTGTCA TGTAATCACA AGAAGCGCCC 540
 35 TGAGTCATCA TTTTTTCAA ATCATTTTA GATAATTCT TATCTTCTTT TTCATTTCT 600
 TTGTAATGCT GATCAATTAC TTTTACAAAT TCTTGATCCG ATTTTAATAT TTCATCGATG 660
 CTATAAACAT CGCTGTCACT TTTCTTGGCA TCTCCCTTTG CAATTTTCCC AGAAGCCCCA 720
 40 TAGGTATCTC TACCATGTCC ACCACCATT TTAATTAGTA TATTTTCAA TTAAACATTC 780
 GTTATACCTT TGAATGCTT ATCTATATCT TCTATAAATG GCGTGTCAAT AATTTCTTTC 840
 45 ATTTTCGAAT CTAATTGAGA TGCATAATCA TATAACTCaT TTTGATAATA CCCCATTAAAT 900
 TTAGATCCTT GTGGAcCTAC TACACTACTT GTTAATGATA TTGCGCCATC TTCGTCTAAA 960
 GAACTGACAT CGCTTACCGC ATCATCCATT GTTGTATCTA CATCTAAGAA GTCTTGACCC 1020
 50 TcTATTGCAT CTATTACACT TTGGATAGAT GACTTTTCAT TGTcATAATC AGCTGTTAGA 1080
 TATTCAATAT CTTTTGTCAT GTCATGCACC TATCCCTCAA TATTATAGTA AAGCTTGGCA 1140

CCACCGAGTG TACTCAATGG ACCTTTGAGA CCACTAATGA CTGTTGCAGC ACTACTATAG 1260
 CCATTTTCCA TAGAATGTGC AGCTTTTTC A TACTGTAGT AATTTAATTG CGCTATTTTT 1320
 5 CCAAAGTTTT GAGCTATTTT ATCATACTTT TGACTTATGC TTCCAATTTC TTTTACAACA 1380
 TGTGCAATCG TTTCAGCTTT AACACTAATT TTCCACTCA ACGTCATTAC TCCTCtGcTt 1440
 TATtAATATG ATTTTcATCA GTATCGAATC CAAATAATTc TCGTGATAAA nGTATTGAA 1499
 10 (2) INFORMATION FOR SEQ ID NO: 811:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 620 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 811:
 20 CnCGCTGCAC CGAAGAATGC TTTTGGTTTG TGTAAGATG CAGGATCTAA ACCACCTGAT 60
 AATGTACGAC CACTTGGTGG AATAACyAAG TTATAAGCGC GTGCTAATCT CGTTATAGAA 120
 25 TCCATTAAAA TAATGACATC TTCCCAATT TCTACTAAAC GCTTGCACG TTCAAGTAAT 180
 AATTCAGCTA CTTTAACATG GTGTTCTGGT GGTTCTGCAA ACGTTGAATG AACGACTTCA 240
 GCAGCTTCTA CTGAGCGTTC TAAATCTGTT ACCTCTTCAG GACGCTCGCC AACTAACAAA 300
 30 ATAAATAGCT TTGCATCTGG TTTGTTCTGTA CTGATTGCAT TCGCTATTTT TTTTAATAAC 360
 GATGTTTTAC CTGCTTTAGG TGGCGCCACT ATTAAACCAC GTTGACCTAA ACCAATCGGT 420
 GTTACTAAAT CCATGATGCG CGTTGAATAA TTTTGTATTT CTGTCTCTAA TTTAATACGC 480
 35 TCATCTGGAT AAAGTGGTGT CAAAGCTTGG AAATGCGGAC GTTCTTTCAC TTCTTCTGCG 540
 TTATGGTCAT GACAAAGTCA ACTTGTAATA AGCCATAATA TTTTTCGTTA TCTTTAGGTT 600
 TTCTAACTTT CCCAGTTACT 620

40 (2) INFORMATION FOR SEQ ID NO: 812:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1094 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 812:
 50 CCGGCTGAAA TTAAGTTCTT GTTATATTTT GCAAAAATGA CAAAGAAAGA TAAAAATAAA 60

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TGAAC TATTT GCAATTAGAG AATTGTTAGA GAAAGGTTTG ATTGGTGATT GTATTCAACC 180
 TATAATTGAA CCAATTAAAT ATACAACCAC ATTTAAAAAT ACTTTGCAAT ACTGTGGTGA 240
 5 AAAAGCATTc TCTATAAATT TAGTAGTAAA TTCAAAGTTA ACTGAAGAAG AGATTAGTAA 300
 CGAAaCTGTt GCACATTTAA CTGAAATAAT AACAAAAAAC AAAAGTGTTA TTCAAAAAGC 360
 TTACTTGGGT CCTTCTGATG AAGGCAATGA TAGGTTGAAA CAGCAATTTT CAAGTAATAG 420
 10 TTTAGCTATT TTAACAAGTG TAGATGATTG GGAAATGTTT GGAGATAAAA ATAAACTTGA 480
 AATGGTTTTT GTACCAGATG ATAGACACAT TAAACGTAAA TTGCGTAATA TTCCAAACAA 540
 15 AGGCATsATT ATGGATCCTT TTAATAAACT AAGTCGTAAT GTTGATTATT TAGATAATGA 600
 TGACGAGTTT TATAGCGACG ATCACCTTTA TTATAAGGAA GATGGATACG TAGCATTTTC 660
 AGACTATTCT GTTATAGGTG GAGAATATGT AGACGGTGGC TTTTCGCCAT TAGCtATTGc 720
 20 GrTACATATT GTCTATTTTG ATGAGGCTAA TGAGCTAAGA GTTAAGCATT TtGTCTCTGa 780
 TTCTAATAAT GATAGATCAA ATCCAGGTAA AAnGTTTTTT GAGGCTGTAG ATAAATTAGT 840
 AACATGGTCA AAAAaCTTAG ATATTAAAA TAGATCTTAT GCGCTTGGAC AATTTGAAGA 900
 25 ATTAAATGAA AATAATAAGT ATCCAGGATT AGGTTTAATT AAAnGTTATC TATCAGCATC 960
 ACCTAGAAAT TATGAATAGA TACTGGGTCT CAAAGAAATA GGAAAAGTTT ATATCGAACT 1020
 30 GAACTGCAAG AATGCATTGA CATGGATGAA CACACGGGTA AAATGATCGC AGCTGAAATG 1080
 ACTATGGTAT TAGC 1094

(2) INFORMATION FOR SEQ ID NO: 813:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 930 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 813:

45 CACCTATCAT CGTCTCTTTA ATTCTATCTA TCTATTTACC CCAATCGTAA ATATGATGGA 60
 CGTTATAGAA TACCAAGAGT TGCAGGTATn TCTATTATTT ATCTAGCTGT AGTAGGTGTT 120
 ATTACGTTAA TTGTTAATTT ATTGATACCT ATTATTGGTT CGCAAGTAGA TAGTTTAGTT 180
 50 AAAAATTCAC CGCAATATCT AGAAAAATTA ATTAATTCTA TTGATAAAAT AGCAAATAAT 240
 ACGTTTTTCT CTTCGTATTA TAGTCAAATT AATGATTGGT TAAATTCTTT ACCTAAGAAA 300
 ATACCATCTA TGTTAAGTGA ATTTACAGAT GGCTTTGGGT CTAAAATTGC AACGTTTGCA 360

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CTTAAAGATG GACATCACTT CAAAGAATTT TCAACGAATA TTATGCCACC GAAATTCCGA 480
 AAAGATTTTC ATGATCTACT TGAAAAATG AGTGTTCAGG TTGGTTCATA CATTCAAGGA 540
 5 CAAATTATCG TTTCAATTCTG TATCGGTATA CTGTTGTTTA TCGGTATTTC GGTATCGGG 600
 TTGAAATATA GCTTAGTATT AGCTAGTATT GCGGCAGTTA CAAGTGTGT ACCATATTTA 660
 10 GGGCCTACTA TAGCGATTTT TcCAGCTATT GTAATnGCTG CTATAACaYc GCCGTGGATG 720
 CTCTTAAAT TAGCAGTAGT ATGGACTTTA GTACAATTTG TTGAAGGGCA CTTCAATTTCA 780
 CCAAATATCA TGGGTAAAAC ACTTAAGATT CATCCACTTA CAATCATTTT CATTTTACTG 840
 15 TGTGCAGGCA AATTGCTTGG TATTGTAGGC GTTATTTTAG GTATTCCGGG ATATGCTATT 900
 TTAAAAGTAT TtAGTTACTC ATTTATTCCA 930

(2) INFORMATION FOR SEQ ID NO: 814:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 814:

30 GTATGATTGC TGTTTAAATA CCAGATGATG GCAGTGGCAA ATCTTATGAC TATATGCTTG 60
 TGAACCCAAA AATTGTAAGT CATAGCGTTC AAGAAGCTTA TTTACCAACT GGTGAAGGTT 120
 GCCTTAGTGT CGATGATAAT GTTGCTGGTC TAGTTCACCG TCATAATAGA ATTACAATTA 180
 35 AAGCCAAAGA CATCGAAGGT AATGATATAC AATTACGACT AAmAGGATAT CCAGCAATTG 240
 TTTTCCAACA TGAAATTGAC CATTTAAATG GTGTAATGTT CTATGATCAC ATTGACAAAG 300
 ATCACCATT ACAACCACAT ACAGATGCAG TAGAAGTTaA aACACATTTT cTAATTATCA 360
 40 AAgCTTAGGA TAAtATGATG tCCTAAGCTT TcCTTTACAA CTTTTCGGAT AACCAACAGT 420
 TAATATATCA CCTTCTAACC AAACTTTTAA TCCCTCATT A 461

(2) INFORMATION FOR SEQ ID NO: 815:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 815:

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AACGATATAA TAGAATTGAA TAAAGTGGGT GATAATGTGA CTAAAAATGA GATTAGAAAA 120
 TACATTTTAC ATAAAAATGAA GAATTTTAAAT AAAGCTGAAA AGCGAAAAGC AGACACATGG 180
 5 TTAAGAAATC AATTTTTTGC AACTGAAGAA TACAAAGAAG CAAACGCAAT TCGCGTAGTT 240
 CTTTCTTTTA ATCATGAAGT AGATACTTTT TCTATTATTG AACAAAGCCTT AATGGATCAT 300
 AAACGTATTT TTGTACCGAA AATGGATTAT TTAAATCATC AAATGACTTT TAAAGAGATA 360
 10 TTTAATCTCA AAGATATTGA TGTCGATAAT AAGGGGATTT ACTATCCAAC TTCAAAAGGT 420
 GAAACAACGA ATAACCTAGA TTTAATTGTT GTTCCTGGTG TTGGATTTC AAGACGATGGA 480
 15 TATAGAATTG GGTATGGTGG TGGCTATTAC GACAGGTTTT TAGCTAATTA TCAGACAAAG 540
 ACAATAAGCT TATTATACGA TTTTCAAATA ACA 573

(2) INFORMATION FOR SEQ ID NO: 816:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3989 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 816:

TAGTTTAAACA ATGTCTATTC TCATAGAATT TGTCCAATA AATGTAGACG ATTCACTAAA 60
 30 CTTCTAAAAA AATAAACCCC AAATTATAAT AGTCTCAATA TTAATATATT ACAATTTATT 120
 CATAGGATTT TTATCATTTC AATTAATAGG TTGTATCAG GGTAAATAA ACATTTTTTG 180
 35 TAATAGTCCT TTTTACGTT CTTTAAATAA CTCAATTCTA TTCATTTGAT TATTCATTTT 240
 ATTGTCTATA GATTTTAAACA ATGCACTTAC TTTATCTGT TCAGTGAGAC AAGGTATTTT 300
 AAGATTTATA TTGCATAAGT TCGCATGAGT TAATTTAGCT GGTGCATTAC CTGTGACAAA 360
 40 TGCTCGTAGT TCTTTAAAAT TTAAATAATA ATTCATAAAA AACAAATTAT GATCATTACT 420
 TTTAACTACA TGCGCATGAT TATTTACCCA GTATTGCCCA TTAGCAATAA AGCTACTCGT 480
 CTCAAAGTGC CCCCATTTTG CACCATCTTC TCCTATTAGT AATCGTTCTT CATTATTGAA 540
 45 TAAATAATCT TTTACGTAAT CAATAATTCC AGTTGCACCA TAGTAAGGGT ATAACCCCTT 600
 TTCTCTTAAT GAAGAAGTAA TTGGTTTTCT TCTATTATTT TCAAAGATAA AGATGTCCTT 660
 TATGAATTTG TTTTCCCACT CTGGATATTC TTCACCATT TCATCTTTGA ATCGCAATTC 720
 50 TTGTGTGAAG ATTTTCTGCA TATAGCCTTT TTTCTGTTGT TGAAGCAATT CAAGTTTTTG 780
 TTCTTCTAAT TCAATTTGTC GGTGAGTTT GCTGAAGAAC TTGCCTATTT TTTGCTGTTT 840

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	TCGACTACCT CCACTTTGTG CAAGGAAAAT TTTCTTTTCTTG ATAATAGATA	960
	CTGTCCAAAA AAATTATAAT AATACTCTTT TTTCAATCTA ATAATACATA CATGTTGATT	1020
5	TAAATTAGCA TCGTTTCAA CTATCGAATT AATGGCTGTT CTACCTATTG ATGCTCCTGT	1080
	AATATTTAAA AGAACATCAC CATAGTACGT TCTACTATTT TTCATCTCAT CATCTATATC	1140
	TTTACTAATA TAACTAAGT CATTAAAGATT TAATTTACCA TTTCTAATAT TTTGACTCCT	1200
10	TAAAAATGGT ATGCCTTTGT TTGTATAGTT TTCACTTCCA CCTTTGGGAG TCTTTCCACT	1260
	ACCTATTTTG GTAGTAAGAT TCCCTAACTT CTTCTCTTCC CATTCGCCTT CAAATCCTGG	1320
15	GAATCTCAAC TCTGGCACAT TTTTCGTTTG TGTATTACTC ATCTTTCAAC ACCCCAAGTT	1380
	CTTTCAGGTA TGCAITGATT TCTTGTTCAA TTTCTGCGAT TTCTTTGTGCG ATATTTTTC	1440
	AATCTTGTG GACTTGATCT AAATCAATTG GTGCTTCTTC TTCGAATGTA TCAACATATC	1500
20	GCGGTATGTT TAAGTTGTAA TCGTTATCGG CGATCTCTTG TAATGTCGCG CTGTAGCTAT	1560
	ATTTATCAAT CGTTGCTTTA CGCTTATATG TGTCTATAAT ACGTTCGACT TGGGCATCGC	1620
	TTAAATGGTT TTGATTTTTT CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT	1680
25	TGTCGTCTTG TTGGCGACAT TTTTAAATA CTAAAATACA TGTGGAATA CTTGTCCCAT	1740
	AGAAAATATT GGCTGGTAAC CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT	1800
	AGCGACGAAT CACACCTTCT GCGGCACCAC GGAATAATAC ACCATGTGGG aGTACGACTG	1860
30	CCATGGTACC TTCATCGTCT AGGTAATGTA CCATGTGTTG AATAAAGGCA AAGTCTGCTT	1920
	TGGaTTTTGG CGCAAgCTTG CCGTAACCAC TGAATCGTTC ATCATTTTCA AATTTTGAAT	1980
35	CTGCTGTCCA TTTCGCACTG TATGGTGGGT TCGCAATAAC CGCATCAAAT GTATTGCCTA	2040
	AAAAGGCTGG ATTTTCCAAT GTGTCATCAT TACGGATCTC GAAGTTCTCA TAACGCACAT	2100
	CATGTAATAA CATATTCATG CGTGCTAAGT TGTATGTAGT ATTGTTACGT TCTTGTCCGA	2160
40	AATAACGATA CACTTGCGTT TCTTTACCAA CACGTAACAA CAATGAACCG GAACCACATG	2220
	TTGGGTCGTA CACGTGACGT AATTTATCTT TACCGTCTGT GACAATCTTC GCCAGTATCT	2280
	TAGATACTTG TTGTGGTGTA TAGAACTCGC CTGCTTTTTT ACCCGcTGTC GCCGCAAAGC	2340
45	GCCCGATTAG GAATTCATAT GCATCACCTA ACATATCAAT TTCCATGTCA CTGTGAACGA	2400
	ATGGTAAGTC GTCAAGATTA ACCATGACTT TAGAGATTAA AGCAGTACGT TCTTTGACAT	2460
	TGTTACCTAG TCGCGTTGAA CTCAAATCCA TATCGCTGAA CAGCCCGATA AAGTCATTTT	2520
50	CACTTTCTTC ACCTAATGTA GATGTTTCAA CTTTGCGAAT CGCCGTCGCT AGATGTTCTA	2580
	TATCGAAATC TTGCGTTTCA ATTCACGAA TCATCGCACT GAATAAATCT TGTGGCTCAA	2640
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CCCATGCTTC TTGATACGTG ATGTCTTCAC CTGACAAGGC ATCTGCATAT TCTTGTTCGG 2760
 CTTTTTCAGA TAAGAAGCGA TAGAAAATCA AGCCTAAAAT GTAATTACGG AATTCACCTCG 2820
 5 CATCCATGTT CCTCTTAAA TCATTGCGAA TCGACCATAA TTTTTTATGT AATTCAGCTT 2880
 GTTGCTGACG TTGTTTTTCA GTAATAGACA TGTGATTCCT CCGCCTTTGC ATAAGTAATT 2940
 TATCTCTTTG TGTAATAGAT TTATTATAAC ATTTGGTTAT GTTGCGATGT TGATAATTTG 3000
 10 GATGTTGGTG GTGGAAATTT TGAGTTTTAG TGGCGCAATT GTTATTGAAA AATTTTATAG 3060
 AAATGTTGTA GCTTTCAAAT GCTTTCAAAA TCATTTATAT TCTTAATGAT GTCAAAAAGT 3120
 TGTTCAATTCA TACATAAATA AAACCAATCA ACAATTGAGT TGGTGAAAAT CAATCGTTGA 3180
 15 TTGGCTTTGA TGCATATTAA ATAATGCAAT ATATATTAAT AAATGTTAGT TATAGTATAT 3240
 TTTGTCAGGA TTGGGTGAAT GTCTAAGTTT TAATTATTTA TCTAAATTAT CTGCAATGAA 3300
 20 TTTCTTAATT TCAGGAGAGA AATAAACAGC AAATCCTCTT GTGCTTTCAC CTGATGGCTT 3360
 ATTACCGGCA TAGATTACAC CAATAGCTTC GTGTTTACTA TTAAATATAG GTGAACCAGA 3420
 GCTACCAGGC TGAATAATTG CATCCGATGA CACTATATTC CCATTCACTG ATAATACTTT 3480
 25 ACCAGTTGAT TCATACATTT GTAGTTTATT TCCATTAGGA TTTGGATAAC CAATGACTGA 3540
 TATAGGTTCA TTTTCTTTAG CTTCTGATGC TATATTAAAT TTACTAGTGA AATCTTTGAA 3600
 TTTTCTACCT TTTGGTTGTG TTGATTTTTT TCAACTTGT ACAACCGCAA TATCTTCTTT 3660
 30 ACCAGGATAA TCTACAATCT TAGTAACTTT ATAAAGTCCA CCACCGTTAT TATAAAAACC 3720
 ATTAGGATGT GCTTTGATTT CATCACCGAC TTTCATGTGA TAGGTAACAT GTTTATTGGT 3780
 AATGATTGTA TGATTTCCAA CTACAAATCC TGTTCCAGCG CCCATCCATG TAACACCACT 3840
 35 GTATGGTGCA ACATTTGTAT TTGTAATTTG TTAAACAGTA TTTTCGGCTT TGGCTGTTTG 3900
 TTGAATACCT TCAACCATTG TTGTGCCGAC ACCAGTTATT GATGTTAAAA TCGTCAATGC 3960
 40 TGCAATACTT TTGATGATTA TATTTTTAT 3989

(2) INFORMATION FOR SEQ ID NO: 817:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 904 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 817:

CGTTGAGCAC AGTTTTAGAT AATAGATAAT CTTGctCTAG TTGTTGCAAT GTCTGCGATT 60

TATGCGTGTA ACGTTCAGTT ATCGTTTCTA AGGTATACTG AGATGTATTT AATTGATATC 180
 CTTTAGATTT AATACTTACG ATGATATCAT CCATAAAATT GCTATTGATA ACATGGATAT 240
 5 CATTGCGAAC TGTGCGGTTT GAAACATTGA CATGTTTAGC AATTTCAATTA GAACTAATGT 300
 GCTTTGATGG ATTTTTTAATA AAAAAGCTGA GTAGTTTAA GTGTCTATCA AGCATTTAAC 360
 ATGTACCTCC TTTCTAAATT TTTCGTGTAA GCGTTTAA GGGTGTATTA ATATTATTAA 420
 10 ACATGAGAGC TTATACATAC GTCAATGACA TTAAAGCGAA CTTTATATG ATTTTAACAG 480
 AGTGCGAATT ATGCAAATAA AGAACAGCAG TAAGATATTT CAAATAGAAA AATATCTCAC 540
 TGCTGTTTTT CTGAATTTAT GCATCTGTA CTTGTGGACG TATCAGGCAA ATGATTAATT 600
 15 TTTAGGTGAT TGTGCTTGAG GTGTTTGTG AGAAGGCGTA TTGGTATTAT TTGATTTATT 660
 AGCAGGTGGT GTGTTCTGTT GTTGATTATT TTGGTTGTT GTTGACGATT GACTGCCACC 720
 20 ACCGTGAGTA TTATTTTTAT TTGAATTTGA GTCTTTTGGC TGAGCTGGT GCGTATTGCA 780
 TGGTACTGTT GAATGGTTGT TAGGAACATT TGACGGTGAA GATGGTTGAT TGTCAATAGT 840
 AACGTTATTG CCATTATTTT GATTtTTATC TGTTTTGTCT GCACTATCAT CTTGTTGATC 900
 25 ATTT 904

(2) INFORMATION FOR SEQ ID NO: 818:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 818:

TTTAACAtGa TAATAAAAAA TCTTTTGTTA TATCATTAGG AATATTGAT GAACTTGATA 60
 40 TTAAGGTTAC ATTTTGAGAA ATGGACTTAG GGATATTTCC ACTATTATTT AGTAAGAAAT 120
 CTTTAGCTAA TAAAGATTTT CCTACACCAT TTTTACCAAC AATGTGATTG ATCTGACCAA 180
 GATAGAAATT TAAATCACAA TTGTCAACTA GTTGTGTTT TTTAACTTTT AAAGAATAGT 240
 45 TATTTAGTTT CATGTATACA ACTCCTATGT ATAAAGGGAT TTATTACACC GATATTTAAT 300
 TGTATTTTTA AAAATTCTTT CACATTATGT ATAGAWGTTA TAAATTAGTA TATCaCACTA 360
 TATTTtGkCT AAATGATAAA TATATCGTTA TATTTTTACA ATATTCTGAA ATTTATGTTC 420
 50 GCCTCTGAAT GCTATATCCA GTGTAATGTG TTTTGCATAT ATGAAAGCAA TTTCAAAATG 480
 TGAATATAGG TTCATTGTGG TATGACAAAC TTCATTGCTT GTCATGAGAT GGATATAATG 540

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GACGGGACGT TTTTAGATTC AAAAAAGACA TATGATAAAC TTAGATTGGA AGCGATTTT 660
 ACTGAACTTA GAAATAGAGA TATTACATTT ATTGCTGCGA GTGGCAATCA ATATGCGAAG 720
 5 TTGAAGTCTA TTTTCGGGGA TAGAGATATG TATTTTATTT CTGAAAATGG TGCAGTTATT 780
 TATAATGGCA ATGAGTTATA TAATTATAAA AGCTTTAATC GTCAGGTGTT TCAACAGGTT 840
 GTCGATTACT TAAATATGAA GCAAAGTATT GATCAACTCG TCATCTGTGG TTTGAAAAGC 900
 10 GCGTATATTT TAAAACATAC TTCTGAAGCG TTTAAAGAAG ATACGAGATT TTATTATCAT 960
 CAGTTAAAAG AAATTGACAG TCTACAGCAA TTACCTGAGG ATGATTATGT CAAAATAGCA 1020
 15 TTTAATATTA ATCGTGAGAC GCATCCGAAT GTTGACGAAG AAGTAGCAAC GCAATTCAGC 1080
 AATGATATTA AACTTGTCTC AAGT 1104

(2) INFORMATION FOR SEQ ID NO: 819:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 819:

CCCnTTTTAC GGATTAAnGG CTTTTTCCTA TTTAAACCT ACGGCATTIT CTTTTCAACC 60
 30 ACGGCCGCTC CCATATGGAT GGTATnGGGA TTGGGGTTTA TAAAATGGGG ATTGGAAATG 120
 GTCCATCCTA AATACTCAGT TTAGTGCTTA TTTCTTTAG TGCTGACGAA TAAATATGAT 180
 35 CTAACCTCTAC GAAACCTAAT AACGTATCAA ATGCTTCATC ACCATTTTCA AATTTACTTA 240
 AACTATTTTT AAAATCATGT CGCAAATCCT CTAAATATAG TGATGGTTTT CGATCTACAT 300
 ACATTTTTAT ACTAACCTCC GATATATAAT CATCTTTATT GTACCTAACA TTTTATTAAG 360
 40 ATAATACTAA TACACTATCG AACTTTGGGC TGATACTGAA ACAGCACAAA GAAACTCAAA 420
 CAATTCGAAT TATGTATCAA AACCTTCAAT TACAGGAAGT GATTTTAAAA TGATTTAACG 480
 CAAAAAACA CCTGTTACCG TTATATAGGT ACAAGTGCTT AATTGATAGA GATGTTATAC 540
 45 GTCTTTAAAT GATTCCACAA CTTTTGGATG TGGACCATCC ATAAGCGGTT CTCTTTGTCTG 600
 AACGCCACCA CTTTGGTTGC CAATTGATTC GCTATCAAAG TACGATTTAT CTTGATTTGA 660
 TTGTTCTTGA ATATGTTCTT CATTATCAGT TGTTGCATAT TCACTATCCA CCTCTGTTTT 720
 50 TTCCATTGTT GCTGTATGGA ATTGTACGAA GTTCTCTTCT TCTAATGCTT TGATTTCTTC 780
 TTTGATAAC GCTCGATACC AATCTTTCGC TTTTTCGCC GCAaTAGGAa CAaCatCTTT 840

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TACTTCAAAT TCTTTCCATT TTTCGGGGTA ACCTTTCATT GTAAAGGGCA TTCCCTTAAC 960
 CTCCAATATG TTATAATTCA TGTTATATAC CACCATAATT ATAAAATGAA ACATATTAAA 1020
 5 CACAATTTTT TAGACTCCCG TCATAATAAC TTCAGACAAA CGTTAGTCTG ACCTGATAAA 1080
 TATTTAATTT TAAACGTTCT TGTCTCTCTC ACGAAAACCA TTGTGTTGAA TATTCATCAT 1140
 TGCTGATTGA ATATAATTAT ACTGTGGTAA ATCTGGTAAT ATCTTTATTT CTAATTCTGT 1200
 10 ATTTAATTCG AAATGCTTAG CGATGTTTTTC AAATATTGCT AAATACTCGC CCATTAATTG 1260
 TTCATTTATT GTAAGTCTAT CTTCAATTAGC CATGGCTCTA TTTAACATAA AGCTAATTTT 1320
 15 TTCTAATGCG AATAAGCTAG GATAATAATT TTGAATCAAT GTCTTATCAC TAAATAATTC 1380
 ACCATTAGCT GCATTATAAA CTGCGTGCA TGTTATTTAA TTTGC 1425

(2) INFORMATION FOR SEQ ID NO: 820:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 820:

nCGnCCTTAT ATATGTTTTT CATGTCCTAC AAAAAACGAA ATATTCCAAT TGCCTATATA 60
 30 CAGATATTCA TTAATGACAC ACTCAATAGC AACCATnACA ATATTATGTT ACCTATTTAA 120
 ATGAAATAGT TCTTTTAAAG AAATACATTT TTCACATATT AATCTATAAT CAAAATCAAC 180
 35 TGACCGATAT TCTATAATTT ATGATTAAAA TAAGTTATAA TATAATAGTA AAGATAAAGA 240
 TAGAGGTGGC TATAATGTGT GGACTTAGAA GTATAACATT AGGTACaACA AATATAGAAC 300
 AGACaAAACa TTTCATGGTT GACATATTAG GATTAAATTA TGAAGAACTT CTTGAAAACT 360
 40 CAATTCGTTT CGGCGATGCA GATATAAGCC CAGGAACAAG ACTTCAATTT ATACAAGTTC 420
 CAAGTGAGCA ATTAGAAGAA TCTCACTTTG TGGGTATTGG ATTACGTACA CCAACTGACT 480
 CAGGTTTAGA GGAGTATGCG GAAATATTAT CGAATAAGGA TATTCCATTT ACAACAGTTA 540
 45 AAGAATTAAA TGGCAATAAA TATTTCAAGT TCGAAGATAA CAATGGTCAT ATTTTCTCAA 600
 TATATTCAAA CGAGAATAAT TATGGCGTTG GTTTAGGTAT GCCTTCTTyT GAGAGTGCGG 660
 TCAATCCGTT ACATCAAGTG CAAGGTTTAG GACCACTGAT TCTTAAAGTG AATCATGTAG 720
 50 ATATTACAGG TCAAATTTTA ACAAATATAT TCGGACTTGA AGTATTTGCA GAATACCAAC 780
 CCTTCGACAA TGCTGACTAT CATGTCCAAG TATTCAAAGT TGGAACGGGT GGTCTAGGTG 840

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ATCAAGTTGA GTTTGAAACG AAAGATGCAG ATTTCTTTAA TCAAGCGAAA TCGCGCTTAG 960
 ATGAAGTGGG AATACCATAT CAAACGCTTG AGCAAGATGA TATTGAATCA ATTAGAaTTA 1020
 5 CTGAAAACAG TGGATTATCG TTTATATTCA CTTTACAAAA ATAATTTTTT TACGATAGCG 1080
 AGGACAAAAT TTATGTTACA TGAACTTGG AAAGAACGTA CACCAATCAA GAAAGTAGAA 1140
 GTCATTAATA CAGATGCAAA GAAAT 1165

(2) INFORMATION FOR SEQ ID NO: 821:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 821:

TCGCCCAATT ATTATGAAAT ATTCAATACA GTTTATTGAT CAAAAACAA AAATCCATTA 60
 TGAACCTTGT CATCACGAAT ATTAACGTAC GTTAGATGGA CCTCTTTAAT GATAGAACAA 120
 25 TTAATAAATA ATGCACTTAA GTATGCGAGA GGTAAAGATA TATGGATTGA ATTTGATGAG 180
 CAATCCAATC AATTACACGT AAAAGATAAT GGTATCGGTA TTAGTGAAGG nACTTGCCTA 240
 AAATATTTGA TAAGGGCTAT TCAGGTTATA ATGGCCAGCG CCAAAGTAAC TCAAGTGGGA 300
 30 TTGGTTTATT TATCGTAAAA CCAATTTTCA ACACACACAA ACCATCCGTT TCCGTCGTAT 360
 CTAAACAAAT GAGGGTACAA CCnTTACGAn TnCCATTTCC 400

(2) INFORMATION FOR SEQ ID NO: 822:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 760 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 822:

TGATATAATA CTTTTGTAAA GAAAAGCATG TGTGGGAGGT ATGACCTGTA TGTCGAACGA 60
 AATACTTATC GTAGATGATG AGGATAGAAT CAGAAGATTA CTAAAATGT ATTTAGAAAG 120
 AGAATCTTTT GAAATCCATG AAGCAAGTAA TGGCCAAGAG GCTTATGAAC TTGCAATGGA 180
 50 GAATAATTAT GCTTGCATAC TACTAGATTT AATGTTGCCT GAAATGGATG GTATCCAGGT 240
 GGCAACTAAA TTGCGTGAAC ATAAACAAAC ACCGATTATT ATGTTGACTG CTAAAGGTGA 300

TTCACCAAGA GAAGTAGTCT TAAGAGTTAA AGCACTTCTA AGAAGAACGC AATCTACAAC 420
 TGTAGAACAA AGCGAACCTC ACGCACGTGA TGTGATTGAA TTTAAACATT TAGAAATAGA 480
 5 TAATGATGCA CATCGCGTAC TTGCTGATAA TCAAGAAGTT AATTGACTC CTAAAGAGTA 540
 CGAATTATTA ATATATTTAG CTAAAACACC AAATAAAGTA TTTGACCGTG AACAATTATT 600
 AAAAGAAGTT TGGCATTATG AATTCTATGG TGATTTAAGA ACAGTTGATA CTCATGTTAA 660
 10 ACGcTTAGAG AAAAGTTAAA TCGTGTGTCT AGTGAAGCTG CGCATATGAT TCAAACAGTC 720
 TGGGGCGTTG GGTATAAATT TGAGGTTAAA TCTAATGATG 760

(2) INFORMATION FOR SEQ ID NO: 823:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 465 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 823:

25 CAAAGGAAAT TGCACAATTA GAAGACCGAT TACGTTACAG CTTTGAATGG GGGCTAATTG 60
 TTGATATTAC GCCACCAGAT TATGAACTC GAATGGCAAT TTTGCAGAAG AAAATTGAAG 120
 AAGAAAAAATT AGATATTCCA CCAGAAGCTT TAAATTATAT AGCAAATCAA ATTCAATCTA 180
 30 ATATTCGTGA ATTAGAAGGT GCATTAACAC GTTTACTTGC ATATTCACAA TTATTAGGAA 240
 AACCAATTAC AACTGAATTA ACTGCTGAAG CTTTAAAAGA TATCATTCAA GCACCAAAT 300
 CTAAAAAGAT TACCATCCAA GATATtCAAA AAATTGTAGG CCAGTACTAT aATGTTAGAA 360
 35 TTGAAGATTT CAGTGcAAAA mAACGTACAA AGTCAATTGC ATATCCGCGT CAAATAGCTA 420
 TGTcTTGTcy AGaGAGCTTA CAGATTTCTC ATTACCTAAA AATTG 465

40 (2) INFORMATION FOR SEQ ID NO: 824:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 824:

50 CACCGCGGTG GCGGACGCTC TAGAACTAGT GGATCCCCCG GGCTGCAGGA ATTCGGCACG 60
 AGGTAAGGAG GTCTCTGTAC CATGGCTCGT ACAAAGCAGA CTGCCCGCAA ATCGACCGGT 120

55

GGAGGGGTGA AGAAACCTCA TCGTTACAGG CCTGGTACTG TGGCGCTCCG TGAAATTAGA 240
 CGTTATCAGA AGTCCACTGA ACTTCTGATT CGCAAACCTC CCTTCCArCG TCTnGTGCGA 300
 5 GAAATTGCTC AgGACTTTaa AACAGATCTG CGCTTCCAnA GCGCACTATC GGTGG 355

(2) INFORMATION FOR SEQ ID NO: 825:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 1099 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 825:

TTCACCTGGC TTGTTGAcTG ACTTGTAaAT GATGATGTGC TTTGTGAATC GGATTGCTC 60
 20 GTGCTTGATC TTGTTGAGTT TGAGGCACTT TGGCTTGCTG AGTTTGAGTC TACTCCGCTT 120
 TGATTCATTG AGGCACTTAG TGACAATGAT GTACTCGTTG AGTCAGACAA ACTTGTAATC 180
 GTTGACGTAC TTGTACTTCC TGATGTTGAT TGAGACATAC TTATGCTCAT TGATGTTGAA 240
 25 TCGGATTTAC TTTCACTTGA TGATGTTGAG TCGGATTCAC TTTCACTTGT AGAACCCTT 300
 AATGATGTGG ATGTACTAAT GGAATCAGAT TTACTTGTAC TGATTGAATC ACTTGTCGAC 360
 ATTGATGTAC TTAATGAATC AGACTTACTA TCACTTGTGG AATCACTTAA TGATGTTGAC 420
 30 AAACCTGTAG AGTCAGACAA ACTTGTAATC GTTGACATAC TCAGTGATGT TGAAACACTC 480
 TCGCTCTTAA ACGTTGACGT TGATTCCTG ATACTTGTCG ATGTTGAAAT GGACGTACTA 540
 CCACTTGTTG AATTACTTAA TGATGTTGAT GTGCTACCAG ATTCTGATGT ACTGTCTGAT 600
 35 AATGACGTAC TCTCACTTGT CGAACTACTC ACTGACTCTG ATGTTGATTC AGACGTACTT 660
 TCACTTAATG ATTCACCTAA AAAGGCAGAT GCACTTTGTG ATTCTGAATC GCTAGTACTA 720
 TTTGATTCAC TTAATGATAT AAACGTGCTC TCTGAAGCAG ATATTGCTTC ACTTATAGAG 780
 TCGCTCGTTG ACGTTGATTC ACTTATTGAA TCAGACTCTG ATGTACTTAA GCTTGTTGAA 840
 TCACTCaTAG ATGTTGaTGT ACGTTCTGAA TTACTTGTAC TTAACGATGT CGAAGTACTT 900
 45 ACCGAACCAG ATGTGCTCGT AGAAGCACTT TgTGATATTG ATTCACCTGA TGCAGTTGAT 960
 GCTGATTTGC TATCACTCGT TGAATCACTA AACGACGTTG ATATGCTCaT TGAATCGGAT 1020
 TGACTTGAC TCAntGAACC AGACGTACTT TGTGATTCCG AAGTACGTAC TGAAGCACTT 1080
 50 GTCGACGTTG ATGTACTTG 1099

(2) INFORMATION FOR SEQ ID NO: 826:

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(A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 826:

10	TATGCGTATC CTGATAGTCA CTTTGATTTT GATATGGAAT TAGCGAAAGA GCAATCTCAA	60
	GACAATCCAG TTTACTATGC TCAATATGCA CATGCGCGTA TTTGTTCAAT TTTAAAACAA	120
	GCGAAAGAGC AAGGTATTGA AGTGACTGCT GCGAATGATT TTACAACGAT TACTAATGAA	180
15	AAAGCGATTG AATTGTTGAA AAAAGTAGCT GATTCGGAnC CTACAATTGA AAGTGCTGCT	240
	GAGCATAGAT CGGCACATAG AATTACTAAT TATATCCAAG ATTTAGCCTT CTCATTCCAT	300
	AAATTChATA ATGCTGAAAA GTGTACCACT TGGTATTG	338

20

(2) INFORMATION FOR SEQ ID NO: 827:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 838 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 827:

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	GTATTTTCTT TCGCGAATGA TTTTATTACT TGAATACCAC GAATAACCTC CAATACCTTT	60
	TCCACTAATT GGTPTTGTAC ATTATGATAC GcTGCGCAT TTTGTCGACT CTTTCTTTCT	120
35	AATAATTGAA TCGCAAAAAA TGATAGTAAT ACGCCAATGC ATGCTAATAA TGATACTGCG	180
	CACGAACTA CAAGTAGAGA CAATATGAGT ACTGTAATTA ATATGTATCC ATTAACAACA	240
	ACGTCCACCA TTTTCATAGC AAAGTTTTCT AAAAAGGTTA AATCTGTTGT TACTATTGTT	300
40	GTAACTCAT TTGAATGATG CGAATTAAAA TAACCTAACC TTACATTTT CAATTTATCC	360
	CCTATATCTA AACGTTCTTT CGCACTCATT TCATAAGCGA TGCTCTCATG GCTTTTGCTT	420
45	TTGAAATATG CTGTAATAAA TCGTCCAATC ACTAATAAAA CCATGATAAT TACAACATTC	480
	AATATATCTT TCATATAAAT AGGTTTATGA GATAGCACAT TATTAAATAT TTTTGCAGCT	540
	AAAAAGATAG GTAACGCAAT AAAAATAGCA TTTAAAAATG ACATGCTAAA TCCTAAAATC	600
50	ATTCTTGCTT TATATGGTCT TATCCAGTTT AAAATTTTAA ATGTAATTG AAACATATTT	660
	GACCTCCTTT TCTCATTAGT TTAATTATGT CCAGTATTGA TTCCCAATC TTTTGTATGC	720
	ATGTGCGTAT CCCACATTTT CTTATAATTA CCGTTTAATT TTAGCAATAA GTGATGTGAC	780

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(2) INFORMATION FOR SEQ ID NO: 828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 898 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 828:

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TCCnAAAGAA GAAATAaCAT TATCATaAAA TCCATTGAAT ATAAATTCAG TCATCCCCTC      60
TGAACtCTC CATAAATATA ATGGTGAATA AGTATTTGTA ATGCAATTAG TAGTTGTTTG      120
ACTTATTAAA TAAGCTTTTA TAATTAAATT TTTAAATCCA TCAGTCTTAT AACCATTTAA      180
TCGAACTCTA TCTCTAATTA TTTCCATATT GTAATCACTA GGCAACTTAA CATGATATTG      240
CATTGCATGC ATTTAGCATA CCCCCTTTTA TAAAAGGAT AGCAATAATA AGTAAAATCT      300
CATATTATCC AATTGTGATA TAGTTATCAT AAAAAGTGAT AGGTGATTAA ATTGAACTTT      360
AATGATTTGG AAATTTTTAT AACTGTATGT GAAGAAGCAT CTATCAATAA AGCTGCAATT      420
AAACTTAGAT ATGCACAATC TAATATATCT CAAAGAATTA GCAAGCTTGA AAATGAATTA      480
GGTGTAGTTT TGCTTTTTAG AAATCAAAAA GGTGCTAAGG CAACTAAAGC AGGCGAAGAA      540
TTCTTAGCGT ATAGCAAAAA AGTATTAAGA GATACAGAGA CTATAAAAAA TAAATGAAA      600
AATAATACTA TGTCTATTTT ATGCTCAGAA CTGTTATTTA ATTATTTATC TGAGAGCGAA      660
GAAATTATGA TGTCGAATAA CTCAATTAAT TTTATTCTA GTGGAAATAT TAGAAAAGCT      720
ATAGAAAAAA ATAATTATGA TAAGGTTATT TCATTCATAA AAaTTAACGA CTCAAATTAT      780
AGACTTAGTA ATGTTGATAC TATGaaAGTA ACGCTTTACA GTAATGGAAG TAATTATGAT      840
AAAGAGGCTT TACTAATAAA TAAAGATGAG TTTGGTCCTT TAAGGnAAAT AACTTTAG      898

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(2) INFORMATION FOR SEQ ID NO: 829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 798 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 829:

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AGTAGGAGTC ATAAATCGn ATTTCAAAG CAATTAATGC AAAATACTGA GTCTACAGTG      60
CTATTTGCGA AAGCGTCcAT ACGAAgTTGA GcAATGCTAA TAATAATGGT CTATCAAAAA      120

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AATATGTTGA TAGTTACACT GATTCTCTTA CTGGAGTAAC AACTTCTGCT TTTTAAATA 240
 AAGATACAGG CAAAGTAACT CTCGGGATGA CTGGGACTAA TTTACAAGAC GAAGCCTTTA 300
 5 AAAAGTTAAA AGAAGGTGAA TTTTCAAGAC AAAATGTTAC CAATGCTTTG GAAACAGTTA 360
 AAGATGGATA TGCAGATCTT AAAATATTAT ATTCTCCTGC ATCTGATCAA AACTATAGAT 420
 ATGCGAATAC ACAAGAATTT ATAAATAAAA TAAAAAGTAA GTATGACATT GATTTTATTA 480
 10 CTGGACATTC ACTAGGTGGA AGAGATGCGG TAGTTCTAGG AATGAGTAAT GGTATTCCGA 540
 ACATTGTGGT TTATAATCCA GCTCCTATTT CTATAACTAG TTTGAATCCT AATTCCCCAG 600
 ATGGAACG TTTATTAGAA TTATATAAAA ATTATAAAGG TAATATTACT AGGTTTGTG 660
 15 CAGAAAATGA TGCATTGACA GAAATCTGA AGAAATATAA GCATTATGTT TTTTTCGGTA 720
 ATGATAAAGT CTTTAAAAAT GGTAAAGGTC ATGAAATGKA AGGCTTTCTG ACCGAAGAAG 780
 20 AACAAAAAGC tATAAAAn 798

(2) INFORMATION FOR SEQ ID NO: 830:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 830:

AATATCAATC TCTTCATAAG CTGAATTATT TTCATGCACT TCTTGATGTG ATGATTTGTC 60
 35 ACGAACnGCT ACAACTAACA TTTTATCGTC TAAAATAAGT TGTTTATATT TTTCTAATTC 120
 ATCAGGCGCT AAGTTGTAGC GTGATAAAAC TGCATGTTCA CCATCTTCTC CTGTAAACAG 180
 TTTAGTCATT CTATCACTAA ATGTTCCACT TGTGAGATA AGGGGAGATT TCAGAGTCGT 240
 40 GTAAGTCATT AGGTGTAATT TACTTTTACT AATAATTGTT AGCCTGATCT AAATAACTTC 300
 AGATTCTTTG ATTGATAnGT GnATAATCGC AGTGCATTAC ACAGAATACT GCCAAGTGCG 360
 CCCTTAAAT TGTTATTAnC TTACCTCTAT ATAAGAACCC 400
 45

(2) INFORMATION FOR SEQ ID NO: 831:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

AAGTCTGCAT GACTTTTATT TGCAAGTTCG ACTGCTTGAT CAAAAGCGCG ATGATCTTCA 60
 GGATTAGCAC TTTGAACTGA GCTGAAATTC GGATCAGGTT TACATTGTGC TTCTACAAGA 120
 5 TTA AATTGAT TGAAATTCAA AGATTGTAAT AACTCAGGTA CAATCGGAAC ACTTGTACCA 180
 TGCAAACTAG TGAACACAAC TTGTAAATCA GATTTAGGAA TATAGCCAAT CATATTTTGA 240
 ATGTGTTTCA TATAGTCATC AGTTACAGAT TTCGGAAAAG GCTTGaTATA AGATGTATTT 300
 10 TGTTTAGAAA tAGGTATATC AATCTGTAAT GGATCGCCAA CTTCTTCGAT ATAACGACTT 360
 GCAAGCTCAG ATGCATCAGT CGATAATTGC GCACCATCAG AACCATATAC TTTGATGCCG 420
 15 TTATAGTCTT TCGGATTATG ACTTGCTGTA ATCATAATGC CAGCAGTAGT ATTAA 475

(2) INFORMATION FOR SEQ ID NO: 832:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 724 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 832:

CTTGAATTGA AGGATACGCA AATGATGCAT AATCAGCTTC TGTATAAAGC TGTAATGTAA 60
 30 TGTCAATCAAG GTCACCTTTT CTAACAAGCA CCTTATTAAT AGAAGTATGA TTCGCTTGCC 120
 AAGTACCTTG ATTATTTTGT TCTAAATGAA TGACTTCGCC TAACGATTTT AACGTAATAT 180
 CTGCACGCTC GTCTTCGCTA ATAGTATATG TCTTACCATC TCGCAAATTG AGCATCTTCA 240
 35 ATTGTTTGTT ATATTTTATA ATCAATTTAT GCATTGTCTT TGCCTCAGTC CTATACTATT 300
 TTTTCTTTT AGCTTCTTGG CGTTTTTCTT TATCTTTTGG TGCTTGTTCT TTTTGTCTT 360
 TTTGTTCTC TTCTTGTTGC TTTAATTTCT CATCTTTTCG TTTTGCTTTC TCTTCTTCAG 420
 40 ATTTGCTTTT TTCATCTTTA ACTTGTTTTT CTTTGTCTAA AATATCTTGC AATTTATCGT 480
 TATACTTTTT CGTTTCTTCA GAACGTTTAT CATTCGATAA ATCTCCGTTA TTTTAAATCT 540
 CATTTAATTT ATTAATCAAC GCTAACTTTG TAATATCGTT ATCATCTAAA TAAGTGGCAA 600
 45 TATTAATCGC TTCATCAAGA TGTCCTTGTC CTAATTCAT CCAATATAAT AAGTAGTCTT 660
 TGTTTGAATT TGGTGTGACA TTATTAAGTA AATTTTCTTT CGTATCTGTn TCTAAACnT 720
 50 GTTn 724

(2) INFORMATION FOR SEQ ID NO: 833:

(i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 994 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 833:

	AGCAGTTTGG CTCGTAGAAA TCTCCCGTCT CTATTCTATG TATTAACTTT TATTATATTT	60
10	GTTATGATAC TATCGATATG AAAGCGTTGT CAATGGTTTT TGTA AAAATT TTGTCAAATT	120
	TAATTTTTCA AGTCTTTATA AAAGTAGTTT AATTTGAAAA CTAGAAATAC CAATCCTAAC	180
	TAATTTATTT ATGACGCTCT TTTGTTTAAT TGACATTCTT CAGCCATATT TTTTATGACT	240
15	AGTTGCATTT TTTACTAATA AACACCTCTA AAACTTTAAT GATTTTAATC GTTTTAGAGG	300
	TGCTAATTAT TTTATTTGAT TATTTTTTGT TTGATACCTA CTGCATATCC CATATGAAAA	360
	CGGCTTTTTT ATTATGTTAT ATGACTAAAT CTCGTGAAAA ATGAAATTTT TGCAGACTTA	420
20	TGATTTACCA AAGTTTATCA TAACTAGTAG TTACATATTT CGCTCCATTT TTAACAGCTT	480
	CATTGACTTC ATCTATTGTA TTAATTAGGC CACCTGCAAT GACTTGTGTG TTTGTTTCTT	540
25	TCTGAATATG ATGAATCGCT TTA CTGCAA CACCTGGAAG TACTTCAACA AAATCAGGTT	600
	CAACTTTTTT TATCAAATCT ATACTGCGTT TCAATGCTTG ACTATCAATA ATAAATACTC	660
	TAAAAATCGT TAAAGTATTT AATGATTTAG CTTTTTTTAT TACTTTAGAT TTAGTCGATA	720
30	CGATACCTTT TGGCTTGTAT TGCTGAATAA TAAATTCAC TGC AAATTC TCGTGGCTTA	780
	AACCTTTTAT CAAATCTATA TGAATAAAAC ACTCTATATG ATTTTGCTTC AGCAATTCCA	840
	TAATACTTTT TATATGTCCT ATATGCATAT CTAGAAGCAC ACACATTTTA TAGTCTGTnT	900
35	TAATCCAGTT TCTCTAAATC nTTAATGTTT CCTATAAGCA GGCAATATGT TGTTAATTCA	960
	CTnGATCCAT CCTCTCTACA TCACACGCTT AAAT	994

40

(2) INFORMATION FOR SEQ ID NO: 834:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 783 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 834:

50	Tc nACAAAGT CGGTATTAGG CTATGGGCCA TTTnACTATT ATA ACTAATC GGAAATATAC	60
	CACATAACAT CATTATTGAG TTGATTCTAT CATTTGCTT ATTAGGGTTT TTTATCATAA	120
55	TGATTTGCAT TTTGCTACTA GTTTATAAAA TGATTAGGAA CTATGATCCA AACACTATAG	180

ATTTAGTTGT AAGTGAATTT TGGTTTGTGT TGTCTATTT TATTACAAAA GGACGGCGTC 300
 ATCATGGCTA AGAAAGTTTT TATTATGGAT AGCGTAAAGA CAATAATTGG TACGTTGCTT 360
 5 ATAGCTTTAG GATTACAATT TTTAGCTTAT CCAATTATTA ATCAACGAGT AGGTAATGAA 420
 GCGTTCGGTT CTATTTTAAC GATTTATACA ATAATAACAA TCACGAGTGT TGTATTAGGC 480
 AATACGCTTA ACAATATACG mTTGATTAAT ATGAATCTAT ACAAATCCAA TCATTACTAC 540
 10 TGGAAATTG CATCGATACT TTTAATCTCA ATTCTGATTG AGAGTATAGC TTTAATTATT 600
 GTATTTCTTT ACTTTTTTAA TTTGAACATC ATCGATATTA TCTTTTTAAT TCTACTTAAT 660
 15 ATTTTAATGT GTTTAAGGAT TTATCTGAAT GTATTTTTTA GGATGACTTT AAAATATAAT 720
 CAGATTTTGT ATATTGCTCT TATTCAATTT TTAGGTTTGC TGATAGGACT ATTTCTATAT 780
 nAT 783

20 (2) INFORMATION FOR SEQ ID NO: 835:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 794 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 835:

30 TTACCTAATT TTTCAATCaT AAGATTCCCC CTATTGTTTA AACaTAAAAA TATTATaCGA 60
 TTAAGCACGA GmCACTTCAA TATATTTTTC AGAATATTCT TATAAATATT AATATGATCA 120
 35 TTTCATATT TAAACACGTT TAATATTAAA ATAAGTTATT CATATAAACT GGTGCTGTTT 180
 GATCCAATTG CAGACTTACG AGTCATTGAA AAGTCTCACA AACTATTGmA AGTAAAtATC 240
 TTAAATAGA AAGTGAATGG TTAATTAAAG TATATTTmAA AAATATTAAC CTTTTTAAGC 300
 40 ACTGCTATTT AGGATATACT AAATAATAAC TAAGTTTAGA AAAATAGGAG GAACATCGTT 360
 TATGTTAAAC AAGGTTTGGT TCCGAACCTG CATCGCTCTG ATTATGCTGT TCATTCTCAT 420
 CAACTATTT ATGGAAGTGC ACGAAGTATT TACTCCAATA GCTACAATCA TCGGTTCTGT 480
 45 ATTTCTTCCA TTTTAAATTA GTGGTTTTTT ATTTTATATC TGTCTACCTT TTCAAAACTT 540
 ACTTGAAAAA GTCGGTTTTT CAAGATGGGC TAGTATAACA ACAATCATGT TAGCTTTGTT 600
 50 TGCTATTATC GGCTTAATTG TTGCGTTTGT TGCACCAATC ATCATTTCAA ATATCAACAA 660
 TTTAATTAGT CAGACACCTG gCCCTACAAA AAGGAAGCAG AGCAAATTAT TAAATTCGCA 720
 CTGGCTCAAA TGGnTAAATT ACCTGGAGGA TGTAACCAng TGGATTACCA ATATGGTAAA 780

55

(2) INFORMATION FOR SEQ ID NO: 836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 836:

TGTTTATACT GTGCCTGAAT TAGAAGAGGT TTAAACACCT ATGAGACAAG ATGGAACCTCG 60
 TGATATTTAT GTTAATTTAG AAAATGTGAG TtATATGGAT TCGACAGGTT TAGGTTTATT 120
 CGTAGGTACA TTAAAAGCAT TAAACCAAAA TGATAAAGAA CTATACATTT TAGGTGTGTC 180
 AGATCGTATC GGTAAGTAT TTGAAATTAC TGGTCTTAAG GATTTAATGC ATGTTAATGA 240
 AGGAACGGAG GTCGAATAAC ATGCAATCTA AAGAAGATTT TATCGAAATG CGCGTGCCaG 300
 CATCGGCAGA GTATGTAAGT TtAATTCsTT TAACACTTTC tGGCGTTTTT TCGAGACTGG 360
 TGCCACATAT GATGATATTG AAGATGCCAA GATTGCAGnT 400

(2) INFORMATION FOR SEQ ID NO: 837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 837:

ATTGATCCAT TTTGCGGTTC GGGTACAATA GCTATAGAAG CTTGTTTAAT TGCTCAAAAT 60
 ATCGCACCTG GTTTTAATCG CGAGTTCGTA TCAGAGCAAT GGAACATCAT GCCAGCAAAT 120
 ATTTATGATG ATTACCGTGA TGAAGCGGAT AAGATGGCTG ATTATGATAA AGAAATCGAA 180
 GTATATGCTT CTGATATCGA TCCAGAAATG GTAGAGATTG CTAAGCGTAA CGCTGAAGAA 240
 GTTGGGTTGT CTGATATTAT TAAATTTAGT GTAAAAGATG TCAATACATT AACAATTGAT 300
 ACAGAAGAAC CGGTGGCGTT AATTGGAAAT CCTCCATATG GTGAACGTAT TGGTgaTCGT 360
 GAAGAAgTtG AAGAAaTGTA CCGTTATATT GGTAaACTAA TGAACAACA TCCATTTTTTA 420
 TCTACATACA TTT 433

(2) INFORMATION FOR SEQ ID NO: 838:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 926 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 838:

	ATTGGGCCAA CTAATCCTGT ATATCCAAAT CCAGCAGACA ATGGTGTTC TTTAACCTGA	60
10	AGAACGTAAG CAATGATTCC AGTAATTATT CCATTTATAG TCAATGGTAT CGAAATAATT	120
	AAATTTTTC AGTAACTGG GATCATCATT TTTGCAGCTC CTATGAGTAA AACTGCATTT	180
	ACACCAATAG AATTGACACG CAATGAGCCA AATAAGAAAG TAACACAGGC AGCCACTATA	240
15	CCTAGGTTTG CTGCTCCACT TCCTAGTCCG TTAAACTAA TCGCAGTTGC AATCGCTACT	300
	AACGATATTG GTGTTACCAT TAATAATGAA AATGCCACAC TAATAAGTAT AGACATTAAC	360
	AACGGATTTA AGTCTGTAAA AGAATGAATT ACATTTCCAA TTGCTTGAGT AATTTTTCGA	420
20	ATGTAAGGTA ATGTGATTAG ACCGATACCC CCACTAACGA TAGGTACTAA AACTGGTAAT	480
	ATAATTAATT CAAAAGATCC AAGTTTGTTC TGTAATACCA TATATATAAG ACATGCAATA	540
25	ATAACAACCA AACTCGTATT TATAATGtCa CCTATACCTT TTAACATAAA ACTATTATTG	600
	CTATATACAA CAGCACCTGA ACCAATCATA GCTGATGTAC CTACTATAGC AGCACCTGCA	660
	CCATTAAATT TAAATTGATG AGCAGCTAAA ACCCCAATAA TAAATGCCAT AAATGATTGA	720
30	ATTAGTATCA CTAAGTATA CGTTAATTCT AAAATTTTCAT TACCACTTTT AAATATTTTt	780
	AATACTTCAC CTAATAAAGC ATTCGGAACA AGTGCAATAA CAACACCAGC ACCAATAGAA	840
	TTTAAAATCT TACTGAAAAA CTGTTTATTA TCAGCATTAT TTGCGTTACT CATAAACGAC	900
35	CTCCAATTTG AACATTAnAC TCATCA	926

(2) INFORMATION FOR SEQ ID NO: 839:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 839:

	CTTCGAAACG TACTTGGTCA TTCCCTTTAC CAGTACAACC ATGTGCAATA CCTACTGAAT	60
50	TTGTTTTCTC AGCAATCTCT ACTAATTTTT TAGCGATTAA TGGTCTTGAT AAAGCTGAAA	120
	CTAATGGATA TGCATTTTCA TACATTAAAT TTCCTTTGAT TGCATAACTT ACATACTCAT	180
	CACTAAATTC TTTTGTGCA TCAATAATAT GACATTCAAC TGCTCCCAT TCTAAAGCTT	240

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CGTATCctTT GTCGATAAGC CATTGAACGG CCACACTTGT aTCTAGtCct CCKGAATATG 360
 CTAACAAT TTTCTCTTTC ATAAAATTCA CCTCATTGTA 400

(2) INFORMATION FOR SEQ ID NO: 840:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1043 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 840:

GGATCGCGGT GTTGTGCTTG ATATACTTTG TAGCGATAAC GTTTACCTAC ACAATCATAA 60
 CGACAATGAA AATCGTCATC GACTGTAACT ACATTGTTGA CATAAATATC ATCAGGTAAC 120
 GTTCGGTTCA TTGCATATTG CCATTGTGAC ATAGGTATAT TCAGCTCTGT GTCGAAATGA 180
 AAGTATTGCT GTATCGCATG TACACCTCTA TCAGTCTTAC TTGAAGGATG GATTCTCACA 240
 TGTCTTTTAT GCATGCGTTG TAATAGCTTT TCAAATTGTT GCTGTACCGT TCGACCATTT 300
 TGTTGAATTT GAAAACCTAG AAAATTATTT CCTTGATACG CAATTTCTAC TAATATACGC 360
 ATGAATTTAC ACTCCTGAAT ATTTTAATAC GAATAAAATA ATTGCAATTG GGATAATCAT 420
 GGTTAAAGAT ATCGTATCTC TCAATTGCCA TTTAAGCTGT CTGTAGCTCG TTCTCTTAAC 480
 ATTGGCATCA TAACCCCTAA CTTCCATTGC GACCGCTAAT TCTTCGGCGC GTTGGAAGC 540
 TGAGATGAAT AGTGGCACTA GTAATGGAAT AAATGATTTA ATACGTGTTG CAATGTTCCC 600
 TGAACCTATT TCAGAACCAC GCGACTTTTG CGCCAAAATG ATTTTATCTA ACTCATCCAT 660
 TAACGTCGGG ATGAATCGTA ACGCAATGGA CATTATCATA CTTAATTGAT GAACTGGTAA 720
 TTTAAACATC tTTAGTGGTG CAAGTAATCT TTCAAACGCA TCTGTAAAT CAATTGGACT 780
 TGTAGATaGT GTCaTAATTG TTGCAATCAT TAcAATCCCA ATTAAACGCA GTGrTATATA 840
 TAGCCCTTCT AAAATACCAT TAGTTTCAAT CGTGATGCCA TGCCATTCAA CTAATACATA 900
 TCCACCTTTA GTTAAAAATA TATGCATCAT TAATGTGAAG ATTAAAAAGA AAAATATTGG 960
 TGTTAAACCT TTGATTAGGA ACCATAATTG AATTTTGTCT AATCTCATAA TGAAnAnGAT 1020
 AAGTGCAAAC ACCCAAAGAT ATG 1043

(2) INFORMATION FOR SEQ ID NO: 841:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 343 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 841:

5 TCGAAATCAA ATTATAATAG ACAATTTT TAG GAGGTGGACT TTCGATGACC AAAGGAATCT 60
 TAGGAAGAAA AATTGGGATG ACACAAGTAT TCGGAGAAAA CGGTGAATTA ATCCCTGTAA 120
 CAGTAGTAGA AGCTAAAGAA AATGTTGTAT TACAAAAGAA AACTGTAGAA GTTGATGGAT 180
 10 ACAACGCAAT CCAAGTTGGA TTTGAAGACA AAAAAGCATA CAAAAAGAT GCAAATCTA 240
 ATAAATATGC TAATAAACCA GCTGAAGGTC ACGCTAAAAA AGCTGACG Cn GCACTGAGAG 300
 nTCCCCTCAT AATTTCCTCCA AnCGTAACCA TGTGTGAATA AAT 343
 15

(2) INFORMATION FOR SEQ ID NO: 842:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 430 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 842:

ATGAGTATTT TAATGATGCG CTACGAGCGT ATGGTCTTAC TGTGAnAACA GGTGAATTTG 60
 GAACACACAT GAATGTTAGC ATAAATAATG wtGGwCagTC TCTGGTAGTT TAGAATTAGA 120
 30 AGAATTAAAG CAATTTAGAC AATGGGGTTC TAAAACACCA GGTCATCCTG AATACAGACA 180
 TACAGATGGT GTAGAAGTTA CTACCGGACC ACTTGGACAA GGTTTTGCTA TGTcmGTAGG 240
 ATTMgCTTTA GCAGrAGATC ACCTAGCAGG GAAATTTAAT AAAGAAGGAT ATAATGTTGT 300
 35 AGATCATTAC ACATATGTAT TAGCTTCTGA CGGTGATTTA ATGGAAGGTA TATCGCATGA 360
 AGCAGCTTCA TTTGCTGGAC ATAATAAATT AAGTAAATTA GTTGTTTTAT ACGATTCAAA 420
 40 TGGATATTTT 430

(2) INFORMATION FOR SEQ ID NO: 843:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 843:

GGACTGCCCG ATGATTTGAC AAATGAATTG CTGATTTGAT TTATATATTA TCTGnAATTA 60

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TCATCTATCC AACAAATATGT CTTATCAATG GTATAGTCTT TGCACACCAA TGGAGGnAAA 180
TAAATCTCAA CCTTACTATA TTAATATATA ATCAAATCTT AGATTAACTA GTGTAATGAT 240
5 ACAGATGGAT AATTGAGTAC AAATTTAAAA CCCTGAGATT TTCGCTTTAA TTTGAAAACC 300
TCAGGGnTTA TTTGATTTTT ATATAATGA 329

(2) INFORMATION FOR SEQ ID NO: 844:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 844:

20 AGATGAAGAA AGTGTTCAT CGATTATCTT AACAGTTGTT GCTTTATATA CTACanTTCT 60
TCCTAGATCT TGTACCGTTG AAAAGAGACC TGGTTGTAATG ACATTTTCAA 120
TCACCACCCA GTCATCAACA TTAAAGTTGC CATCTGATAT ATCTCTTTTCG ATTTGTATAA 180
25 ATTTCTGTTT ATCTATTGCA TAAAATTGTA TCCATTCTCC TGCTTCGTAC ATTGACATTG 240
GTTACAGCTC GCTGCTAAAT ACTTTTAACG GTGTGCGTCC AATAATTTGC CATCCGCCAG 300
GGAAATCTGA TGGGATATAG TCCTGTTTGA TTATTGCGAA TACCTACAGA ACCTGGCATG 360
30 AATTTTTTAA CCTTGGGCnG ATTACGTCTA nGGnGTATGT 400

(2) INFORMATION FOR SEQ ID NO: 845:

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 535 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 845:

CATAAGTCCA GTAACCTTCA ACTGTGTCCT CATCTTTAGT TCCAAATATA TCAACGTATT 60
45 TATTTCTTAA CTGATTAAATG TTTCCCCAAC TCTCGGATCC AAACACTTGA ATATGACTAT 120
ACCAAACCCA CGTTTGCAAT GTTGCAATGAA TGCTACCATT GGGCTTTTGC CATAACCATT 180
TTCCAGATAA TGAAAAATGC GGCTGAGTGT AATATTTGAT TAGTTCATTG ATATTAGTCT 240
50 CGTTTTCACT GATATTATAG GCTTTTGCTT CAGATGAAAA ACTGATTGGT GTTTTAGGAA 300
GTTGTGTTGA TGTAGTTTCT AAAAGTAACA ATGCTGTTGA TAAACTAAT TTATTCATGA 360

ACCGATTCCG AATTAAATAA AAGCTAAAAC TATGTTAAAT AAACCTAAAC AGTTAGTAGT 480
 GTTATTTAAG CAAAACCTTAT CATTTTTAAG TTGGACAGAA CAGATCAATA AGAGC 535

5 (2) INFORMATION FOR SEQ ID NO: 846:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 509 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 846:

TCAATCGATC AAATGGTGAT TGACCTTTTA AATTTGTATG ATCAAAATAA TGATTGTTGG 60
 CCATATCTTT ACTATGCTTA CGTGCAGTTT CAGAATTCTG TTTAGAATAC TTCAATGTAG 120
 20 ATAATTGATG TTGTTTTCTT TCAGCATTAA CTAAATCAAA ATTTTGTAGT TCAAAACTAT 180
 CTGCAAGCGA TTTCGATGGT GTCCTATATT GTTCTTTTAA TCTATTTTCC ATAGCATCAC 240
 TTACTTGTA AAGAGCTGTT ACATTATTAC GTCGATGCTT ATCATAAAAT ACCGTCGTAT 300
 25 AAATGTGATT TTTATGGAAA ACATCATATT CTTTATTATT TTGTTTCGTAA CGCACTCTAC 360
 CTTTAACAAT CTCTGTTTCT GGTTCGCCTA ATCTTTGCCT TACAACCGAT TTAGGTGTAT 420
 TGTATTTAAT TTTTGATTTT GAAGTGATTA TATTTTGATT TGTATATAAC GCATTAACCT 480
 30 TATCTTTCAT GTAACCTATC ATTATAAAA 509

(2) INFORMATION FOR SEQ ID NO: 847:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 847:

CGTATTGATC TATAAATAGT GTTTAGATGC TATAGTCGGA TGCTTAAGTA ATTTAAAGAA 60
 45 AGTATCTTTA ACATCGATGT GTGTATAATC ATTTTITAGAA GTATTATAAT CTTTTTCTTC 120
 TCCCTTCTAA AATATATACA GGTGCTTCAT CAGCTAGTGG TTCAACTGGA ATGTCAGCAT 180
 AAACCTCGCA TCATATGTTA AACAAAAACG ATTGTATCTG TACTTCACCT ATAACAGCAC 240
 50 TATCCAATTC GTGCTTATCA AATAAACTAA GATTTTTGTC AGTACCTTTT CACAACCTAGT 300
 ACATACGTCT TGAGTTCTGA AGCATCATTT CATAAGGAGA ATACTGGCCA CGTGTGGACT 360

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(2) INFORMATION FOR SEQ ID NO: 848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 848:

TACCACTTGA ATACATTGCA TATAAAATAC GACGTTGTAC TGGTTTTTAAA CCATCACGAA 60
 CATCTGGCAA TGCACGCTCT TGAATAATAT ATTTACTATA TCTTCCAAAG CGATCACCTA 120
 AAACATCTTC AAGTGATAAA TCTTGAATTA TTTCCTCAC TAGATTTCTT CCTCATCAAA 180
 TTGATCATTT TCAAGCACTT GTACTTCAGA ATTATCTAAA ATACTTTGGT CCTCTTGCAT 240
 ACCAAACTCA ACATGCTTTT CAATCCATTC ACGTCTAGGT TGTACTTTGT GCACCCATTG 300
 AATGTTGTGA CACGTTTAGA TGAACGCAC TTGCATCTTG CAACTTGTGA CACGnATTGA 360
 AAGTTnCGTG TTTGCGGGGG TTnCACGCTC GTTTGCCCCAT 400

(2) INFORMATION FOR SEQ ID NO: 849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 849:

TTTATATGAT TTATTTGAGG AGTTAAGAGA TTTATTTAAA GAAGAAGATT TAGAACCATG 60
 GACATCATGC GAATTTGATT TTACAAGAGA AGGTGAATTA AAAGTTTCAT TTGATTATAT 120
 TGATTGGATA AATTCAGAAT TTGGTCAAAT AGGTCGACAA AATTACTATA AGTATAGAAA 180
 ATTTGGAATT TTACCAGAAA CGGAATATGA AATTAATAAA GTTAAAGAAA TCGAGCAATA 240
 TATTAAAGAG CTAGAAGAAT AACTATCTT AATGTAAGAC TAAACAATAA AGCTTTGTTT 300
 AGTCTTTTTA GCGTTTAAGT AAAAAGCaAT AGATACCGTA AAGTTGATGC TCATCAAATA 360
 ATAATATAaA GATAATTTTA GGTTTTTTAAA CTTTTAATCG 400

(2) INFORMATION FOR SEQ ID NO: 850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 923 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 850:

5 CAGGCCATAC TTACAATTTT GGCCATCGTC CGGATGTATT nGGAATCGTT GGATAATAAG 60
 CATCAAGGTC GTGACTATTT CGTAAAATTC CAACTGTCCC AGAATTTACA TCATTATGTC 120
 CAATTACTGG GCAACCAGAT TTTGCCAACT ATCTATATtT CaTATATTCC aAATGTTAAA 180
 10 ATGGTTGAAT CAAAATCTTT GAAATTATAC TTATTTAGTT TCAGAAATCa CGGTGATTTT 240
 CACGAAGATT GTATGAATAT TATTATGAAT GATTTGATAG AGCTTATGGA CCCACATTAT 300
 ATTGAAGTCT GGGGCAAGTT CACACACGTG GTGGAATTC TATTGATCCT TATACAACT 360
 15 ATGGACGTCC AAATTCTAAA TATGAAAAA TGGCTGAGCA TCGTTTGATG AATCATGATT 420
 TATATCCCGA AAAAATAGAT AATCGTTAAA TGTATCATTT AATAAACACA CCAATAAGTT 480
 20 GATTTTCCTA ACTTATTGGT GTGTTTTTCA TTTAGCATAC ATAATAGGTT ACATTAAAAT 540
 AACATTTTAT ACCAAAGTAC ACCAAAAGAA TATTAGTACA CGAATTAAAC AACATTTTTA 600
 TAGAAACCTA TTGCACTTTA ACGTCAATAA GTATATTTTT ATATTATCTC TAATTAATTG 660
 25 TGC GCGCTTA ATAACAGAAT ATTCTCAATA TTTTTATTTT TTTGTGATT GTTGGAATAT 720
 TTAGTTGATA AGGCACAATC AAATTTACTT AACTATTGT ATTAGGGGAA GAAAGGATGG 780
 GATGTATACA TGACACAACA AACTCCCAT GGAAATCAAA TTCAAGACAT ACCTCAAACA 840
 30 GGATTTTTTCG GGcATCCTCG AGGACTAGGC GTACTCTTCT TTGtAGAGTT CTGGGrAAGG 900
 KTTAGTTATT ATGGGCATGC GTG 923

(2) INFORMATION FOR SEQ ID NO: 851:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1004 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 851:

45 TTAnTTGCAT CTATTTCACT TGGTGTAAG AAAGCGGAAT TTGATTTTAT TGAAAAGTTA 60
 GctCAAGAAA AATTAATCCC CgAATATATT ACAATAGATA TTGCGCATGG TcACTcAGAT 120
 TCaGTGATAA ACATGATTAA ACATATAAAA ACCCATATAC CTGATAGTTT TGTTATTGCT 180
 50 GGTAATGTTG GTACGCCAGA AGGTGTTAGA GAATTAGAAA ATGCTGGTGC TGATGCTACC 240
 AAGTCGGTA TAGGTCCTGG TAGAGTTTGT ATTACAAAGA TTAACAGG TTTTGGTACT 300

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GCCGATGGTG GTATAAGAAC GCATGGCGAC ATTGCTAAAT CAATTAGATT TGGTGCATCA 420
 ATGGTCATGA TTGGTTCATt WTTTGCGGCA CACGAAGAAT CACCTGGTGA AACTGTAGAA 480
 5 CTTGATGGTA AACAGTATAA AGAATATTTT GGTAGTGCAT CTGAATTTCA AAAAGGCGAA 540
 CATAAAATG TAGAAGGTAA AAAAATGTTT GTAGAACATA AGGGTTCATT AATGGATACC 600
 TTAAGAGAAA TGCAACAAGA TTTACAAAGC TCAATTTTCAT ATGCCGGTGG AAAAGACTTG 660
 10 AAATCATTAC GTACTGTAGA TTATGTTATT GTTAGAAACT CTATTTTCAA CGGTGATAGA 720
 GATTAATATT TATAGTAGGT GAGGTAAATT AAAAAATTCA TAGTAACTGT TGTTCGTTTT 780
 TTATCAATTA TTATCATTGC GCCAnTAACA GAATTTAAAC CATTCAATCA TTTACAAAT 840
 15 GAAGTAAGAC AATATATTGA CATTACATC AATAAGAAA CAATTTCTGC GGAAAATAAA 900
 TTGGATACAC CGAAGAAACA ACAATTTGCC TTTAATAATA TACAAATGAA CATGTCGAAA 960
 20 TCAGATGTTG AGAAAACATT AAATAAACCA AAAAGAGTGA CATn 1004

(2) INFORMATION FOR SEQ ID NO: 852:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 852:

GTTCGCTCCA ATGTACGCAG TTGTATATGC ATAGACACCA AAATCGAACC ATTCCATTGC 60
 ATTACCGATA CCGGTTGCAA CAACGGTTTT TTTAGCTTTC TTTGCATCCA CCATGTTAAT 120
 35 ATTCTCTTTA TTAAATCCA TGAATTCATA CACTCCCTCT TGTATGTTTC ATAATTATAC 180
 GGAGTTAATT AGTTTTGTCA AATTTATAAG AATTTAACT TTTATATAAA TACCAAAGTA 240
 40 TGTTTGTTCA AAAATTTTCGC TTTATCGnAT TAAATTCATG GTTTTATACC TCATACATTG 300
 ATTAGACATA ATAATCTAAA CACGACGTTA CTTTGGATAT ACTnAATGGT nnCACACTCA 360
 GTAGGAAGCA CGCATTCGCT CGATAATGTA ACCATACTCA 400

45 (2) INFORMATION FOR SEQ ID NO: 853:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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GGTGAAATTG TAACTATATA ATCGATATTA CCTTCAGTGT TCAAACTGG AAAATAATAA 60
 TTACCATCAC TCTTTTGTGTT GAATTTATAA ATTTTAAAAG GTTCACCAAG TGTATACGAG 120
 5 GCTTTCTCTT TATTATAGAT TTTATCAAGT GAAGTAACAT AAGAAAGATA GTCTTTTGTG 180
 GCTAAATTAC GTACGTCAGT AGGAACACTC TTGTCCTCGA CATTAACTTG CACATGCTTC 240
 TTATCTTTTG CTTTGATATT TGAATTGCTC TCAGCGTTTG CAATAGGGGT AACACTTAAA 300
 10 GAaAATATTA AACTTAAAGC TATTAATTTT GGAAAGTTTC TTTTCATATA AAAACTCCTT 360
 T 361

15 (2) INFORMATION FOR SEQ ID NO: 854:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 605 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 854:

25 ACnTTATACT AGAnAAAGnT ATTAAAGTAT ATCTGCTTTA CACCATTAAA AAGCGGCAAA 60
 TGCTATAGAT AATCTAAAGC ATCTGCCGTA TGAGnATTTA TTTATTTTGT ATTGTCATAA 120
 TCGTGTGGTT TTAAATTAAT TGTTTCTAGC TTTACAAATT TTGTTTGTG AATGATTTTA 180
 30 TGAATAAAGT AAATCAACGC TAGAATGATT AAAGGTAAAA AGTTTTTAAA AGCATTTAAC 240
 CATTGATCTT TTAAATATA TTCAACTGAG CCACCATAA GCAAGAATAA TAGTGTAGTG 300
 ATGACAATGA TTGGTCCTAA TGGATAAAAA GGTGCTTTAT ATGGTAGGAC CTTATTAGGG 360
 35 TCTTGACCTT GTTTTTTAAT AGCTTGTCGC AATCGTATTT GTGACCAAAT GCTTGATCCC 420
 CAAACAATA TAATCATTGA ACCAATAATT TCAAGTAAAT TAAAAACGGC ATTTGAATTA 480
 40 AAGTTTGCAT AAATAATAAC AATAACAACG ACTGCATAAG TAGTTAATAA TGCTCTTAAA 540
 GGTAACCTAG TTGTCTTGTT TAATTTACTT AAAAATGGG GTGCTTTTTT GTCTGAACTT 600
 AAGGA 605

45 (2) INFORMATION FOR SEQ ID NO: 855:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 515 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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TTGAACAAGC ATTTTAAAT AGTCAACAAC ATCAmGCAAT TAGTGAAGAG GCACAACTTT 60
 TAAATAATCC AGATGAATTA ATGGCATTIT TAAAGAATAA GCGTAAAAAT ATTTTAGAAA 120
 5 ATGCATACAT TATGCCGCAT AATATGAGAG AAATGTTACG AAGTTATTTG GAAAGTATGT 180
 CTCAAGACTT TAATGTTGGC GGATTTTTTA ATAAAAAGAA GAAAAAACTA CAAATTCAAC 240
 AACAGCGATT ATTAACAGCG ACAGATGCGT TACAAGAACA TGTTAATCAA CAAATTCGTC 300
 10 AACCAATGCG AGAAGATATG TCATTGTGTA CGCGTTTTAT CAATAAAAAA GmAGCTTCAG 360
 aTAmAGTATT AAATCAGCAT TATGACGTTA AGCCAGAAAT GATTGAAGGT TTATATCAAC 420
 CACAAACATC AATCAGCAAT ACTTATGTAC TTACATTTTC AGACGAAGTG GTTAAAGCCA 480
 15 TTAAGAAATA TGTTGAACAA CAATCAACAC CAATT 515

(2) INFORMATION FOR SEQ ID NO: 856:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1607 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 856:

GTCATTTTTA AAATTTGCA TTCGCGTTA ATTTTTCTC TTTTTCTTT TTCTTCTAGT 60
 30 GACATACTTT CTTTAGGTGT TTCAACCAAT TCAGATGTAT CTACATCATC AATTTTAGTG 120
 ATTTTGTCTA CATCTTCTT TAAATCTTCT GGGACGTTCT CGAAACGCTT ATATTGCTCT 180
 TTAGAGATAC TAGCAGCTAT TTCATTAGCT CCTAAAATT CATCTATCAA GCCGAAAGAC 240
 35 AAGGCTTCTT CTGCAGTAAG CCAAGTTTCT GCATCTAACA TCTGTTTTAA GTGTTCTTGA 300
 TCTAAATCTT TTGCTTTATC TAAATAAGCT GAATTACTAA CAGCATCTGT TTTTCAAGT 360
 40 AAATCCGCTG TCTTCTTAA TTCTTCTGCA TTACCTACAG TCATAACCCA TGAATTATGA 420
 ATCATTAAAA AACTATTTTT GTGCATAAAA ATAGTGTAC CACTCATAGC GATAACACTA 480
 GCAATTGATG CCGCTAAGGC ATCGACATAG ATATTAATTT TTGCAGGATG CATTTTTAGC 540
 45 ATATTGTATA TTGCATGTCC TTCAAATACA CTGCCTCCAG ATGAATTTAT ATGAACATCT 600
 ATTTCACTGA TGTCTCCTAG TTCATCTAGT TTATTTTGA AATCTGTAGC AGTTACATCA 660
 CTTTCAAACC ATTTATCACT TACAATATCA CCATAAATGa ATATTCACC TTTACTTTTT 720
 50 GATTTTCTTT TCATTGAAA ATACTTAGCT TTCATTGACA TTTTATCAC CACCTTTCaA 780
 AGATTTTCTT AATTCAAGTG GCGTGTCAAT TGGGTATAAA TCACCGCTTA ATTAGCGGCT 840

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AACCCTACG AACTGCTTTA AAGTACACTT CTGCTTGTGT TGCCTATCA GCCCTTAAAT 960
 AAGATTTAAC GTTAAATTTA AAATACCTAT TTTTTCTCT GTCTGTTTAA GTAAGTAGTT 1020
 5 TCCGATTAAa TTCTTCTTCA TACTGTTTGA CGATTGGCAA TAAGGTATGC TGCAAGTAAA 1080
 ATCTGTTTAA CTCTTCATTT TTCGCGAAAT TTGTATTTGA TCTTGCAATT AAGAATATTG 1140
 AGGGCAATTG AAAAACGTTA GCTACTCTTT CTCTTGTTAA ATTCTCGCTT GCCACTATAT 1200
 10 CTTCAGAGAC ATATTTTTTA GGTAAGGTT CGATTTCAAC ACCAGGCTCT TGAATAATA 1260
 TTCCACCGTT TTCTTCATAG TACTGTTTGA AATCTTCTAA CACTTGTTGC CTTTTTCTG 1320
 TACTTACATT GGAACCATAT TTAAGCATAA AAGAATCTGG TTTTGCATT TCTGTAAGAT 1380
 TAAAGGTTCT TACTGCATTG TCAAAATCAG TTGTATTCTT CAACACATCA ATCGGACTAA 1440
 TACCTTGAAC CATATTAGAT GCCACGATGT GTTTAAATG CAACATGTCC aTATTATGAA 1500
 20 CAATCAATTT ATTTCCAGTT GCAGCATGAA TGAATAATA AAGTTCACcG TGATTGGTTT 1560
 TCAATTAACA TTCAACAAC ATCTGGATTT AATAAGAAAA GCTTTGA 1607

(2) INFORMATION FOR SEQ ID NO: 857:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 857:

35 ATGCGCATTT AACCGCATTT AGAGATGCTG AAGATCAGTA TAAAGCTTTG TTAGAAATTA 60
 CAACATTACC AGAAGGTAGA ATTTATGTTG CTCGCCAAGA TCAACTCATT GTGGGTTATG 120
 TCACTTTCCA CTATCCTGAT GAAATTGAGC GCTGGTCTAC AGGTAAGCTT CCATATTTAA 180
 40 TCGAATTGGG GGCAATTGAA GTCAGCATCA ATTTTAGGCA ATTACAACTT GCAGAAAAGC 240
 TGATACAACT TAGCCTTCTA CACCAGAATT CGAGAATTAT ATCGGnATAA CTACAGGATA 300
 TTACCGGCAT TGGGGGTTTA AAAAATTCCC AGTnAGAGGT ATTnCC 346

(2) INFORMATION FOR SEQ ID NO: 858:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1176 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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ATTACTATAA TGAATCTTGC GAGATATTTA GAAGTAATGA TACAAnATAA TGGACTTTAG 60
 AATTTmAATT TACAATAAAT AGTTCTATGA TTAAATGTCA GTTTTATGAC ATTTATTTAT 120
 5 TGAAAATACG AACGAATGaG CGATaTGATA ATATAGATAA GAATGATTTT AATTTAGGAG 180
 GCCTTTATGG TGCATAATAA AAACAATACA ATTTTAAAAA TGATCAAAGG TGAAGAAACA 240
 10 TCACATACAC CTGTTTGGTT TATGCGACAA GCTGGCCGTT CGCAACCAGA ATATCGAAAA 300
 TTGAAAGAAA AATATTCACT ATTCGATATT ACACATCAGC CGGAGTTGTG CGCTTATGTA 360
 ACACATTTAC CAGTTGATAA TTATCATACA GATGCGACAA TTTTATACAA AGATATTATG 420
 15 ACACCATTAA AGCCAATTGG TGTCGATGTA GAAATTAAAT CGGGTATTGG TCCAGTGATT 480
 CATAATCCAA TCAAAACAAT TCAAGATGTT GAGAACTTT CTCAAATAGA CCCCGAACGA 540
 GATGTACCAT ATGTATTAGA TACAATTAAA CTTTTAACAG AAGAAAAGTT AAATGTGCCG 600
 20 CTAATAGGAT TTA CTGGGGC ACCATTTACA TTAGCGTCAT ATATGATTGA aGGCGGACCA 660
 TCGAAAAATT ACAATTTTAC AAAAGCGATG ATGTATAGAG ATGAAGCAAC ATGGTTTGCT 720
 TTAATGAATC ATTTAGTTGA TGTATCTGTT AAATATGTAA CAGCTCAAGT CGAAGCAGGT 780
 25 GCCGAATTGA TTCAAATTTT CGATTCATGG GTAGGTGCAT TAAATGTGCGA GGATTACAGA 840
 CGTTACATTA AACCACATAT GATTCGATTA ATCAGTGAGG TTAAAGAAAA ACATGATGTG 900
 CCGGTAATTT TATTCCGTGT AGGTGCCAGT CATTTAATCA ATGAATGGAA TGATTTACCG 960
 30 ATTGATGTAT TAGGCCTAGA TTGGAGAACG TCTATTAATC AGGCTCAACA ATTAGGCGTT 1020
 ACTAAAACAT TACAAGGGAA TTTAGATCCA TCAATTTTAT TAGCACCATG GAATGTCATT 1080
 35 GAAGAGAGAT TGAAACCAAT ATTAGATcAA GGTATGGAGA ACGGTAAACA CATCTTTAAT 1140
 TTAGGACACG GTGTATTCCC AGAAGTGCAC CAGAGA 1176

(2) INFORMATION FOR SEQ ID NO: 859:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 621 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 859:

50 ATTTGGTGCA TTGGTAnAAT TGACCTGAAA GnAAAAAGTG GTTTAGTTGC ACATTGAGTG 60
 nAAGTGCGCA GATGAATTAT GTTGAAAACG TGAGGAAGAG CACCTTTGCT GTTGGTGATG 120
 AAGTAGACGT AAAAGTATTA TCTATTGCTG ATGATGGAAA AATTAGTCTT TcAATTAAGA 180

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AAAAAGCCGA AGATTTTGAA AAGAAATTAA GCAATTTCTT AAAAGATAGT GAAGATAAAT 300
 TAACTTCAAT CAAACGTCAA ACAGAATCTA GACGCGGTGG CAAAGGTTCA AGACGTTAAT 360
 5 TAAATAAAT AAAGACTGTT TCGATAAGGA ATATATTTAG AATGATGCGT ATCGAATAAT 420
 CGATTGCAGC GTTAGACAAT CTAAGACTGT TTCTTAAATA AGGAGCAGTC TCTTTTATTT 480
 GTAAATGATAT AACTAAGACT TATACCATTT TTGAAAATTG TAAAAGTGAG GTGATGTTAT 540
 10 GCAGTTAAAT AGTAATGGTT GGCATGTTGA TGACCATATT GTTGTGCTG TTTCTACAGG 600
 TATTGATAGT ATGTGTTTnn T 621

15 (2) INFORMATION FOR SEQ ID NO: 860:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 544 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 860:

25 TATATTAGGT ACTTGTTGTTG GTATTGTGCC AGCTTTGCTG TCTACTATAA TTTCTAAAAG 60
 GTTTGAACAT ATAAAAGGGA AAGTGCTAGG TGTATTTAAT TTTGTGAGAT ATATTGGAAT 120
 30 GACTGTCGGT GCATTATTAA TTGGTATCAT TTCTCAGCCG TTGGTAGCCT TTTACTTCAC 180
 AACTATAACT ATCATGTAA TAGTAATATT TCTTTATATA AAGATAGTTG ACTTTCAGCT 240
 AAAGTATGCC AAATAAACTT AAAAAAGCAG TGAATCATTT CAATAGATGG AATGATTCAC 300
 35 TGCTTTTTGT TTATAGAAAT TTAAAATTCA TGCCTTTATG CTAACAACAA TATTATTTTA 360
 CTCTCTTACG TTTGCCAATG TAACcGTATA GCAAAGTAAA TGACTGCGAT AATGATGACA 420
 ACATACATat ACGTGAATAG GAAGGAAGAC CAGTCATCAA CATACCAAAG CTATCGCTCA 480
 40 AAGTGCgNCT GGTAAATTAA ACCGAATTCC AnGATTGTAG GAACCCnATT AATGGAAATA 540
 ACGG 544

45 (2) INFORMATION FOR SEQ ID NO: 861:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 651 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 861:

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AATTTAAAAT ACATTTATGC TTTACCCATT CGAAAATACC TTAATCATTT TCATTTATAG 120
 CATTGTTTGA TTGAAGGATA AAAAGTTGTT GTTTACAATA AAAATAATGA GTATCTGAAA 180
 5 TGAGGGATTC AnTATGACAC ATGTGGAAGT AGTAGCGACT ATCGCGCCAC AATTATCTAT 240
 CGAAGAAACT TTAATTCaNa AnATTAATCA TCGTATTGAT GCAATAGACG TATTAGAATT 300
 10 ACGAATTGAT CAAATTGAAA ATGTCACAGT TGaTCAAGTG GCAGAAmTGA TTACAAAGCT 360
 GaAGGTTATG CAAGATTCAT TCAAATTATT AGTTACGTAT CGTACAAAGT TACAAGGTGG 420
 CTATGGGCAA TTTACAAATG ACTCGTATCT TAATTTAATA TCAGACTTAG CAAATATCAA 480
 15 TGGCATAGAT ATGATTGATA TAGAATGGCA AGCAGATATT GACATTGAAA AACATCAACG 540
 AATCATTACA CATTTGCAAC AGTATAATAA AGAGGTGGTT ATATCACATC ATAATtTCGA 600
 AAGTACGCCT CCATTAGATG AATTGCaATT TATATTTTtn nAAATGCAAA A 651

20 (2) INFORMATION FOR SEQ ID NO: 862:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 401 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 862:

TGTGAGTGGT AATGACACAC AAGCAGATT AATAGGTTAT AGTTTTAAGT TTGACGGTGC 60
 GATTTCAAGG CAAGAGGCTT CTAAAGATGT ACATGCAGTT ATATTATCGA ATAAAACACT 120
 35 ATATTTATTA GATGTATTAC AAAAATTACC GATAGATAAA ATGAATTCAT TGAATATCCA 180
 TCAAGAAATT ATTGATGAAA TGTCAGATAT CATTTTAATG TTATATCGTG AATATGCAGG 240
 TATGTTTTTT AAAAGTCAGA AACTAATCAA CCAATTAAAA AGATTGGAmC AATAACaTAA 300
 40 AATAATAAAa GGTATTCAAG TAGCCACATA GATGTGTTTA TTTGAATACC TTTTkGAATA 360
 GaaAAGaGAT ACTGGCaATT TTAATAACCA GtATCTCTTT T 401

45 (2) INFORMATION FOR SEQ ID NO: 863:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 863:

ACAAAGTAAT CAATATGTAA TATAAAATAC ACTGGTACTC AATATATAAT GATGATAAAA 120
 TTAATTTTAA TTAGATAGAG TTGCTTTGTG TTTTAAACGC nGATGCTACT ACTTATCTTA 180
 5 ACAGTTGATT AAGTAAATCA TTAAACAGCG AGATTATnCA ACCAGGGGGA TGA CTTAATG 240
 AATTTATTCA GACACCAAAA TTTAGTATCA GAAATTTAAT GTCGGTATTT TTTCAGCTTT 300
 AATGCCAC 308

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(2) INFORMATION FOR SEQ ID NO: 864:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1827 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 864:

TTCTACATCT TAAACGATGA CCTAACTATG ACGTTAATCT GGAAAGATGG GGAGTTGCTA 60
 GTATGATGTT GAAATTTAAA GCTTGGGATA AAGATAAAAA AGTTATGAGT ATTATTGACG 120
 25 AAATCGATTT TAATAGTGGG TACATTTTGA TTTCAACAGG TTATAAAAGT TTCAATGAAG 180
 TAAACTATT ACAATACACA GGATTTAAAG ATGTGCACGG TGTGGAGATT TATGAAGGGG 240
 ATATTGTTCA AGATTGTTAT TCGAGAGAAG TAAGTTTAT CGAGTTTAAA GAAGGAGCCT 300
 TTTATATAAC TTTTAGCAAT GTAAC TGAAT TACTAAGTGA AAATGACGAT ATTATTGAAA 360
 TTGTTGAAA TATTTTGA AATGAGATGC TATTGGAGGT TATGAGATGA CGTTCACCTT 420
 35 ATCAGATGAA CAATATAAAA ATCTTTGTAC TAACTCTAAC AAGTTATTAG ATAACTTCA 480
 CAAAGCATTAA AAGATCGTG AAGAGTACAA GAAGCAACGA GATGAGCTTA TTGGGGATAT 540
 AGCGAAGTTA CGAGATTGTA ACAAAGAACT GGAGAAGAAA GCAAGCGCAT GGGATAGGTA 600
 40 TTGCAAGAGC GTTGAAAAAG ATTTAATAAA CGAATTCGGT AACGATGATG AAAGAGTTAA 660
 ATTTCGAATG GAATTAAACA ATAAATTTT TATGGAGGAT GACACAAATG AATAATCGCG 720
 AAAAAATCGA ACAGTCCGTT ATTAGTGCTA GTGCGTATAA CGGTAATGAC ACAGAGGGGT 780
 45 TGCTAAAAGA GATTGAGGAC GTGTATAAGA AAGCGCAAGC GTTTGATGAA ATACTTGAGG 840
 GAATGACAAA TGCTATTCAA CATTCACTTA AAGAAGGTAT TGAACCTGAT GAAGCAGTAG 900
 GGATTATGGC AGGTCAAGTT GTCTATAAAT ATGAGGAGGA ATAGGAAAAT GACTAACACA 960
 50 TTACAAGTAA AACTATTATC aAAAAATGCT AGAATGCCCG AACGAAATCA TAAGACGGAT 1020
 GCAGGTTATG ACATATTCTC AGCTGAAACT GTCGTACTCG AACCACAAGA AAAAGCAGTG 1080

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AGTGGTGTAA GTAGTAAAAC GTATTTAGTG ATTGAAACAG GCAAGATAGA CGCGGGATAT 1200
 CATGGCAATT TAGGGATTAA TATCAAGAAT GATGAAGAAC GTGATGGAAT ACCCTTTTAA 1260
 5 TATGATGATA TAGACGCTGA ATTAGAAGAT GGATTAATAA GCATTTTAGA TATAAAAGGT 1320
 AACTATGTAC AAGATGGAAG AGGCATAAGA AGAGTTTACC AAATCAACAA AGGCGATAAA 1380
 10 CTAGCTCAAT TGGTTATCGT GCCTATATGG ACACCGGAAC TAAAGCAAGT GGAGGAATTC 1440
 GAAAGTGTTT CAGAACGTGG AGCAAAAGGC TTCGGAAGTA GCGGAGTGTA AAGACATCTT 1500
 AGATCGAGTT AAGGAGGTTT TGGGGAAGTG ACGCAATACT TAGTCACAAC ATTCAAAGAT 1560
 15 TCAACAGGAC GACCACATGA ACATATTACT GTGGCTAGAG ATAATCAGAC GTTTACAGTT 1620
 ATTGAGGCAG AGAGTAAAGA AGAAGCTGAG CGCAAATACG AGGCACAAGT TAAGATAAGG 1680
 AGAGATGGAG ATGCCAAAGA AAACGGTAAC GATTGATGTA GATGAAAAC TATTAGTAGT 1740
 20 AGCTAGTAAT GAAATATCAG AACTATTATA TGAATATGAC AGTGAGTtAA TGTCAGCTGG 1800
 ATGGAAGATG GCGATAATAG GGATATC 1827

(2) INFORMATION FOR SEQ ID NO: 865:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 865:

35 TCAATTGCAT CATCATATGA AATTCTaGGG AATGGTGTGCG CAACTTTTTC AAGTTTTGAT 60
 GTATCACGCT CTAAAATTTT CAACTCTAGT TTACAATTTT CTAAAACTGA TTTTACAACA 120
 TGTGTTACAT ATTGTTCTTG AATTTCTAAA CTTTCAGCAT GATTTGTGAA AGCCATTTCT 180
 40 CCTTCAATCA TCCAGAACTC GATCAAGTGT CTACGTGTTT YTGATTTTTC AGCTCTGAAA 240
 GTTGGACCAA ATGAAAATAC TTTTCCGTGT GCCATTGCTG CAGCTTCTAA GTATAACTGA 300
 CCACTTTGAG ATAAAAACGC ATCTTGATCA AAGTATTTAG TATGGAATAA TTCATTGTA 360
 45 CCTTCTGGCG CACTTGCTGT CAAAATTGGT GGATCAACCT TTGTAAATCC ATCTTTGTTG 420
 AAAAATTCAT ACGTTGCACG AATAACTTCA TTTCTAATTT TCATTACAGC ATGTTGTTTT 480
 50 TTAGAACGTA ACCATAAATG ACGGTGATCC ATTAAGAATT CTGTACCATG ATTTTTAGGT 540
 GTAATCGGAT AGTCATGCGC TTCTGAAATA ACTTCAATTG ATTTCACTTG CATTTCTGAT 600
 CCTAAGTCAG AACGATTATC TTCTGTAATT GTGCCTGTAA CGTATAGAGA TGATTCTTGA 660

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TGCATAAAGC CTGTTCCATC ACGTAATTGT AAAAAGGCGA TTTTACCACT TGAACGTTTA 780
 TTTGTAAACC AAGCACCAAT TGTAACGTCT TGGTTTAAAT GATCTTTCGC TTGTTTAATC 840
 5 GTTGTTTTCA TAACCATTCT CCTATTTATT TTTTCGkTAT ACAATACTCA TTCATTTTAA 900
 CAAAATCCGC TTTCAAGTTC TAGAACTAGA CTAAAAGATA ACGtGTAAAT GGTAATGATT 960
 TACGCACAGA TTTGAACATT AATTATATT AAGACAATAC AATCATCAGT TTCAGACAAA 1020
 10 ATATATAATA AAGCCTCAAT ATTATTAGTA TGAAGGTCGT TTTTGTnCT AACATTCAAG 1080
 TTTAATTATA AAACCTCAAAT TTTGACGACC AAACAAAAAT TCTTGTAACA GAACATAGCA 1140
 15 CATGTCATGT CACAAGAATT TTACTTTGTA TTTCACTTTT TCTTTTTTTG AATTGTCTT 1200
 AATAATTTTC CAAACTGTTG AATGTCGCCT TTTTCTGAC GATAATTTTC AAGTGTGTTG 1260
 TCAAAAAAGT TTTTATAATT ACTGTTTATG AGTCGATCAT CAAATGAAAC TATTATGCCG 1320
 20 CGATCATTTT CATTCTAAT TAATCTTCCA AGTCCTTnGT CTAnAACGTG TAACTGCAT 1379

(2) INFORMATION FOR SEQ ID NO: 866:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 450 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 866:

TTACAACGAA TAGTTCACCG TTCGAGTCTA ATCTATGTAA TGCTTGCTCG AATATACGAT 60
 35 GCACGGTTTC TTTCCCTGCT CTTATTGGTG GATTGGTTAA AATAAAATCA AAACTTTGT 120
 CTTCCACAGC AGACAAAGCA TCACTTTCCT TTACGATCAC ATTATCAATA CCATTTAATT 180
 TTTTGTTTTT TTCAACTAAG GCTAGCGCTC TGTGATTAAC ATCTAGCATT GTAATTGAAT 240
 40 GATGTGGTGA TACTTTAGCA ATCATCAAAC CAATTGGTCC GTAACCACAA CCAACATCGG 300
 CAATTCGCTT ACTTGGACCA GGTGGATGCG CTTTTAAAAA AGTTTGAACA AGAACATCTG 360
 aACCATAATC TACTTTAtCt TTCGAAAACA CTCctTATCA GTTATTAAAT CAATTTTATG 420
 45 AnGGTTnTAA TTGGATATTG AGTACGTTGT 450

(2) INFORMATION FOR SEQ ID NO: 867:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 867:

5 AATGTTAACA ATATAGCACC AATTAACCCC GACATGATAA TAACGTGTAA TGTTTTATTT 60
 CCTATTAATT GTCTCGCAAT ATGAGGTGCA ATTAATCCTA AAAAGCTAAT ACCACCGACA 120
 ACTGAAATTG CGGATCCTGC TAATATTACT GCTAAAATTA ACAATAGCAT TTAAATAGTT 180
 10 TTAACFTTTA AACCGAGTGC GGTGCAACA GCATCACCTA GATTCAATAC ATCTAATTGA 240
 TAACTCCATA AAATGATGAT GGATCGTTAT TAAAACCAGG GAATATAGAT AATATCCGCA 300
 TATCAGGCCA TATAGCTACC TGTACCAAC AGGTTTnTGC TCCAnGGTTC TnTAATAAGA 360
 15 CGCACACGCG ACAATGCGCT TGCTACCATT AGGCAGCTTG 400

(2) INFORMATION FOR SEQ ID NO: 868:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 1132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 868:

AATCCnTnAA GTGCCATAAC ATCATCTCCT AACATCTTTA TTATACATCA ACATTTTATA 60
 30 AAAATAACnT CTTATGATAA AAATGAAAAT ACTAATTTTA ATGAGAGCGT CTTAAGCCGC 120
 AATTGATAAA ACATATGCTA CAATATTTTT AAACACTATA CAGGAGGTAC TCTATGACAA 180
 AATATACATT TAAACCTAAA GATTTCAAAG CGTTCAACGT AGAAGGCTTA GACGCACGAA 240
 35 TGGAAGCTTT AAACGAATAC ATACGACCAC AACTCCGTGA ATTAGGAGAA TATTTTAGTG 300
 ACTTCTTTAC AAGTCAAAC TGTGAAACAT TTTATCCTCA CGTAGCAAAG CATGCTAGAA 360
 GAAGTGTGAA TCCTCCTAAA GATACATGGG TTGCTTTTGC AACAAACAAA AGAGGCTATA 420
 40 AAATGTTACC TCATTTCCAA ATTGGTATGT TTGAAGATCA ACTGTTTGTT ATGTTTGGAA 480
 TCATGCATGA AGCAAAAGAT AAAGCAACaC GTGCAAAAGT TTTTGAAAGA AAATTTAAAG 540
 CTATTCAACA ATTACCTGAT GATTATCGTG TTTGCTTAGA TCATATGAAA CCTGATAAAC 600
 45 CATTTATTAA AGATTTAACG GATGATGATT TAATAGAAGC GATACAAAGA GCCATCAATG 660
 TGAAAAAAGG TGAATTCTTT ATAGCGCGTG CAATCACACC ACAAGATAAA AGATTAAAAA 720
 50 GTGACAAAGC ATTTATTGCA TTTTATAAG AAACCTTCGA TCAGTTCTTA CCATTTTATT 780
 CTGCATAAAT AACTTTGTTT AAATAATAGA GCACTTAATC ACATCCaTGA TTTCGTGCTcC 840
 TTtTTTCTTA ATATTAAATC GAACGTtCAA CATAaTAATT CATACTTTTA AAAAAATTAA 900

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GGTGAGTCAA AATGAATAAT AAACGACATT CAACAAATGA ACAATTAAGT TTAGACGAAA 1020
TAAACAATAC AATTAAATTC GATCATCGCA GTTCAAATAA ACAGAAATTT TTATCATTTT 1080
5 TTGGACCTGG GTTATTAGTC GCTGTTGGTT ACATGGATCC CGGAAACTGG AT 1132

(2) INFORMATION FOR SEQ ID NO: 869:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 418 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 869:

CTCAATGTAT TGA CTGTGAT TTGGAGTGTA TAATGCTACT GTTTTGTCTA TAGCCATCGC 60
20 ATCAAATATT ATATTTGAGT AATCAGTGAT AACGACATCA GACATTAGAA TTAAGTCTTG 120
AGCACTAAGA TACTTTGGTG CAACAAGCGC CTCTTCTGGT AAGATCGCTT CATCAACACC 180
CTGAACCACA ACATGATAGG CTTTGAATAA AGCATCTGAT AGTGGTAATT GTTGCGCACT 240
25 CACTAATCCA ATAGGTGCGT ATAATAAAAC TGGTTTTTGA TCATTTATTT TAAACGATTT 300
CTTATACTGT TGTTGAGTAG TACTTTCGTT ACTCTTTTGT AGTAAATATT GGTGTTTAGG 360
ATTACCATAA GCCAATACAT TGCTTGGTGA CTAGGAAAAG nCGTTTGATA AAAGGGCT 418
30

(2) INFORMATION FOR SEQ ID NO: 870:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 587 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 870:

GAGTnTGTTA CAGTAATTGA TTTTATTGGT AATTnTAAGA CAAATTATTT AATTCCGATT 60
GCGCTTTCTG GGGATCAATC GCAAnATAAA GATAATTATA AGAAGTTTTT AACGAATAAC 120
45 GATTCGATTA ATGGAGTATC TACAATTAAT TTTGAAGAAG TTGCTAAAAA ACAGATTTAC 180
AATTCATTGG ATGCAGTATC ATTAAATCAA AATAAATTAA TATTAAGGC TTATGAAGAA 240
50 GTTGAAAATA GATTGGGACA CATGCCGTTA CTAATGGATT TCATACAACA ACATTCTATA 300
GATCCAAGCG TTATATTTTC TAAATTTAGT AATTATTACG AGTTCTTAGT GAGATATAAA 360
AAAATAGATA CATTATTGAC GGAAAATGAA TCTAAAAATC TGGTTTTCTT TTCAAGGCAA 420

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TTAACATATG ATGAATTAAA AAATAAAATG TTGAACGAAG TTAAGGATAT AACAGAAGAT 540
 GATATAGATA CTTCATTAAG AATTTTAGAT TTTTCATTTT ACAACGC 587

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(2) INFORMATION FOR SEQ ID NO: 871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 971 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 871:

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CTACTAAACC AGGTAATCGG TAGAATCCAA GCAGGAATAA ATAAATTAAT GChACACCAA 60
 TAAACGATGC AAACACAGTn TTATCTAATG CATCTTGACC AAATGGGCA CCTACTGAGT 120
 20 TTGAATAAAT TTCTTTCAAG TCAACTGGTA AAGAACCTGC ATTTAACAAT kCGGCGATTT 180
 GTTTTGCTTT TTAAACGCCT TCTTGTCCTT TAAATCCACC CGAGATTTCT ACGCTATCAG 240
 AATTGATTGG TTGATCAACA CTTGCTGCAG AAATAAATTT AGGGTTTTTC TTTTGTGCTT 300
 25 CTTTTTTATA GCTGTCACCT TTTTGAAT CTAACCAAAC AACCATGACA TTATCACGTT 360
 TCTTAGAGAT TTCTCCGTT ACTTTTTTAA ATTTGTTTTT GTCTTTTACT TTAAAAGTAA 420
 CTGTAGGcTG GTTTGTTTTCC tGtTTAAAT CTTGtTTGGC AGATCCCTGT TTaATATCAG 480
 30 AACCCTTAA TTTtACTTTA TCTTCTGCAT CGCGAATTGT TAAATTAGCT TGAGAAGATA 540
 AAATTTTACG TGCTTCATTC TGGTCTGTTA CACCAGCAAG TTGTACTCTA ATTCTATTAG 600
 GTTCTTCAAC TTGAATTTTA GGTTCCGAAA CACCTAAAAC GTTAACACGA TTTTCTAATG 660
 35 TTTGCGCTGT TGATTGTAAG GCTTTTTTAT CTATTTTGTC GCCTTTATTT AAAGGATCGA 720
 CTTGATAAAG CACCTCAAAT CCACCTTGCA AATCAAGTCC TAAATTGmCA TTCTTTATAA 780
 40 CACTTTTATA AGTTGcAGCC ATTCCGGCAA ACAACAATAC GACTAAAAGC AAGAACGCAA 840
 TTATTCTACT ACTTTTCTTC ACATGAACAC CTCATTATTT ACGTATGTAT TTAGAATACT 900
 TGAATACTAT TTTATAACGC AAGTGAAATC TTTCTTACAA AATTTATTAG CCTTATACAT 960
 45 ATTAACATAC T 971

(2) INFORMATION FOR SEQ ID NO: 872:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 636 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 872:

CTGGTTAACA ACATCTGGTT CGGCATCTCC TTAGCTTCCA CTAAATCTTG GATGTCTTGG 60
 5 nnATCTTGCG CAAGTnGTGC TTTGGCTTGT TCAATTtCTy CTTTAGTCAT CGCATTGTTA 120
 ATGCCGTTAT GACCTTGTTG AAGTATTTGA TTAATACGAT CTTTAAGTGC TTGTTTTTCC 180
 TTATCTGTTA GATTGGATT TCGATCAATT TCGTCAATTA ATGCTTGaAC TTGcTTATCA 240
 10 ACGTCTTTAT TGGCATCAAT TTTTGCTTTT GGTATTTTCAT TGGCATGCAC TTGTTCAATC 300
 GCGTGGTTGC CTGCTGTTTG AACTTGAGAT ACAGCCTGAT TACTTGTTGC TTTATTAATG 360
 15 TTGTTGATGA TGCTGTTTGC CAATTCTTCT GCTTTATTTT TCGCAATAAG CTTGTCTTGA 420
 TCCGTCGCAT TTGAAGCTTC GATTCTTTT AGCTTATTAG CTAAAGCTTG ATTAATAGAT 480
 TGAATTGCCT TGTCTTTAGC ATCTGTAGT CGTTGATCAC CATTAAAGATT ATGGATTGCA 540
 20 TCATTGACTG CTTGGATTGC GCCATTGATA TCATTCACAT tTGTGTaTCA CTATTTAGCA 600
 ATGTATTTGC TAGACGTTgG CATCATCGAA GTTTGT 636

(2) INFORMATION FOR SEQ ID NO: 873:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 659 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 873:

35 CTCTGAATGC ATTCATTAAA CGCTGGGTCT CTTTATATGA AACGTATTTG TCATTTTTAG 60
 AACTCAATCC GTAAAAATTG TCAACTTTCT TTTTAATATT ATCGTAATCA ATGGTTACAT 120
 TACTTAAATC AATATCTAAA TCTATATTTT CTGCATCTTC TTTAAAGCCC GCTATACTGA 180
 40 AAAAGCCTTC AATCGGCTGA TCAATCATTT CAATATATTT TAAAGCTGTG ATTGAACCTA 240
 AACCATGTGT TACAAAATAT GTATCCTTTT TCGGTACATT AATTGTTTC GTCATAGCTT 300
 CAATCCACTG ATCCACTGTC TTCGCTtCAG GGGATTCAAA ATTAAATAAT GTTACGTCAT 360
 45 ATCCTTCTAA AGTTAAGTTA TGCTCCAACC ACTGATACCA ATGATTTCTA CTATTTCCAT 420
 GCATAGAATG TACAATAtTA CATCTGTCAT CTCATTCTCT CCTTTCAACT TACTACTTCT 480
 TTTCTATTTT TAAAAAATG ACTGATTACC TATAATTGTA AAATAAAAAC ACCTTAATTA 540
 50 GAAATGTTAT ATCGCAAAGT GACATTTCTA ATTAAAGTGT ATTGTCATCA TTTCAATATC 600
 ATTCAAAAAC AGCTAAACCT TTGTCTCTGC TTCAATTTC CAAAAATAAT TCCCGCTGA 659

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 874:

AAAATAAAAT CCATTTTAGT ATTCGTAGAA AATGAGAGCC CCCTTTACCA CAATATGTAA 60
 ATGTATATTG TGAAAAGGGG GCTTTTATTT ATGACATAGT TGTTCAACTC ATACATTCAG 120
 TTGATAATGC AGTGC GTTAT GCAGCTATCC ACTTCATATG TATGGCGCAT ACTTGATATA 180
 TGAATATCAT CAAGATTTTA AAAGTATCGC TAATTTTAAA GTCTTAAAC GCAGATTAAT 240
 GGTCATGATG TGTTAnTGCG TTTTGGTTTT TAGAGCCACG TAATCCCAan GGACATATAG 300
 GAGGAACCAT TCCAC 315

(2) INFORMATION FOR SEQ ID NO: 875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 875:

TACACGACCT TGTAAGTCAG CTGCTTTATA AGCTAGGGCG ATGTTATCAA AGTTGGATGT 60
 ACTTTGAGCT TGGCATTTCG TTAATACTTT TAACGAAGGA TTTAATATAT GTCTGATACG 120
 TATATATTGA TTATATTCAA TTCTTaATTt GGATAAGATT GCTGATAATT TGAAGCAATC 180
 GGAGCTAAAT GGATCGAAAA ATGAATAAAT TTCGATTTTA CTTACAGGTG ATAGaTTGAT 240
 ATCTTCACGA CTCTTATTTT CCATTaWTCG TAATTCTCCA GCCATGTTTA TTCACCTACA 300
 ATTAATTTTA GGAATTCACC ATATGaTTAG CAGTTAATCT TaAGCGCTCA AATAAATAAT 360
 CTCCAACACC TTGTGGAAAC caGCgCGaTT AATTGCTGTC TGCATATTTT CTAGCCATGC 420
 ATCTCTTTCA AATTCAGTGA TTGTAAAATC TATATGTCTT TTTCTTAGCA TAGGATGTCC 480
 GT 482

(2) INFORMATION FOR SEQ ID NO: 876:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 670 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 876:

5 ATGCAATTGA ATTCTTAAAA GCAGAAGGCT TTGATGATAT TGAATGGGGC GAAGATTTTG 60
 GTGCGCCACA TGAAACAGCC ATTGCTAATC ATTATGATTT ACCGGTGTTT ATTACTAATT 120
 10 ATCCAATAA AATTAAGCCT TTCTATATGC AACCAAATCC TGAAAATGAA GAACTGTAT 180
 TATGTGCAGA CTTAATTGCA CCTGAAGGAT ACGGTGAAAT TATTGGTGGA TCTGAACGTG 240
 TGGATGACTT AGAATTGTTA GAACAACGCG TTAAAGAACA TGGATTAGAC GAAGAAGCAT 300
 15 ATAGTTACTA CTTAGACTTA CGTCGTTATG GTAGTGTGCC ACACTGTGGA TTTGGTTTAG 360
 GTTTAGAGCG TACAGTAGCA TGGATTTCTG GTGTTGAACA CGTTCGTGAA ACAGCGCCAT 420
 TCCCAAGATT ATTAACCGT TTATATCCAT AAGTTTTAGG GTCGTTACTT AAAATATATA 480
 20 TTATGATAAT AAAAAGAATC GTCCAGCCTA TATTAATAGC TGGGCGATTT ATTCTTGGA 540
 AATGAAGATT GATAACGGCT TATATTAATC ATGAACAAAC TTTTGTTTAG TAACTATATT 600
 TGGAAAATAA ATAGTTCATC TGATTATCCA TAAAGTTCAT TGTAAAATC TAGTGTTAAA 660
 25 AAATACTGTT 670

(2) INFORMATION FOR SEQ ID NO: 877:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 1258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 877:

TGCAAAGTAA ACTGGATGGC TnTCTTGCCG CCAAGGATCT GATGGCGCAG GGGATCAAGA 60
 40 TCTGATCAAG AGACAGATCC TAACCTCTCA TTTCCGATAA GTTTAGTATG TATTATAGGT 120
 GATGATTnTC TTGTTTTCAA CCTTATACAC AATATTTTTG AnATTTATAT TATATTCATA 180
 TAAGGAAGGC GATTAATTAC GATTCATCAT TATATCTCTA CGTGTTAATT TATTAACcTA 240
 45 TACTATATTT ATCaACaCAA CAGTTTTTCC TTTCATTTTC AAACATAACA GAAAAAGCCT 300
 GAGACATACT TAGTCCAGA CTGTTCTATA ATTAATTAAT GATATAACAA GGTAAATCAT 360
 TCAAAGCTAA CATCACATTT ATTCACTGTA ATTTTTCATA AAGAATAATA ATGACTGTAA 420
 50 TTCTATACCT AAGTCAATTT GATGTACTTG CACATCTGAA GCGGTATTAA TTCTACCAGG 480
 AGTGAAGTTT AAAATACCTT TCACACCAGC TTGGACGAGT TCATCTGCAA CTTTCTGTGC 540

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TAATTCATCG TTATCTTTAA CAATAACGTT CCCTATTTTC TGGCCAATAA CATCTTCTTT 660
 TACGTCAAAC GCTTCTGTAA TCGTCATATC GTCATGTATT GAAAAGTTAT ATGTGAGCAA 720
 5 AGCTTTCCCT AGGTTCCCAA CTCCGACAAT TGCgATTTTG ATCATGTCAC TCTCGCTTAG 780
 TTCAGATTTA AAGAAATCCA ATAACTATC TATATTATAT CCGTaCCCTT TTTtACCTAA 840
 TTCGCCAAAA TATGAAAAGT CACGACGAAT TGTtGCCGAG TCAATTGTa ACGCATCGCT 900
 10 AATCGCTTTT GAATTTACAC GATCTATACC TTTAGATTTT AATGAACTGA CAAATCTATA 960
 ATATAACGGC AAACGTTTTA AAGTTGCTCG AGGAATTTTA ACTTGGTCAC TCATTCGCTA 1020
 15 TTTCTCCTT CGTGTtTGAA TGAATTATAT CTATGTATTc AAACGAGTTA GAGCGTAATT 1080
 GTTAGATTAT TAAAAtACAA ATAATTGaTT ACAATGAATA CCTAAATATT ATACATTAWT 1140
 GAATTTTAAA AATAAATATC TTAGTTTCAA GACGCGCTTT TATACTGTAA AATGGTTATT 1200
 20 AATGTAATAA TTACGCTTGT TTCATAAGTT AATAAAATTt GAGAAGACGA AGGTGAAG 1258

(2) INFORMATION FOR SEQ ID NO: 878:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 546 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 878:

AAACAATCCC ChCCAAAGTA ATTCCACCAC TAATTGTAAA TAACTTTGGA AAGGATGTTG 60
 35 TTTGTnATTC CCATGGACAC ATGCCATCTn ATTTAAGTTT TATACTCTAT TTTTCTGATG 120
 TCTTGATTAA TTGCAAGCGG TCTTGCGAGC CTGTTCaAG CTCATATTCT TTATCTACTT 180
 GCTTACCGTT TTCrYTTATT AATCTTACGG TTGCGGTaAT CTTATCACCA TGTTTTTCAG 240
 40 CATCTATAAT TTGTGGTGAA CTAATCATCA TTAAACTTCC TTTAGATACA CGCTTCTTTA 300
 CATCATCATA AAAAGATGAT CCTTTTTTTA TATATGATGA TACAAAATCA AAATCCGACT 360
 GATTAAACGC AGCATTATTC GCTAAAGAAT ATCCAGCAAA GAATTCTATC AATTTGTTCT 420
 45 TCAAGCTGTT TTCTTCTTTT TCTTTCTTTT CAACATAGTC TTCGATATCT TCACTGTCAA 480
 AATTCAAAGT TATCTCTGTA TTGTATTTTA AATCGCTAAG CTTTAATCGT CTTCGTCTGT 540
 50 GATGTA 546

(2) INFORMATION FOR SEQ ID NO: 879:

(i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 870 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 879:

	TTTTATGAATT TTTTATGTAA CATTAAATAT TCTTCTGGCA ATCTTCCTAC TATkTCTkTT	60
10	ATATATCCTT CTCTCCTTC TTTAAATACT AAACCTGTGG GAGTTAGTGT GTTATACCTA	120
	ATTTCTATCT CATTCAAATG ATCATTCAAA AGGTCAAAA ATTCTCTATT AAAATAACCC	180
	CATTTCCCAT TTTGTAATAA ATATTTCTTT CCATCTTCCA TTTCAACTTC TGCATGTAGT	240
15	ATCGTTTTTA GTaGCATATT ATTTGAATGC CCCAAATTAT CkATCACKTc AATTCTGACA	300
	TCATTTATAG AATTAACGTC ATATTTTAAT AAGTAATCTC CTATTTCAGT GATGTAATCA	360
	ACTTCAGGAT CAGTCGCATC AAATGTCTCT AATGTATTAT TTTTAAAAGA ATTTATATAT	420
20	ATATTGACGT CGAGCATATC ATCTAACAAG AGTATCATAT TACTTAGTTC TAAAAATCTT	480
	GATATATCTA TAGATATATT TTCTGTAGTT GAAGAATTCG ATAGTTTTTT TAGCAATAAA	540
	GTATCTAATA CTTCTATTTT ATTCAAGTCT TTTAAAGTTA CTATTCTAGG AAATTCACTA	600
25	ATTTTTTGAG GAAGATTAAT AATAGCGTTT ATTTCTTTGA TTATCACACT AATTTTATCT	660
	ATGaATTGCT GcTTTCTATT CGGtACACGC AATGaAATAC TTGTACCACA AGTCCATTGt	720
30	TTTTCCaAAA ATTTGAGGaT TCTGTGGaTG tCCTTGGaCT GGaTATATAA GATTCTGAAG	780
	GTCTAACGTA ATCTACACTA TTCCTTCTAT AATTAACAAT CTCTTTAAGC CTGTTTTGTt	840
	GAAAAAAATT AACATTTTTA nTAACTAnGG	870

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(2) INFORMATION FOR SEQ ID NO: 880:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 880:

45

	GGTTTACATC TTTATCAACT GTAATTTTCAAT TGACATCTTC ATTCATATTT AAAACACCAT	60
	TAAATGTCCC TGAATATTCA CTTGTTTGTT TAACTGTGGC AGTGACTTGT CGTTACCATA	120
50	TGTCATCATA TATTGTGCAA ATGTTAAAGT CCCCATTGAG TTGACCGACA AAGTTGAATT	180
	TATCGAATTG TATTGAGATT GTAAACTTAG CAGACATTTT TAACCACGAG CATTCTTATC	240
	CAAATAGnCC TTGTCTGTTA TTTTCAAGTC AATTTTCACA ATAGGATCAC TGCATCTTTT	300

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ACCCTCTTTT TCTGCTnCTC ACATAACTTT CAGATGGACT

400

(2) INFORMATION FOR SEQ ID NO: 881:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 881:

15 AAGATATTGC GAAAAGAAGT GACAGTAACA GAGGAATTTT AAAATTTATT CAACCATATA 60
 TTGAAAATTG ATGAAATGGT GCATGCAAAT GAAGCGCGTA TTGCGTATGA AGCAGACATG 120
 CGAAAACCTT TATATAGTAA ACGCATTTAT CAAAATTTAA CATTAGACTC TATTGTTTTT 180
 20 AGAAATACAT TGAGATATAC AGCGATTATG ATGATAGCGG ATATTTATTG CGTTAATGTT 240
 TGATTTTGAA AAAGCATCCT GGATCCCGTT ATCTGCACAT CCAATATTCC TAGGGCCATC 300
 AnCCTATACC ATGCCATCCG AGAGAGGTAT GGn 333

25

(2) INFORMATION FOR SEQ ID NO: 882:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 617 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 882:

ATTGAAAGAA AAAGTACGT ACTTATCCGA TGATAAAATG AAAGAAGTAG ATAATGCACT 60
 AATGATTAGT TTAGGGCTGA ATGCAGTAGC TCACCAGAAA AATTAGGCGT CTATTATATG 120
 40 TATTTTTCAG AGATAAATAA AATATTGATA TAAAGACAA TAACTTTATA ATAATTATAA 180
 CTATTTCTAA ATTCTGTACG AAGAATTTTC TTATAAACAA AGATTTTAGC AAATACCAGT 240
 TATGATATTC ATATTTTTTA TTATAAAGG ATGTCTTAAG TTTTITAGGC TTTAGGTATT 300
 45 CCATCCTAAA GTTTTTTTAG CTTAAAAGTA TCATCTACAG CAAAATTGCA AACGACAAAA 360
 TTGATAAGTG CAATTAAATA AATGTTAGTA AGTGAATCAT AATTATCCTT GCTTAAGCAT 420
 TTGCTTTGTA AGGGAAGTGA GGAGGCAACT AATCGTGGAA GAATTTAAGC AACATTATAA 480
 50 GGGTTTAATT GATGAAAGTT TAACGTGCCA AGATAAAGTA GAATTGATAA AAAAGTGTGA 540
 GAAATACACT GACGAAGTGA TTCGTAAGGA CGTCTTGCCT GAAGACATTG TCGATATTCA 600

55

(2) INFORMATION FOR SEQ ID NO: 883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 583 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 883:

5 GTTGTATTAA AATTTTTCAA TTAAACAACG AAACAATACG AAGAAAAACA TATTACTGAG 60
 15 CCACTGGAAT TGACGAGCTT ATTAGGTAnT ATTTCTCGTC TAGACAATGG TCATTTTGCA 120
 CATTGCGATG CTACTTTCGG TACTCAATCA TATGAAACTT TTAGCGGACA TCTCGCTAAA 180
 GCAATTGTTT CTGCAACTGC TGAAATCATT CTTACTGTAA CTGATTTGGA CATTCAACGT 240
 20 TCATTCAAAG ATGCAGTCGG TTAAATTTA CTTGATCCTC AATAGCACTT TACTTTTTAG 300
 TTGAATCAAA TTTTATTACA AGTTATCATA AGTGCTTAAT CATAAATGCA TTCTCGTTTA 360
 TTAATATACT TCAACGAGTT AAATTAAATT TTAAATTAGG AATTGAATGC GTTTATAACT 420
 25 ATCACATTTG aATGaATAAC TTTTTCATTA GAAAGTAGTG TkTATTATTG aTGCAATCTC 480
 GaTACATCGC TAGAATTTAC TTTtaATTTT ATTTATCGTC TCCCTTnTTG AGACTAAAAT 540
 30 TTTTCAATTT ATGACTTTAA ATTTGTTTTT AGCATATATA CCT 583

(2) INFORMATION FOR SEQ ID NO: 884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 524 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 884:

GCAGAGGGCT TACGATAAAA AGAAAAATCT CGCTCGCCCG CTTCAAGTCAA ACTCACAAA 60
 45 GcTAACGCAt GwyTGCTyCA TTCGTGCGAT AACTTTTGA TACATCTACA CCAATACTTG 120
 ATATCGTTTC AATAATGCTA TCTCCAAATG CATCATTACC TAATTGTGTA ATCATAtACG 180
 CTTGTTGTCC LAACTTTTGA ACTGTACAAG CTACATTGCA TGGCGCGCCA CCAATTTGCT 240
 50 TCGTAAATGT TTGAACATCT TTAAATTCG CATTGTGAAC ATTTGGAATA AAATCAATTA 300
 ACGCTTCTCC TATTGAAAAT AGACGTCTCA TTTATGTTCA TCCTTTAAAT CATATTTAGT 360
 AAATTGTAAA TATACTTGCC CTGATTCTGT TGATGTTTTA ATACCTAGTG CGTCTTCTGT 420

TGTATCAACA AAAATTTGTA ATTGCTTTAA TGGCGTGTCT AATA

524

(2) INFORMATION FOR SEQ ID NO: 885:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 885:

TTAATGATTT CTTCGTATGA TTCACCAACA ATTTGCGCTA AAATATCATG CGCAAGTACT 60
 TCACCTTCAA CCATAAATTC TATTTGCTCT ACTAAAAATT TTACGTCATT CATGCTATTC 120
 ATTTTTGGAA TTAACAAAGC ATATAAGTTT GTAAATTCCTT TTAAATACGC AGCATCAGCT 180
 TTTAAGTAAT GGCCTAATGC GTCACCTCCTA TATCTCCGGA TAACATCTTC TGAATAAAGT 240
 CATCCTCATA AATATCATAA TGATGGCTTG CAGCTGGGTA CAATTTTGTG AAATTCCATG 300
 TAAAAATCCT CCCTAAATAA AAAACTACTT CCAACATGAA GAGTTGAGGC ATGTGCAAAC 360
 TAGCCCATCA CTCATAACAC TTCCACGTGG GACTACCAAC 400

(2) INFORMATION FOR SEQ ID NO: 886:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 857 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 886:

AAGAATTTAA ACAAATGAT ATTTGGAAAC ATTTTAAAGC TGTGAAAAAT AATCATGTTT 60
 ATGACTTAGA GGAAGTGCCA TTCGGTATTA CAGCAAATGT TGATGCTGAT AAGGCAATGA 120
 CTCAATTATA TGATTTATTT TATAAGGATA AAAAATAGTG AGTTGATATG ATGATAAAAA 180
 ATAAAAAGAA ACTACTATTT TTATGTTTGT TAGTCATTTT AATCGCAACT GCTTATATTT 240
 CGTTTGTAAC CGGTACAATT AAATTGTCAT TTAATGACCT ATTTACAAAA TTTACAACTG 300
 GTAGCAATGA AGCAGTGGAT TCAATCATTG ATTTGCGATT GCCACGTATA TTAATTGCAT 360
 TGATGGTTGG CGCAATGTTA GCAGTTTCTG GAGCATTATT ACAAGCAGCA CTACAAAATC 420
 CTTTGGCAGG GCGAATATCA TTGGCGTTTC CTCAGGTGCA CTTATAATGA GAGCCTTTGT 480
 ATGTTGTTTA TTCCACAATT GTACTTTTAC TTACCATTAT TAAGTTTAT TGGAGGTTTA 540

ATATTAGTAG GTGTTGCGTT ATTCGTATTA TTAAATGGTG TTTTAGAAAT TTAACTCAA 660
 AACCCCTTTAA TGAAAATTCC TCAAGGCTTA ACAATGAAAA TATGGAGCGA CGTATACATA 720
 5 TTAGCAGTAT CAGCATTATT GGGATTAATA TTAACATTAC TATTGTCCCC TAAATTGAAT 780
 TTACTAAATT TAGACGACAT ACAAGCGCGA AtATCGGTTT TAATATTGAT CGTTACAGAT 840
 GGTTAACAGG GTTATTA 857

(2) INFORMATION FOR SEQ ID NO: 887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 887:

GATTTATTTT AATATTATTG TTAGAAGGAA TTTTACAAA TTCAGCGAGT GCAATCGAAT 60
 ATTCAGACTT ACATCATAAA AGTAAGTTTG ATTCAAAGCG TCTAAGTAAT GCTAAGATGT 120
 25 CATTCAACAA TCCAACCTCAG CTTGAAAATA AAAACACAAA CGATAGACTG TTGAAGCATG 180
 ATTTGTTATT TCATGACATG TTCGTAAATG ATGATTGGAA AAAGGATTTT AAAGTTGAAT 240
 TTGAAAATGA GGCACCTTCA AAGAAATTTA TAAATAAGGA TATCGATATA TTTGCTGGAA 300
 30 ATTATGGATA CGGATGTCAT GGGGGAGCAA CCAATAAAAC GCAATGTAGT TATGGTGGTG 360
 TTACTTTAAG TGACAATAAT AAATACGATG ATTATAAGAA TATACCTTGT AATTTATGGA 420
 35 TTGACGGACA TCAAACAGAA ATAGAACTAA CTGCAGTAAA AACGAAAAAG AAAATTGTTA 480
 CTATTCAAGA ATTAGAGGTT CAATTAAGAA ATTATTTGAA TGAGAAGTAT AAGTTGTACG 540
 AACAAAGGTGG CGACATTGTT AAAGGGTATG TTAAATATTA TAATGATGAT GAACAAAATG 600
 40 TAGAATATGA TTTTATAAT TTAAATGGTG AGTATGGTCG TGAGGTATTA AAAATGTATG 660
 CnGATAATnA AACnA 675

(2) INFORMATION FOR SEQ ID NO: 888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 888:

AATTCCTAAT TAACAATGCC TTCATTAAAA AACCTTCTTC CATCAATTTG ATGTTTTCAT 120
 GATATTTAGG TTTTCTCTTT TCAAGATAAA CCATTAAAGTy CTCAATAGAA GGTGTAGTGA 180
 5 TATTCACCTTT AkGACCTAAA ATTTCTTTAA ATACTTGCGC ATGTTCTGTT AATCCTATAA 240
 ATCCCGTACG CTTATGTTCT TCATAAATAA GTAGAGATGC TAATTCATCA TCAAGGTCCT 300
 CAATAGCACC ACTCACAAC TGAATATCTTT GTAACAGTTG TTCTTTTGAA CCATTAAAGA 360
 10 TAACTTCACC GTCACCTAAG TGAATGATAT AATCAGCTAT TTTTCTAAA TCTGAGATAA 420
 TGTGTGTCGA CATGAATATT GTTTTATTTT CATCAATTAA TTCTTGCTGA ATTATCTCCA 480
 ATAGCTCATT TCTAGCTAAG GGATCGAGAC CTGAAGTAGG CTCATCAAAA ATATACAATT 540
 CAGCATGATG TGAAAATGCA ACTGCTAGTG ATAATTTTCAT TTTCATCCCA GTCGAAAATG 600
 TTTTATTGTA TTTATTGATT GGTAAATCGA ACTTTTCAAG ATAAAATTCA AATACTTGAT 660
 20 GGTCCCATTT ACGATAAAAA GGGGcAATCA TTTTTCaAG TTGCTTCGTA GTCCATCTCT 720
 CATTAAAATA ATTTTCAGAG TAAACnAACC CAATTCTATT CTTTAACTCT ATCGGATTGA 780
 GAGCCATATC CTCTTCTAAT ACTCTAATAA CACCAGTTTG TGGGTGATAC AAATCCATAA 840
 25 TTAACCTAAT n 851

(2) INFORMATION FOR SEQ ID NO: 889:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 889:

AATCACCTTC ACGCCAATAT TGATTTTCAT GCGTAAATAC TTGTGCCGTT TCATGATACT 60
 40 TTGTCAATCG TGCGTGTTGC TGGGGGGAAT ATTTTTCAGT AGCCCAATTG GCTGCATGAC 120
 CTTCAATGGC TAGTTCAATT GCAGGATTAA TTAAATCTTC CAATGACAAT TTAGCATAAC 180
 GCTTGTGAAT ATAATCAAAC AGCTTTGGAA TTGCTGGCAC ACGACAGTTT TACCATGTGT 240
 45 AGTCATATCA AAAAATGATT TATATTCGCC TGAATCAnCT AGATAAAATT GGTTGGCTAC 300
 ATGGTCAGGG TGCTGGCTCA CGGTGCATCA AACGCnGnTA ATACTGCCCA GTACCTTTGC 360
 50 TC 362

(2) INFORMATION FOR SEQ ID NO: 890:

(i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 747 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 890:

	TTGGTTTATT CCCAAAAGT ACGCGAAAAT TAGTAGAGAA GAATTTGAAA GTTTAAATAT	60
10	TGTCAAACCC GCTAAAAATA ATACTTTCTG GCCTGTTGCA GGATTTGCAG TGTATTAAAC	120
	AACCTTAACA AGAAAATATA TCTATTTGCT TAACATCCAT TTAGAAAAAG AAATAGTTAT	180
	ATTAACATGC TGTATGATAC TTCTAGGTGT TTTCGCATTG TTTATATATA TAAATACAAA	240
15	ATTGAAGTTA CATATTTTTG ATAAAAATAA AAGTAATAAC GAAAAGATCA TATTAATACC	300
	TACATTTAAA AATATTTGTT TATCCTTATT TGCTTATATA TTATTTGGTG GATTGTCAAC	360
	AATGGCTCTG AGTATGTTAG TAACTTCATC CCCTCAAAAT ATAATAGAAT TTCTTGCTTT	420
20	AATTGGCATG ACTGCATGCT TCTTTCTACT GAATATGTCA TCGGTTCTAG ATAAAAAAAT	480
	TCATGTTATT TTAAAAACAA ATAAGTAGTA AAATTGATTA ACTTAGGTAG TATCGGATAC	540
	TTAAATGTTG GTTCATAAAA AGCAATGATT TTAAATCGAG GAGCTATCTT AGAAcAGGGA	600
25	AATAAACAG CCAAAGTTAT AAAAAGTGAA TTAATACTA ATTATATTAT GTTAGCCACG	660
	CTTCAAATAA AAnATAATTA GAATAAGGTG GGATTGATAA TCAAnGCTAn GCGAATCTAA	720
30	AATCATCAAT AAAAACCCCA AATATAG	747

(2) INFORMATION FOR SEQ ID NO: 891:

(i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH: 526 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 891:

	ATTTTGAAAT TTTAGCAGAT ACTGATAATG GTCTCGATGC AATGAACTT ATTGAAGAAT	60
45	ATAATCCTAA CGTTGTTATT TTAGATATAG AAATGCCAGG CATGACTGGA CTTGAAGTTT	120
	TAGCGGAAAT TAGAAAAAAG CATTGAATA TTAAAGTGAT TATTGTAACA ACTTTTAAAA	180
	GACCGGATA CTTTGAAAAA GCAGTTGTGA ATGAtGTGGA TGCATATGTT TTAAAAGAAC	240
50	GTTCTATAGA AGAATTGGTG GAAACCATT AATAAGTAAA TAACGGAGAG AAAGAATATA	300
	GCGCCACATT GATGACTTCA TTTTTGTAG ATAAAAACCC ATTAACGCCC AAAGAACAAA	360
	TTGTATTAAG GGAAATTGGC AaTGGTTTAA GTAGTAAAGA AATAAGTGAA AAATTATTTT	420

55

ATCGTTTTGA TGCTTGGGAA AAGGCAAATG AAAAAGGCTG GACCTA

526

(2) INFORMATION FOR SEQ ID NO: 892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 892:

15 TATTTGATGT AAAAGCGAAn GAACCATACA ATGTAACAAT TACTAGTGAT AAATACATCC 60
 CTAATACTGA TTTGAAACGT GGGCAAGCTG ATTTATTTGT AGCGGAAGGT TCTATCAAAG 120
 ATTTAGTGAA ACATAAGAAG CATGGTAAGG CAATTATAGG AACGAAAAAA CATCATGTTA 180
 20 ATATTAAGTT ACGTAAAGAT ATTAATAAAA TCTATTTTAT GACAGATGTT GATTTAGGTG 240
 GACCAACGTT TGTCTTAAAT GACAAAGACT ATCAAGAAAT AAGAAAGTAT ACAAAGGCAA 300
 AGCATATCGT CTCTCAATTT GGATTCGATT TGAAACATAA AAAAGATGCT TTAGCATTAG 360
 25 AAAAAGCGAA AAATAAGTT GATAAATCTA TTGAAACAAG AAGTGAAGCG ATAAGCTCAA 420
 TATCAAGTTT AACCGGAATA TTATTATTTG TAACATCATT TTTAGGTATT ACATTCTTGA 480
 TTGCTGTATG TTGCATTATA TACATAAAGC AAATAGATGA AACCGAAGAT GAGTTAGAGA 540
 30 ATTATAGTAT TTTGAGAAAG CTTGGATTTA CACAAAAAGA TATGGCAAGG GGAATAAGT 600
 TTAAAATTAT GTTTAATTTT GGGTTACCTT TAGTTATTGC ACTATCACAT GCATATTTTA 660
 35 CATCATTAGC ATATATGAAA TTAATGGGTA CAACGAATCA AATACCGGTT TTCATAGTAA 720
 TGGGATTATA CATTTGTATG TATGCTGTTT T 751

(2) INFORMATION FOR SEQ ID NO: 893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 893:

50 GGATGTTGTA CATTATTCAG ATTACTTTGA AGGGGCACAA AAATATTTGA GCTATTTAAA 60
 ATCAACAGTA GATGTTAACT TTGAAGGTTT GAAAATTGCT TTAGATGGTG CAAATGGTTC 120
 AACATCATCA CTAGCGCCAT TCTTATTTGG TGACTTAGAA GCAGATACTG AAACAATTGG 180

TAGCTGAAAA AGTAGTTGAA ACTGAAATGA TTTTGGGGTT AGCATTGGA CGGCGATGGG 300
 AGACAGAnCC ATAGCAGTAA GATGGAGAnG GnCCAATCCG TTGACGGTGG ACCCAAT 357

5

(2) INFORMATION FOR SEQ ID NO: 894:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 464 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 894:

15

GCTAACCTGC AAAATTCGAT AAGCGATTCA ATaCTGAcGC CTGcATTTCG CAAATTTTTTC 60
 ACTAAATAAA TCCAATTTAA ATCACTATCA TTATATATTC TATATCCATT TTCATCTCGA 120
 TTAAGTGGTG GAATCACACC AACCTTTTCA TAATATCTTA AAGTGTCTTG AGATATATTC 180
 ATGAGCGCTA CGACTTCTTT AGTTTTCATT GCGACTATCC TTTCAGTTAT GTTTGGTCGT 240
 CTAAAGTAAT GTTGCTTTAT ATATTGTCAT CTCGTTTGA ATACTTCTTA TTTTATTACT 300
 CAAATTTAAA TTTGTCTCTT TTTTAACATT TTACATTTCA TCGTTTTTAA TTACTTTAAA 360
 AATTGTATAA CTkAAATATT TAAATGATA TAAwCACTAA GATTGaTAAT AtTTAATTnT 420
 TTGGAAAATT ATnTTAAGTT GCCAATTTTG GGGGGATGCG GAAA 464

30

(2) INFORMATION FOR SEQ ID NO: 895:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 599 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 895:

40

AnAATGAAAG AGTTACAGGA CTTTATTGCT CGTTTCTCAG TAACGCTTCT AAATCTAAAC 60
 AAGCAACAAG TCGTAAAAAA CAACTCGAGA AAATTGAATT AGATGATATT CAACCATCAT 120
 CAAGAAGATA TCCTTTCGTT AAATTCACAC CTGAGCGCGA AATCGGTAAT GACTTACTAA 180
 TCGTTCAAAa TCTATCTAAA aCGATTGACG GTGAAAAAGT ATTAGATAAT ATTTCATTCA 240
 CAATGAATCC AAATGATAAA GCAATTTTAA TTGGGGATAG TGAAATTGCG AAAACCACAT 300
 TGCTTAAAT ATTAGCCGGT GAAATGGAAC CAGACGAAGG TTCATATAAA TGGGGTGTA 360
 CAACGTCATT AAGTTACTTC CCTAAAGATA ACTCAGAATT CTTTGAGGGC GTTAATATGA 420

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GCGGCTTCTT AGGCCGTATG CTATTTAGTG GAGAAGAAGT TAAGAAAAAA GCTAGTGTAC 540
 TTTCAGGTGG AGAAAAAGTA CGTTGTATGC TAAGTAAAT GATGTTATCA AGTGCAAAC 599

(2) INFORMATION FOR SEQ ID NO: 896:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1057 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 896:

TCATTAGTAG AAATCGTTAA AGATGCATCT TGCAATTTAA AATCCGAATC TTTGTATTGT 60
 TTGTTACAC TATCTACGTT TAACAATGTT GTCATATCCA TGCTCCTCTT TGTTTAATTT 120
 TAATAAAAAC GTCTTCTCTT CAATAAATAA CTAAAGGCGT TATATATGAA AATAGCAATG 180
 ATAAGTAGCA AACTAAAGCT TTGATTAATT CCAGTAGTAA TTGAATAAAG CCCAATTACT 240
 ACAATGGCTA GTATCAATAT TGATAAGTTG ATCGCATATG TTTTAAATAA TGCAATTAAT 300
 TCTATATGGC GTTCACCTTC ATCCAATATT TCCAATCGCT TTTCAGTGTA ATTCTTATCT 360
 GCAATTTTTG GTATTCTGTC ATCAAACCTT CTATTAAACA GTGTAAATTG TGTATTGAAA 420
 ATAGCACTAG CAAAAAATGG TATTAAAAAG AATAGTATTG CATTTGCTGC AGCGTGCCCT 480
 ACCACAAAAA TAAGCAATAC TAAAAAGCA ATAAGTGTCT GCAGAATACT TAATATACTT 540
 CCATTTAAAA CATAACGATT CGCAAGCAAC TCATATTGAT CTGTTGCATC GATATCTACC 600
 TCTTTATCTA CAAGTTGCTT ATACTTCAAT GCACGTCTTT GATTCATCAA AACAATGGCT 660
 TCTACCAATA TGATAATAAT CGTCGCAACA ATCGATATTA CAACGACATT GTTATATGTC 720
 GCAAACGTCA AGTTCTCAAT ACCAAATCCA TCAAAATTAC CTAAAATTCC ACCTATGATA 780
 CCCCCTACAA GTCCACCCAG TAAAGATAT CCGATATATC TTAGTATTTT CATGCCTCAT 840
 CCTCCTCAAT AATAAAAACA GTTCCACCG TTTCATTGAA AATGCGAGCA ATTTTATTG 900
 CCGTTAATAC TGATGGCATA AAATGTTTTC GCTCAATTAG CGATATGGTT TGTCTTGAAA 960
 CGCCCGCTTG TTTAGCAAGT TCGGTTTGGT TTAAGCCATC TCGTGCTCGT AATTCTTTCA 1020
 ATCGATTACG CACATCGCAT CAACTCCnTA ATTACAC 1057

(2) INFORMATION FOR SEQ ID NO: 897:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 897:

5 AAATTATTGA GTTAACAAAT CATTACGGAG CACATAATTA TTTACCATTG nCAATTGTCA 60
 TTTCAGAAGC CGAnGGGGTA TGGGTAAAG ATCCTGAAGG CAATAAATAT ATGGATATGT 120
 GAnCTGCATA TTCCGCTGTT AACCAAGGTC ATAGACATCC GAAAGGTATT CAAGCATTAA 180
 10 AAGATCAAGC TGATAAAGTG ACTTTACTCT CACGTGCTTT TCATAGTGAT AACTTAGGTG 240
 AATGGTACGA AAAAAATTTGT AACTGGCAG GTAAAGATAA AGCTTTACCA ATGTAATACA 300
 GGTGCTGTAA GCAGTAGAAA CAGCTTTGAA AGCAGC 336

(2) INFORMATION FOR SEQ ID NO: 898:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 898:

TGnTGnTTTC TTATTGTTGA CCAATTATTT TGCATACCAA ATCCAAATCA TGTATTTATC 60
 AATCACATCC TAATGCTAAA TCCAATGTAT TACATTGTTT AATGGTATAG CACAATCTAT 120
 30 CATATTTGGT ATATCAAGTA TGGAAAACAT TCCATATCAT TTTTACTTTA TTTTATTCTT 180
 ATGTTTAATA GCTGCAGTAA ATTCGTATT AGCAGGTATA CGACACACGG CAATTTATAA 240
 TAAACATCT AAAGTGACAC AACTGATAA TCAACAGGGA GTTTCAAAGA TAGTCAGACG 300
 35 GG 302

(2) INFORMATION FOR SEQ ID NO: 899:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 469 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 899:

CCACTAGCTG ATACAGTAGG TATACCAAGA TTCGTCATCG TTACGACATA TCAATTTGGT 60
 50 CAATATGCGA TGTTATTCTT AGCGCCGACT GGACTTGTTA TGGCCACACT ACAAATGTTA 120
 AACATGCGAT ATTCACATTG GTTCCGATTT GTATGGCCGG TAGTTGCTTT TGTATTGATT 180

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TATAAAAAAT ACTAATGGGG TTTTATGCAT CTCGTAGGTT TGTAGAAATA CTAAACTAAG 300
 CGAGGTGCAT TATTATTTTT GATTAAGAAA ATAATGACGG TAATGATAAC ACTAGTAAGT 360
 5 AATTGATACA ATGCTCTATT TAATAATGAT ATTTTAAAAA TTGTTTTTTA ATGTAATGTT 420
 AGATCTATGG TATATTATAT TTAACGTGGT AAATATGTAT TTGCTGTAA 469

(2) INFORMATION FOR SEQ ID NO: 900:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 821 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 900:

CTTTATTGGT AACTCTCTAT aATATtTTaA CATTTTTACG CTATCGTGCA AACGCAAcCa 60
 CTTTGAATTy TCTGATATTT TTAGCATATA ATTTACACCC TGCACGATGA ATTGTTAATC 120
 CAGTTGTATA AATATCGTCA ACGAGTAATA TTTCTTACC ATTTAAATCT AATTCCGTAT 180
 25 CAATAATAAA TGGATTTTCA TCTGCCAGAC GCTCTTTCTT AGTTAAATGA GACTGTTTTG 240
 GTCTATTTGA CATCTTTAAA ATCTTATCaA AGCGAATCCC TTTAGCTTTT AGTACTGCCT 300
 CTACCGGGTT AAATGTTCTA GATAATCAT GTGCCGGCGA AGAAGGAATT GGCACAATAT 360
 30 AGTCATAAGA TGTTTGTTGGT ATTTCAATCA AATGTGCCAA TAATTCACAT AAATAATAGT 420
 CTTTCAAAAA TTTATACTGA TGTATCATCT CTTTCATTAA ACCGTCATAT TGAAATTGAC 480
 AATATAATTG TTCCATTAAA TTAAAGTGTG CCGATAGAAA CTTGCAGTCT AAACAATACG 540
 35 CTTCATCTTG ATTTAAGTGT TTTAAGCACC TTGAACATCG CCTTGCTTTA ATATCAAGTT 600
 TAATATTGTC CCAATTCTCT TTGCATCTGT CACATAATCT ATTAGGTTTC TTGAACAAAT 660
 TATAAATGGT TATATTTTCA TATAACTTAG CACCACAACCT CAAACAATTA TTCATCAATC 720
 40 CAACCTCTTT TTAATGCTAA TTGTTCATC CTTTGAATCT CTTTTTTAGC TTGAATCATA 780
 TTCATACTTA CCCCTTnCAT GAAAAAACAA TACTTTTTCC A 821

(2) INFORMATION FOR SEQ ID NO: 901:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TGATGCTATT AAAAAGTTAA TTGTGCGGTC TGTTTTGATA ATTTTAATAA TAACTTCAGG 60
 TAACTAAAAA TCCTAATATT GAAAAACAA AGCCATTTAA AACATAACCT AGTATATTCC 120
 5 ATGTATGATT GTAACCTATT TGCCAGTTnT GTACTGACTT GCATAATTCT GTCACGTnCG 180
 AACCATGTAC AAGCCTGCAA CTACTGCTGA ATGATTCCTG ATGCGTGAAC AATTCAGCAA 240
 TTAAATACGT AACAAATGGT GTTACAATTG AATAATTGAA ACATATTAAT GTTTCATATC 300
 10 CTCGACGnCA TCAATGTTAA TCCGGACCTT ACTAATGCAT ACCTATAAG 349

(2) INFORMATION FOR SEQ ID NO: 902:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 902:

CAAGTGGTAT AAATTTACCT GGTGAAATGT AGGTCGTGGT GGCGATGATA CATTATTTCG 60
 25 TAAAATCGAC GCGTTGTTA AATTCGAACG TAAAGGTCGC GACAAAAAAC AAGTTTCTGT 120
 ATATGCAGTT AGCTGAATAA TTTTGTCTAG TTAACACCAG AAAGTGAATC TTCTGGTGTT 180
 TTTTACTTTT TATAAAATGT TTTTCATTAT TATTTTCATT ATGnTATTTA AAAATGGGGA 240
 30 TTTTAGACGT TATACTAAAT GTGCACTGTA TAGGGGCCCT AATCACTAAC TATAGGGGGA 300
 CAAGGATACA GTGCAGCGTT AAGGATAACT GnCCACATTG GTCTGGGAAT ATAGGATTTA 360
 AGCAAGGTTA TAAAGTACTC nTAGGCCCTA 390

35

(2) INFORMATION FOR SEQ ID NO: 903:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 903:

GGAATAGACG TATATGCGCG TTGAATTTAA TCCTAATAAG CTTTCGCATG ATGAAGTGCT 60
 TTGGTTAAAA CAAAATATCA TCAGTTATTT GGACGATGTT AGTTTACGA GATTAGATTT 120
 50 GGCTTTTGAT TTTGAATTTG ATTTAAAATG ACTATTATGC ATTGTCAGAT AAGnCGGTAA 180
 AAGAACTAT ATTTTATGGC CGAATGTAAA ACCAGAACAA AATATTTTGG TGnCGAATA 240

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GATTCACATT CTATGCGGTG GAATTGATTA AACG

334

(2) INFORMATION FOR SEQ ID NO: 904:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 904:

15 CAAGTTGGGG ACACTGTTTC AAATGAAACA ACAGTGTGTA TTTTAGAGGC AATGAAACTA 60
 TTTAATGAAA TTCAAGCAGA AATTTAGGT GAAATTGTTG AAATCTTAGT AGAAGACGGA 120
 CAAATGGTAG AGTATGGCCA ACCGTTATTT AAGGTGAAAT AATGAAAAAG GTTTAATTGC 180
 20 AAACCGCGGT GANTCGCAGT TAGGATTATT CGCGCTTGTC GTGATTTAGG CATCCAACT 240
 GTTGTCATCTT TCTGAGGGGA TAAAGATCGC TACATCTCAA ATGCTGATGA GGCATATnCG 300
 TGGGCCnCTT GTCTAAGGTC ATATTTAATA TCCG 334

25 (2) INFORMATION FOR SEQ ID NO: 905:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 905:

35 TTCACCCTGT AATTCTTaaC CGTCAATTGA CCTTTATGCA GATTTAATAT TCCTAAAACG 60
 TATAACTCTT CTAATGATAA TTGACACATA TTAAATAAC ACTTTAGATT CCGCAATAAT 120
 40 TCTTGTGACG ACAATAAATA CGATACATAG TCACAATAA AATCAAATGT ATATTGACCA 180
 AAATAACGTT CAATATAGTC ACTAAGCTCA TTATTCATAT ATTCTATTn ATCTATATGC 240
 ATTTTATTAA TCGAAATAGT CAATTTACGT TGATCCCTTT GATCTCTTCC TTTCAATAGC 300
 45 CATTGATGAT TGnTAAATA ACTTAACATT TGAAGAAGGG CCATCTTAGA TTGGATTCT 360
 TTCATnTTA ATAACTATC TATTGAAGCG CTATTGGAA 399

(2) INFORMATION FOR SEQ ID NO: 906:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1478 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 906:

5	TACATTTTTC AATTTATGGC AAAATnCACa ATTTTCATCG AAATATTTTG TAnAnAATCA	60
	TTGCTAGGTG ATGAGTTATC TCGGTTAATT ACAAACGAT ATCTAAGTTT AAATATTAGA	120
	TCATAAAAAA ACTATCTACT GAATATCCCT CCATAGCATC ATTTTCTAA GCAAAAGTTA	180
10	AACTTAGTTA GATAAAATGC AAATGAGATT ATTGTAGATA GTCTCTTTT AATGTTTAAA	240
	AATGATTAAT GCCaTAAACA TAAATAATTC CaAAGAATGC CGCGCCACTA AGCACTGTTA	300
	ATATAAGACT TAGTAACAAT GTGCGTTTAT AATGTTTaAC AAATGCtATG AACAAAATGA	360
15	CTACATTATA CGCAAAGAAA AGTCCGAATA ATGTCATTGT TATTTTCAAA TCAGAATAGA	420
	AAATATTTAA TAGTAATACA ATGACTGCAT AAATTAAATA CGGAATAACT ATAAATTTGC	480
	GTTCAAATCT TAATTGTTcG AAaCGtTTAT CTTcGTTTGT CATGATATGC TCCTTTATGA	540
20	TTTAAAAGTA AATAAGTTTA CGGAAtATCT TGTCCGaTAA TAGCGGTGTA AAtGTCAAAC	600
	CACGACTGAT CATCtAAATT AAGTkGTAGC CctTCGATTG CTTGATCAAT ACGCTTTAAC	660
	TGACTTGTTc CAAGTATCCG GCATGATACG ATGCGGTATT TTTACTAACC ACGCTATCAT	720
25	CACAGCTGTG TCACTyACAC mATATTGTc AGCTATTGAT TGAACAACtT TCATAATACG	780
	TTGCGCTTTA ATATCTTCCT TGTCGAAAT TTTACCGCCT GCAAAAGGAC TCCAAGCCAT	840
30	GATTTGAACA TGGTTTTGAT ACATTGAATC CATTGTTCCA TCTTGTAAC TATCAACGTG	900
	ATATGGCGAT AATTCTAATT GATTGATGCT AATATGTAGT CTTTCTTTCA TAATATATTG	960
	ATTTAACAAT TGGTATTGTG AATGATTAAA ATTCGACACC CCGAATGACT TCAACTTACC	1020
35	TTGTTTAACA AGTTTAGTTA ATGCATCAGC AACTTGTTCT GGaTCCATCA ATGGTGaAgG	1080
	ACGATGAATG AGTAGACTAT CTAAATAATC TACATTCAA TTGATTAAATG ACTGTTCAAC	1140
	AGATTTACAG ATGTGCTTAC TACTCAAATC ATAACGATGT CCATTTGTAA AATCAAATTG	1200
40	CTTAGAAGGC AAAATGATAC CACATTTCGT AACAAATTGA ATTTTATTTC TTAATTcGGG	1260
	TGATAAATCC AAAGCATTAC CAAACAGTGA TTCACATTGA TAATCTCCAT AAATATCAGC	1320
	ATGATCCATC GTTGTAATTc CACGTTCAAC TAATTCATTT ATAAAATAAT TTAActCTTT	1380
45	CGCAGTCATC TTCCATTcAT TTGCACGCCA AAAACCTTGT ACAAGCCTAG AAAAATGAAC	1440
	ATAGTGATTA ATCATTATTT GTTCCATATn TCATCCAC	1478

(2) INFORMATION FOR SEQ ID NO: 907:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 543 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 907:

	TTCTATGAGA ATAGATATTG TTAAATTAAG AAAGTAGTCA ATTTTATTAT GACAAAAGAA	60
10	AGAAGAACAT TTAGTTCAGA GTTTAAGTTA CAAATGGTTA GATTATATAA AAATGGTAAG	120
	CTTAAGAATG AaATTATACG AAAGTATGAT TTAaAACCT CAATTATCTC AAATTCGATA	180
	AAACAACACC AAAATACTGG ACCCTTCAAT CATCAAGATA ATTTAAAAAG TGATGAAAAA	240
15	GAGTTAATAA AATTACGCAA AGAAGTTCAA CATTTAAAA TGGAACATGA TGTTTTAAAG	300
	CAAATTTTAA AGTTGATTTA GAAACTGAAC TTTTAAAGA TACATTACTT GAAGATTCTA	360
	ATTTATCTGA TTATATAAAG AACCAACTTC CAACGATATG GAGAGACTAA GAAATAGTTT	420
20	AAATTTATTT AATTTCAATA AAAACTCATA ATAATATTTA AGTAAGTTAG ATTGCTTTTA	480
	GCATTAGGAA TTCGCTTATA ATTAGATGTT CAATATAGAC TTTTTTACAC ATACATGAAC	540
	TAT	543

25

(2) INFORMATION FOR SEQ ID NO: 908:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 751 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 908:

	TTTnCGGTnG AACATGATTn CGATATTACT TCTAAAACGA TTCAACCAA ACCAGGAGAA	60
	AGTGTTGGAC GTTTAGTTAA TGTGATTGT AAAGATACAG TACTGGAGTA TTCAGAATTA	120
40	GATCCAGAAG TTGCAAATCA ATTTAACAAT GCTAATATCG GTATTCATGC ATTTAACTT	180
	GGTTTTATTT TAAACGCTGT AAATCGTGAG TTACCTTATC ATTTAGCTAT TAAGAATTTG	240
	AAGCAATTAG ATGAGAACTT TGGTGTTATT GAACAACCA CTTTAAAAIT CGAATTGTTC	300
45	TATTTTGACA TATTTACTTA TGGAACTAGT TTTGTACGT TACAAGTTCC TAGAGAAGAA	360
	GAATTTTCAC CTCTTAAAA TAAAGAAGGT AAAGATAGTG TTGCAACTGC AACAGAAGAT	420
	TTACGTAGAA TGGGTTTAAT TTAATGATAG GCGGTGACTA TGATGTCCAA ATCAACTAAA	480
50	AAAAGTAATG ACACAATCGT AGAAACATTT AAGGATATCA TCCCTTTATC ATTTGGAGAA	540
	GAAATTGGTA ATGCGGCATC TCATGGTGTT GCAGCTTTGT TAACATTATT AGTGTTACCC	600

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TATGTTATTT CTATCTTTAT GATGTTTATT TCATCTACTA TTTATCATTC TATGCAAAAT 720
GAAACACCTC ATAAATATAT TTTAAGGATT A 751

5 (2) INFORMATION FOR SEQ ID NO: 909:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 394 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 909:

AAATTGTCAC AATTCAGTCT AATTTAAAAG GAAGTTAATT ACAAATTAAT AAAATCATGC 60
 ATCGTGTCAT TTAGATATTG AAAAAGATGA GTCAAATTTG TTTCATATAT TTTCCAATAA 120
 20 CAAATTATTA TATCTAAATA TACAATCAGA AATATATGAA TAGAAATATC AATAAGAAAA 180
 ATAATATGAT TAAAAATGAT GAATGGCATA CTTATAAAGT GTCTAAATAT TGGCGGTCAA 240
 TATTACTTAC AAACACGAAT GTTAAGTAAT GTAGACAATG cTGaAAAAAC AATaAGTAGa 300
 25 AACTCTATAT AGAATGTTTCG TTTTATTTT TaATAATTGa ATAATCaTTA TTGGGTGGAT 360
 TTTAATATGG nATTCCGGTC GGCACACGGA TTAC 394

(2) INFORMATION FOR SEQ ID NO: 910:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1022 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 910:

40 TAAAGCTAAG AAAAAAGAAA AACGTAAAGC TTATAACCAA CGAATGAAAG AACGTAGGAA 60
 AAATCAACCT AGCGCAGTTA GTCAACGTCG AATGAATTTT GAAGAGCGAC GTCAAATTTA 120
 CAACAATGAT ATTTCTGAAG AACGCAATTC AAGTGAAGTT AAGGACAAAA AAGAGCAAGA 180
 45 ATAAATATTG ATGATACCCA GATTAGTAAG CAGAGGTCTT TTGCTTATTA ATCTGGGTTT 240
 TTATATGAGG TTAATTATCG ATAACGTTTA ATTAAAGTGT TTAGGTGTCA TAATTTTAAA 300
 TGACGATTTC CCCATTACKA TACACCTAAA TtATCATCAA TCTGaATTCA GATGTTTATk 360
 50 ATAAAAATTA GATGAAAAAT ATGTTAATAT ACAAGkAaTT TAATGTGcGk ATATCTATAG 420
 GCTCGTAGTA TACTTATTAA AATATTAAAC AAAGAAAGGA TTTTAAGATG AATAGAAAAC 480

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GGCTATCCTA TTTTCTTTA AAAAGTGGTA ATGCATCACA ACGTGAAGAA TTAGCGAAGC 600
 AATTATCTCA GAACGGTGGC AAGGTTTCTT TAGATATGCT TCAGACAACA ATGGGTGCAT 660
 5 TAGCAATTAT TTTATTAATT TCAACACTTT ATGGTATATT TGCACAAATT TGTATTAAAG 720
 GACGTAGAAA ATTATCGATT AACTTTTTTG TTATCGCGAT AATTGTAAGT TTGATGGCTC 780
 TTAATTTAAT TGCAATTGTC TTATGGGTTA TCGTGATGAT TATGTTGATT TCTAAAAAAG 840
 10 AATCAAAAGA AACAACACAT AAGGACGATG AGTATATTTA TCATTAATAT GTTCATAGCA 900
 AAAGAAAAAC CATTAAATG TTAAGTTGTT AATTATTAGA TACAACCAAC ATTTTAATGG 960
 15 TTTTATTTTT AACTTTGTAG TTCTTGAAT GTTGAACGA TTAAATAGAC ATTTAAAATA 1020
 CT 1022

(2) INFORMATION FOR SEQ ID NO: 911:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 274 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 911:

GGTACTTTAT TTTTATTTTT GGTCTTAGTG ATTTTACAT TATTACATA TAAAGCGCCT 60
 30 AATGGTATGC GTGCCATGGG TAGCATTAGC TAATGCAGCA ATCGCAACAT TTTTAGTGGA 120
 AGCATTTAAT AAATATGTnG GTGGCGAGTA TTCGGTATTA AATTTTGAAG AGAGCTAGGA 180
 35 GACGCTGCGG AGGTCTAGGT GGTGTCGCTG CCGCTGGATT AACAGCATTG GCTATCGGTG 240
 TGTCACCACT ATATGCATTA GTTATAGCAG CCGC 274

(2) INFORMATION FOR SEQ ID NO: 912:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 679 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 912:

CTTTAATTGT TCACTTTATC ATTATTATCA ATCAACTCTA TGATATGAAA TTGTGTTAGA 60
 50 GATAAATCTA GTTCCTCATT TTCCTTTTTA TACTGTCTTC TTTTATCGGC ATTTTCTCTT 120
 TCTATAATAA ATTGTTGTAA TTTTAAAATA ACTTCTCTCT TCATATCCAC TATTATTCCT 180

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TTGTTGTAAT TAACATATAT TTAAGTTAGTT ATGCACCATT TATTCGCGAT TTCACAAATC 300
 CACCTATAAT ACAAACTATC ATTTTAAATA AGCAGAATTT ACCCTGTCTT CCACACAAAT 360
 5 TGTTCGAC ACTTTAATGT GCCTACTATC CAAAAAGTT ACTCATAACA AATTGCGCAT 420
 TTTAATAAAT GTAGCAATGC CATTGCGATG CTGCAAAAAT ACTCGTATTC ATATTTATGT 480
 10 TTTATATTAT TAAAGTTTTT TAAATCCATA TTTTATAAC ACTTGCTATG TGATAAAATT 540
 AATnTTATAT ATAAAATCTT AAGATTCAGA TTATTTAATA GCAAAGGAGA TAGTGATATG 600
 GATGTTTTAA CAATAGAACA TTTAACAAAG AAGATAGGCA ACAAACGAT TCTCGAAGAT 660
 15 GTATCATTTA AGCTGAAAC 679

(2) INFORMATION FOR SEQ ID NO: 913:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 564 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 913:

GCCATCCTTC AGTGCTAATT TTTTCAAATT CTAATGCAGA TGCACCACTA ACCATACCAT 60
 30 ATATAAGAA AAAGACCACG AAAGnAATAA GTAGTAGTAT AGATGCACAT ATCATAATGA 120
 CATTGGAGTT TTCAGCGCCA AATTTAAATG TCAATGsGAA AATGATAGAG TATGCCCCCTA 180
 TGATACCAA ACTCATTAAA CCTGACATAA TACCAATCAT CACACTTTGG GTCACAATCG 240
 35 TAGTCACAAC TAATCCAATC ATTAACTTG CACCGAATAA GATTAAATAA AAGGCAAAGT 300
 ATGACTTAAT ATAATCACTA CGTTTAACCG GTAAAGTAGA TACATAATAC ATCCATCTTG 360
 AGTCTTTTTC aTGTTTAATA TTATCAGTAA TAGGTGTGAT TAACATAACC CCAGCCATkG 420
 40 CCGAACTCAT CAACGGATTA AATACTGCAA AGTATCCTGC AGCTATAATA GCGACTATAA 480
 AATAAATATA TGTTTGCTT CTCGTTGCAT AAAAATACT TAGGAACATA CCTTTCATTA 540
 45 TACTTCACCT CGCATTATGA TTTT 564

(2) INFORMATION FOR SEQ ID NO: 914:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 643 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AAAGAAGAAG CAAGTGCAAA TAATTTAAGT GATATATCAC AAGAGGCACA AGAGGTTCAA 60
 GAAGCTAAAA AAGAAGCACA AGCAGAGAAA GACAGTGACA CATTAACTAA AGATGCAAGT 120
 5 GCAGCAAAGG TAGAAGTATC AAAACCAGAG TCACAAGCTG AAAGATTAGC AAACGCTGCA 180
 AAACAGAAGC AAGCTAAATT AACACCAGGT TCAAAAGAGA GTCAATTAAC TGAAGCGTTA 240
 TTTGCAGAAA AACCAGTTGC TAAAAATGAC TTGAAAGAAA TTCCTCAATT AGTTACTAAA 300
 10 AAGAATGATG TATCAGAGAC AGAGACGGTT AATATAGATA ATAAAGACAC TGTTAACAA 360
 AAAGAAGCTA AATTTGAAAA TGGTGTATT ACACGTAAAG CTGATGAAAA AACAACTAAT 420
 15 AATACAGCTG TTGACAAGAA ATCAGGTAAA CAATCTAAAA AAACAACACC TTCAAATAAA 480
 CGAAATGCAT CAAAAGCATC TACAAATAAA ACTTCAGGTC AGAAAAAGCA ACATAATaAG 540
 AgATCATCAC mAGGTGcAAA GaAACAAAGT AGTTcmAGta AGTCaACTCA AAAGAATAAT 600
 20 CAAACTAGTA ATTAAGAnTT CAAAAACAAC AAATGCTAAn TCC 643

(2) INFORMATION FOR SEQ ID NO: 915:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 915:

AGGTTTAAGG GAAAAATCCT ACCTGGAGAG ATTCAAAAAC TAAATGGACT ATTTCCAAAA 60
 35 ATAAAGGGCA ATCACATGGT GGTCTTATT GGAAGTTAAT AAATAACAAA GGAAAAAGAA 120
 TAGCTTCTTT AACTAAAGAA GGAAAAATCT TAAGGGAATA AGGTGTTGTA AATTATGTGC 180
 TTTGATATAA ATAATTTGGA TATAAAAAAG TTGAATTTTA GAAAGGTAAA AAACGCAATT 240
 40 CATTTAAGTT TAAGTGGCGA TAAATACCAG TTTTGGAGG ACGGTAAAAC TATCAATAAT 300
 ACTTATTTTT TAGCTGTATA TGATAATGCA ATAAACATTT TTGAAGATTT GTTTtCGCCT 360
 tCTGATTCTA TAAATTTGGn TCATGTAGTA TATGTTTATA 400

(2) INFORMATION FOR SEQ ID NO: 916:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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CCCAAAGTTC GATAGTGTAT TAGTATTATC TTAATAAAAT GTTAGGTACA ATAAAGATGA 60
 TTATATATCG GAGGTTAGTA TAAAAATGTA TGTAGATCGA AAACCATCAC TATATTTAGA 120
 GGATTTGCCA CATGATTTTA AAAATAGTTT AAGTAAATTT GAAAATGGTG ATGAAGCATT 180
 TGATACGTTA TTAGGTTTCG TAGAGTTAGA TCATATTTAT TCGTCAGCAC TAAAGGAAAT 240
 AAGCACTAAA CTGAGTATTT TAGATGACAA TTTCAATCAC ATTTATAWAC ACAATCCTAT 300
 ACATCATATG GAGCGACGTG TGAAAGAAAT GCGTAGTTTA ATAGAAAAGC TTAATCGTAA 360
 AGGATTACAG ATTAGCGCAG AAAC TGCCAA AGAACATATA 400

(2) INFORMATION FOR SEQ ID NO: 917:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 917:

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GAAAATTACT ATGAAGATTG CATTAGGATG CGACCATATT GTTACAGATA CAAAAATGCG 60
 TGTATCTGAA TTTTAAAAAT CAAAAGGACA TGATGTCATT GACGTAGGAA CATACGATTT 120
 CACAAGAACA CATTATCCAA TTTTGGTAA AAAAGTTGGC GAACAAGTTG TTAGCGGTAA 180
 TGCAGACTTA GGTGTTTGTG TTTGTGGAAC AGGTGTTGGT ATTAACAATG CTGTAAATAA 240
 AGTACCGGCG TTCGTTTACG ACTAGTACGT GATATGACAT CAGCGTTATA CGTAAAAGAG 300
 GAATTAAATG CGAACGTTAT TGGCTTCGGT GGACGTATTA TAGGTGAGTT ATTAATGTGC 360
 GATATTATCG ATGCCATTAT TAATGCTGGA TTATAAACCC 400

(2) INFORMATION FOR SEQ ID NO: 918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1220 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 918:

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GTCTCCAGCC ATTWACCAC ACATACCTGT CCATTTACCT TCTTTATGTG ACGCTTCAAT 60
 AACTTGTTTA ACTAAACGTA AGATTGAAGG GTTATATGGT TGGTATAGAT ATGATACACG 120
 CTCTGACATA CGGTCAGCAG CTAATGTGTA TTGAATTAAA TCATTTGTAC CGATACTGAA 180

GATTCCTAAT TCTATATCAT CCGAAATGTC ATGACCTTCA TTTTAAAGGT TTTCTTTTTC 300
 TTCTAATAAT ATAGCTTTAG CTTCTCTAAA TTCGTTAATT GTTGCAACCA TTGGGAACAT 360
 5 GATATTTAAC TTACCATAAA CTGATGCACG TAATAATGCA CGTAGCTGTG GTCTGAAAAT 420
 ATCTTGTTGC GCAAGGCATA AACGAATCGC ACGGTAACCT AAGAATGGAT TCATTTCTTC 480
 10 AGGCAAGTTT AAGTATGATA ATTCTTTATC TCCACCTATA TCTAAAGTAC GTACAACAAC 540
 ACGTTTACCG CCCATTGCTT CTAATACTTC TTTATAAGCT TCAAATTGTT CTTCTTCTGT 600
 AGGCATTTGG TCACGACCCA TATATAAAAA CTCAGTTCTA TATAAGCCGA TACCTTGTGC 660
 15 ACCATTTTCa ATAACACCTG GCAAATCATT AGGTGTACCA ATATTTGCAG CAAGCTCTGC 720
 GTGAACACCA TCAACTGTAA CAGTATCAGC ATCACGTAGw TTTTGTAATT CTTTCTTGTC 780
 AGCAAAATAA CGCTCACGTT TATCTTGATA AGCGATTAACT CATCTTCAG TTGGATTAACT 840
 20 GATTACATCA CCATTTAATC CATCTACGAT AATCATGTCG CCTTGTTTAA CTTCTTGAGT 900
 AATTGATTTT GTACCAACAA TTGCTGGaAT TTCTAAAGAA CGACTCATAA TTGCAGAGTG 960
 aCTTGTTCTT CCGCCAATGT TTGTAGCAAA ACCTTGACG AATTCTTTAT TTAATTGAGC 1020
 25 AGTATCAGAT GGCCTTAAGT CATTCCCTAC AATAACAACG CTTTCATCAA TCATACTCGG 1080
 ATTCGGTAAT TCTACACCTA AAATATGTGA TAACACACGT TTAGAAACGT CGCGAATATC 1140
 30 AGCCGCACGT TCTTTCATGT ATTGTTATC CATAGATTCA AAAATTGTAA CAAATTGTGT 1200
 TGThACATCC GCTTAATGTG 1220

(2) INFORMATION FOR SEQ ID NO: 919:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 919:

45 TTAGATTGAC TGCAAATGCC GACTCAAAAG AACAAGCACA ATCATTGATT CAACCTGTTA 60
 AACAAGAAAT TCTTGATCGT ATTGGAGAAT ATTATTATGG TTCAGATGAC ACATTAATTG 120
 AGCAAGCTGT AATAAAGAAA ATTCATGAAC CTTTTGTAAT ATATGATGGT ATTACTAATG 180
 50 GTGCTTTATA TCATCGATTG AAAGAAGTGG ATTTAAACGA TGTTCTAAAG GGTATGATTA 240
 ATCACAATGA AAACTTTGTt GATATTAATa AACCTATTGA GCaGCAATTA AAAGATGCAG 300
 TGCAATTTGT TAATA 315

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 920:

ACTTTGTAAA CCTACAAATG TAATGAATAA TCCTATACCT GCTGAAACAG CCATCTTCAT 60
 TTGATAAGGA ATTGCATTAA TAATAACTTC CCTAAACCCT GTGACGGTTA ATATCGCAAA 120
 GAATATACCT GAGAATAAAA CGCCTGTAA ACCAACTTGC CAAGGAATAC CCATGGTTAA 180
 CACAACAGTA AATGCAAAGA ATGCATTTAA TCCCATACCT GGTGcTAACG CAATTGGATA 240
 TTTAGCTATT AGCCCCATGA ATAGCGAGCC TACAAATGCT GCTAATGCAG TCGCTACAAA 300
 AATGGCACCT TGGTCCATTT TCATATCTTC TGATACGCCT TTAACACCTG CTAAACTTAA 360
 AACTTGCGGG TTAAGTCTA AAATATAGGC CATAGATAAG AAAGTTGTGA TACCGCCTAA 420
 GATTTCTCTT TTA 433

(2) INFORMATION FOR SEQ ID NO: 921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 921:

CTATTTTATT TGTATAGCGC TTGATGTAAA GTTATTTTAG CTGTCATACT ATGTGCTAAA 60
 CCAAATTCAG TTGTGTCATA TCTTCGCTTT TTGTCACTG TTATAATAGG TATAATCGGA 120
 TATAATGAAA AGGkGAGGGA GGATTCAAAA TGCGTAGGTT ATTATATTCA TTTCTTTTTT 180
 ATATGATCAT AGGTTTATTT AGTGGCTTTT TCTATAGAGA GCTAACAAAA GCATATGATT 240
 TTACTGGTAC AACACAATTA TCACTTGTA ACACACATAC ACTTATTTTA GGTATGTTTA 300
 TGkKTTTAAT ATTATTACCA TTGGaGAmGT TATTTAAATT ATCAAGTTAC TACTTATTTA 360
 ACTGGtCTTC TATGTATATA ACATAGGTGT TATCGTTACT ATAGGTATGA TGGTGACAAA 420
 AGGATTCTTC CAAGTCACT 439

(2) INFORMATION FOR SEQ ID NO: 922:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 474 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 922:

GTAATATCTA TATACGTATA TTTAAATGAT ATATCTGGGT ATTTTCTTTT TAATAGCGGC 60
 10 TGTAGCCAGT CATAAATATC TtTCGaTGTT GGCGCATTAA CGCAACTTGC ACATATAACA 120
 TCTGCCCCAT AAAC TACCAC ACTCACGTGC TCCATATATT TATCCCCCAT TGGTTTGATA 180
 GATTTTTTATT ACACTATCTA TTATAATATA sTmATAAAGA TTATCAAATT CATCTCTCGA 240
 15 AAGGAGACTT GCCTGATGCC TACTGAAGAT ACAACGATGT TTGATCAAGT AGCAGAAGTT 300
 ATTGAACGTC TTCGTCCATT TTTATTACGT GATGGTGGCG ACTGmTCATT GATTGACGTG 360
 GAAGACGGTA TTGTAAATTA CAATTACATG GTGCATGGTG GnACATGCCC CAAGTTCTAC 420
 20 AATCACTCTT AAAAGCTGGG TATTGAGCCG TGCATTACAC GAAGAAGTGC CTGG 474

(2) INFORMATION FOR SEQ ID NO: 923:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 554 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 923:

TCAACTTGTG AAGAAAATTT ATTAAC TTTA GTAAC TCTC CAACAAAACC TTGTGATGTC 60
 35 ATCACAGCCA TATTTGAAGT TATACCTGAT TTAGATCCCT TATCAATTAC AATTGTATTC 120
 ATCCACTGAT CCGGATTTCT TGCCAAAACC GTAGTAGAAA TAGGATCAAA TTTTGAAATA 180
 TCTTTTAAAT CAAGCTCTTT TTTTAATTTT TCATTTTCCG CTTCTAATTG TTGGTTCTTA 240
 40 GATTCTAACT GGCTAATCTT ATTTT TAGAT TCTTTAGAAAT CTCCTTTTTT AAAAAAGTCC 300
 CCAATCGTAC CAGCAACAAA ATTAAC TGA TAACTCACAA CTCGTTGTCC AAAAGACACA 360
 GAATCACCTA TATATTGTTT AGGAGGTGAT TGAGATTGTG AACGTATGGA CAGCCCAATT 420
 45 AATGCAATAA AAACGATAAT TGCACATAAA ACAACAATTA ATTTGGTATT TTTAAAAAAC 480
 TTAAGCACCC AGAACACCTC TATTATGTCA nAATATTGTA TATCCTTTTC TAATTnATAT 540
 50 TACTCCCATT ATGA 554

(2) INFORMATION FOR SEQ ID NO: 924:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 575 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 924:

	ATCTTTAGGC ATTAAGCAAG TTTATGTAGA AGACTTTGAA CATAAATCCT TTAGCAAAGC	60
10	TAAAAAGCC TTAGAAGAAA AAGGGTTTAA AGTTGAAAGT AAGGAAGAGT ATAGTGACnA	120
	TATTGATGAG GGTGATGTGA TTTCTCAATC TCCTAAAGGA AAATCAGTAG ATGAGGGGTC	180
	AACGATTTCa TTTGTTGTTT CTAAAGGTAA AAAAAGTGAC TCATCAGATG TCAAAACGAC	240
15	AACTGAATCG GTAGATGTAC CATACTACTGG TAAAAATGAT AAGTCACAAA AAGTTAAAGT	300
	TTATATTAAA GATAAAGATA ATGACGGTTC AACTGAAAAA GGTAGTTTCG ATATTACTAG	360
	TGATCAACGT ATAGACATTC CTTTAAGAAT TGAAAAAGGA AAAACAGCAA GTTATATTGT	420
20	TAAAGTTGAC GGTAAACTG TAGCTGAAAA AGAAGTCAGC TATGATGATG TATAAATATA	480
	ATTGAAGTAA ATGTACCGAG GTTCTATTT GGAAGTCTCG GTATTTTAT GTTGGAGATT	540
25	GCGGTAGTTT TAAATGCnT CnTGTcTCA TATAC	575

(2) INFORMATION FOR SEQ ID NO: 925:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 307 base pairs
30	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 925:

	AAAAACGCTG CTGAGTTTAA AAAGCAACAA TTAAATGAAC AAGGTATTTT CAAGAAACCA	60
	GTGATTACAC CTATTAAACC ATATAAAAAT TTCTATCCAG CTGAAGACTA CCATCAAGAT	120
40	TATnACAAAA AGAACCCCGG TACATTATTA CCAATATCAC CGTGGGTCAG GTAGAAAAnc	180
	GTTTATAGAT CnCATTTGGG GGATCCAAAG CTTAAAAAGA TAAAAGTGAC TACCAGATAT	240
45	AGATATATTG TTACACAAGA AACGGCACTG GACCACCATT TATGAATGAT ATTGGACCAT	300
	TTGCTAA	307

(2) INFORMATION FOR SEQ ID NO: 926:

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(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 926:

5 CTCTACGCAC TCATTGAGAT ACACACATTG CGCATTGCTC ATAGAATCAG GTGTACACAT 60
 TAAAGAAATA CAAGAACGAT TACGGCATAA AGATATCAAT ACCACTATGA ATATCTATGC 120
 TAAATCACA AATTCATACA AAAAAGACGC CTCCCATAG TTTAGTCACC AAATGGAAGA 180
 10 CGTCTCGTAA TTAAAATATA TTTGCGTGCA TTCTAATTTA TACTTAGAAT GAATCATACT 240
 CGTGCATAAT GTAATTTTCT AGTTAGTCAA AACTATAAAC AGTTTACAT CATTCTGGC 300
 ATGCCACCCA TGTTAGGTTG GTCATTATTT TTTTCTGGAA TTGATGCTAC AACCGCTTCA 360
 15 GTCGTTAAGG ACATTGCTGC AACACTTGCA GCAGTTGnAA 400

(2) INFORMATION FOR SEQ ID NO: 927:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 809 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 927:

25 TTTAGGTGGT TTTAATnGTT ATGGTCATTC TGGACACCTA CTTATAATAA AATTTCAAAT 60
 30 CAAACTGAAC nTTTTGTACC GTTTGATTAA ACTCAAATTT ATTAGCTCCG TATTTAAATT 120
 TTGGTTGGGC TATATTCGTT TCGGTACTTA TTTCAACACC GTTTTTATAA ACTCGGAAGC 180
 TATCATAAAC AATTcTGCT CCAGCTTTTA GTTTGATCCC TTCGATTTTC ATTATTTTCTAG 240
 35 CATGCGTTAA ATTCCATACA AACGATTCTG TATCTTCGCC TAAATAAATT GTTATCTTTT 300
 TATACATGTT GAATTGGTCG TTAGGAGCAC TACCATGATA GTAAACTGTA CCTTTGCTCA 360
 AATTTTCAAA TGTATACTTT CTTTGTCTC CGCCTGCATG CCAATCAATA TTAAAATCAA 420
 40 ACGACCACAA TCCAACCTTT TTGTTTTCTT CTAACCTCTAG GCTTGTTCCA ATACTTTCAC 480
 CGTATGGTAA TTCTGTAGTT TCGAATTTTA GTTCAAAAGA AACTTTATTA CCTTTTGTGTT 540
 TAGGGTTTAT AACTCCGTTA AAAATAACTT TATACTGTTT ACCATTTACA TAAATTGTT 600
 45 GATCGTGTCT TGAATATTCG TAATCCGGGA AGTTGTTTTT ATCTAATTC ACGTAATCAT 660
 CAGAAGTTGG TTGAGTAAAC CTGTAATTCA ACTCTCTTT TCTTCTGATn TCTCGCAAAT 720
 50 ACATAGGTTT TATGTCTGTC GTTAACGAAT ACAACATATC TCGCATATAA GCAATGTCTG 780
 AACGATTTTT AACTTTACAA AAACAAGGA 809

(2) INFORMATION FOR SEQ ID NO: 928:

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(A) LENGTH: 1016 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 928:

10	nAAAACTATT ATCGCATCTA CaGTaATCGC TGCAGGTCTT TTAActCAAA CTAATGATGC	60
	TAAAGCTTTC TTTAGTTATG AATGGAAAGG TTTAGAAATC GCAAAAAATT TAGCAGATCA	120
	AGCTAAAAAG GACGATGAAC GTATTGATAA GTTAATGAAA GAGTCTGATA AAAATCTAAC	180
15	TCCTTACAAA GCTGAAACTG TTAATGATCT GTACCTTATT GTTAAAAAAT TAAGcCAAGG	240
	TGATGTGAAG AAAGCAGTTG TCAGAATTAA AGATGGTGGT CCTAGAGATT ACTATACTTT	300
	TGACTTAACT CGTCCTTTAG AAGAGAACAG AAAAAATATT AAAGTTGTTA AAAACGGTGA	360
20	AATCGACTCG ATTACTTGGT ATTAAAAAAC ATACTGAATT AAATAGTTGT ACGCCAAACG	420
	TTAGAAAACA ATGCTAACGT ATTGGCGTGC TTTTtTATT TAAGTAACTT CCAATTTATT	480
	TAGCATCTTT ACGACTGTTT AATAAAGCAC GTATGATTAA CACGGTTGCC ACTATATCCG	540
25	TTACAATTTT TATGATTGTT AATACATTCG ATTCCTTTT CACAATAGCC ACCTCGCTTG	600
	TTCAAAACAT AAACAACAT TGCATTCACT TTTAAGTAAT TATTTATATT ATTTATCCCA	660
30	ATAAGCTCAC CATTCAAATA AACACAATAT TATAAAATAA TTATACCTTT GGATATAGCA	720
	AAAAGCCACA CTCTATAGCA TGGCTTCTAT CAATTATTTT AAAGTATTAT ATTTTAAAC	780
	TAGATCGATT TGTCTTTGTA ATTTTTTCTT TTCATAACTG TGTGGAAAT GAATTAAATT	840
35	AACAGCTCTT TGTGCTTTAC GGTGTGTTGC AACAGTTCTT GTACGTTTGA AAAAGTTTAC	900
	AGCTTTTTGT GCATCCACAA CTTTTtTATT TACTTGwTTT kTAAAGTTTG TTGATACTGA	960
	TCATATTTTT TAGCAGCTTC ACCGTTnTTA GTTGTGCATG AGATCACCGG CAACCG	1016

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(2) INFORMATION FOR SEQ ID NO: 929:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 929:

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AAATGAAATC ATACCTAAAA GAGATATTAT TACAGAATCA ATGATTGTG ACTGTATTCA	60
AAATGCAGGT ATTGATTTAG AAGTATTTAA AGACGACTTA CAAAAAGTA AACTAACCGA	120

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CGTTTTCTTT AGTGAAGATG TTCATGAAGA AGGTTTAAAA GTCGAAGGAT TATACCCATA 240
 TCACATCTAT ACTTATATAA TTAATGAATT GATGGGTAAA CCTATCGAAA AGAATCTTCC 300
 5 TCCTAAATTA GAAACTTATA TACAGCAACA ACAACTTGTA ACGATGGAAG AATTACTTAC 360
 TATTTATGAA TGGCCAGAAA AACTTTTAAA CAAAGAGTTA 400

(2) INFORMATION FOR SEQ ID NO: 930:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 930:

20 TATTTCTGAC ATGTATCATG CTCCTTCGTG CTTTATTCTA ATGTAATATA CACAATTATA 60
 CATTGAAATT CAAATTTGTG AACACATTGT GAACTGACAT AAATTATACA CAATTCATA 120
 GCGCATAATG TTTTAAAAAT ACACATTATA GCAATTATAA TTAAGTTCAT TGTGTTGTCA 180
 25 TCAAAAAAAG AAAAAGGTGA TGTTTTAAAT GGATACAGTT GAATCAGTCG GTTTTTGACA 240
 GCATGACTTA GCAGTTCATA TCATTTTGCA ACGATGGTGT GGTATGCTTA ATGTCGCAAT 300
 TCAGATTTTA GGATCGCAAA ATGACTCATA TATAGCATGC CAAGTGGCAA GTATCATACG 360
 30 ACATGGnGTG TCAGGCATAn GGCTCATACT GTGCAATATG 400

(2) INFORMATION FOR SEQ ID NO: 931:

- (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 543 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 931:

CCAATCAATG TTGCCAATGG ATCACCTAAT GACAACCAAG TAATTGCTAC CATAGTAACT 60
 45 GCTGTTTTAA TTTTACCTAA TTGACCAGCT GCACTTACGA ATCCTTGTTT AATTTGTAGT 120
 AAACGTAAAC CAGTTACGGC AAATTcTCTG GCAATaATAA TGATTGCTAC TACAGAATTT 180
 GTTAGTCCTA GTTGCAACAAG TACAATTTAA GCACTTGCAA CTAATAATTT ATCCGCTAAT 240
 50 GGATCCAAAA ATTTCCCCAT ATTTGTAACT AAATTCCATT TTCTAGCTAA ATAACCATCA 300
 ACAAATCGC TAAGGGAAGC CAATATAAAA ATAAAACCAC TGATTAATAA CTCAATTCTT 360

ATAAAACTG GTATTAACAC TACTCTAAAA ACCGTAATCT GGTTCGGAAT ATTCATTATA 480
 CATCCTCATT TCTCACTAAT TTATTTCTGT TAAAAATATT AAAACTAACC ATGATCCATA 540
 5 ACC 543

(2) INFORMATION FOR SEQ ID NO: 932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 932:

GATTGCGAAT GAGATTAGTG GGATGATACC GGTAGAATGG GAGCAAGTAT TTACAATAGC 60
 20 TTATGTAAC TATCAAGCTG GAGAAGTCAT CTTTAATTAT ACTAAACCAG ATAGTGATGA 120
 ATTAAATTAT TATTCAGmCA TACCTAAAGA TTGCAATGTC TCAAAAGATA TTTTTAAGAA 180
 TTCATGGTTT AAAGTTTATC GAATGTTTGA TGAGTTAAGA GAAACTTTTA AAGAAGAAGG 240
 25 GCTTGAACCA TGGACATCAT GCGAATTTGA CTTTACAAGA GATGGCAAAT TGAATGTATC 300
 TTTTGATTAT ATAGATTGGA TAAATACAGA GTTTGATCAA TTGGGCCGTC AAAATTATTA 360
 TATGTACAAA AAATTTGGGG TTATACCAGA AATGGAATAT 400

(2) INFORMATION FOR SEQ ID NO: 933:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 759 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 933:

ATTTTTACAA AGAAATAGTA GTCTTATATA TCTTAACATT TAATAACTAA ATCAAACATA 60
 TTTTGAGCCT TTTTTTGAAA ATTAACATTT TAACCTTTTT GATTTTACAA CAAATTATAG 120
 45 CTACGTATTG AAAATTAAAG CmTTGGtTTA AGTGTGTGT TAAAgyTTT TATGTTTAGA 180
 TTGTTATATT ACTATGTATT CTTAAATTTG TTTAAAAAAT TAATGCTTTA AATTGATGTA 240
 TAATGGGAAT AAGAAATAAA TAAAAACGAC CCGCAGGATT AACGTACGGG TCCACTACTA 300
 50 AAGGGAGTCA AATTTTTACC TcGTTTGTAT CATGCAGCGT TTTACACATA CTTTTAAGAG 360
 ATGTTIATTC GTTATCGAAG GTACACCTTT ATTATAACTT ATATCATTTT TATTAAAATA 420

ATAATGATTA TTAAATAGTA ACTAAATACA AAATTACATG GGGTGAATGA TAATGAAACA 540
 ATACTTAATT ACTGGTGGGA CTGGTATGGT TGGATCTCAA TTAGTTAATG AAATTAAAAA 600
 5 ATCAGATTCA CATATCACGA TATTAACGCG ACACGACCAA ATTTCAAATG ATAAGAAAAT 660
 TTCATATGTC AACTGGGCTA AATCTGGGTG GGAACACAAA GTTCCTCAAA ATATCGATGT 720
 GGTCAATCAAC TTAGCAGGTG CTACATTGAA TAAACGATG 759

10 (2) INFORMATION FOR SEQ ID NO: 934:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 934:

GATCAAGCTG GGAAGTCAT TTTAATTAT ACTAAACCAG GTAGTGATGA ATTAAATTAT 60
 TATTCAGACA TACCTAAAGA TTGCAATGTC TCAAAAGATA TTTTAAAGAA TTCATGGTTT 120
 25 AAAGTTTATC GAATGTTTGA TGAGTTAAGA GAAACTTTTA AAGAAGAAGA GCTTGAACCA 180
 TGGACATCAT GCGAATTTGA CTTTACAAGA GATGGCAAAT TGAATGTATC TTTTGATTAT 240
 ATTGATTGGG TGAATTCAGA ATTTGGACCA ATGGGAAGAG ACCATTATTA TATGTATAAA 300
 30 AAATTTGGnA TTTGGCCTGA AAAAGAATAT GCCATAAATT GGGTTGnAAA AATAAGnTT 360
 ATGTTAAGAG CAAGnTTGAG CTGAACTATA GGGGAGATAA 400

35 (2) INFORMATION FOR SEQ ID NO: 935:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 935:

45 CTGAATATAA TTTTnCAAC TACATCTCGT TTATTAGACA CCGTGCACTG ACTAAGAAAA 60
 TTTCTCTTGA CTCCATTAGT CCTGACGAAT ACTAACATTT AACTACCTTG CTCATCGATA 120
 GAAACAACCTT GTAATGTTAA TTTCCCTTAT TTTCTTAGTT TTAATCTATC AGCGATTAAT 180
 50 TCGATTGCAT CTTTTTCATA AGCAATTGGA TAACTTGAC CGCGGTACAC CTAACGCTCG 240
 AAATATGATT TnTATCGTC ATAATCTAAA ATATTATnGG CAAAATCACA GCAGTTTTCA 300

55

(2) INFORMATION FOR SEQ ID NO: 936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 619 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 936:

GTTATCATCA TCTTCTGAAG TATCATCTTG CCCATCGACT TGACTTGCAT CAGTTCTCTT	60
TAAATCATCA AACTCTGGAC TAGCTAATGT ATTATATAGT GTTTTAGGTA AGTAATAATA	120
TTCGTTTAGC ATATCTTCTT TTAATAATC ATCTACTTGA TACATAATTC TTTGAGCCAG	180
ATACATATTA TCTTCAGAAT TTTGATTTTG GAAAAAATTA GGTAAATATA AGAACATATT	240
TACTAAAATA TCATCTAAAT CTGAATGTAT AGATGGTATA TCAAAGAAAT CTTGGCTTAA	300
AAATGCATGT TCTAAATACA AAAATAATAA ATCTGTATAT TGTGTTTTAG TACGATACAC	360
TTTAATTTGA GATTCCGTAT ATGATATACG TGTATCTAAG CGAAGATCAA TTAATTTAGC	420
AGTACTTGGG CGCTCAACTT TAATAGAATT TAATACGCGC ATATCTTCTA ATAATTTAAA	480
AAGTTGTTGG ATAAAATTTA GGGtGTTTAA AAGTTTATC TTGtACTACT TCATTTACAA	540
TTTGtACATC CaTCATATGA TAACCGTAAG CAGCTAACAT AACATCTGTT TTAAACCAG	600
CCATTTTCGAT ATGGCTTGG	619

(2) INFORMATION FOR SEQ ID NO: 937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 937:

TAATCCCTTT CATAATGGGC ATCAATATCA TATTAATCAA TCTAAAAAAC TTACAAATGC	60
TGACGTTACT ATTGCAATAA TGAGTGGTAA CTTTGTCTATG CGTGGCGAAC CAGCAATCTA	120
TAATAAGTTT ACTCGTGCAA AAATGGCATT ATCAACAGCT GATTTAGTTA TCGAACTACC	180
AGCAACTGCC AGTTTATCAT CTGGcGATCA TTTTGCCGAA CTAGCAGTTA AAGTCGcGAA	240
TTATATGAGT GTCGATACAA TTGCATTTGG TAGTGAAAAT AATGAtATCA AAACATTAAA	300
rCmATTAgCA CACAGCATTa ATGaAATTGA mCAATCTGaA TCCTTTTCAC aAAAAAGTrAA	360

AAGTCCTAAC AACATACTTG GTATTAGTTA CCTGAAAGCA ATTGCTAAAA ATGCTAAAAA 480
 CATCAATGCA ATTTCTATCA AACGAGAAAA TGCTCAACAT CATGATTCAT TAATTCAACA 540
 5 CCATCAGTTT GCAAGTGGTA CATCTATTAG AACATCAATC ATTAGTCAAG ATGATCATTG 600
 GCATCATGTG GTACC 615

(2) INFORMATION FOR SEQ ID NO: 938:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 938:

20 AGAATTGAAG ATGGTAAAGT TTCAAAATAT CATTCCGGTTA TCATAAAAGA CGCACAAGCA 60
 ACTTCACCAT ATTCAATTTT TATCAGAGGT GCTATTTATC GCTTTGAACC ATTAGTATAA 120
 ATATACGTAA GTGCTATGAG CGAGAATGCC CATATGAATA ATGACAAGCA CAATGGAAAG 180
 25 AATCGTAATA TATTATTTAA TCGTGATGCT TAATTAAAT GAAAAAGATT GATAATATAA 240
 ATGTGAAAAA GTAAGTATAC CCGTAAACTA AAGTATTCAC GGTGAGAGGT GTCATGTCA 300
 TAATGATGCA CGTGTCATAA TTATAATAGC TTAATATATGT CCATACAACA CCATGTAGAT 360
 30 ATGCATATAC AGGGTATGAT AGACATAGnG TCTGnGAAAT 400

(2) INFORMATION FOR SEQ ID NO: 939:

- (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 466 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 939:

GTACAGGTAT GATTGGTGAT CCCATCAGGT AAATCAGAAG AACGTGTGCT ACAAACAGAA 60
 45 GAACAAGTAG ATAAAAATAT CGAAGGTATT AGTAAGCAAA TGCACAATAT TTTTGAATTT 120
 GGAACAGACC ATGGTGCAGT GCTTGTTAAT AATAGAGACT GGTTAGGACA AATCTCATT 180
 ATTAGTTTTT TACGTGACTA TGGTAAACAC GTCGGCGTTA ATTACATGTT AGGTAAAGAT 240
 50 TCAATCCAAA GTCGTTTAGA ACATGGTATT TCATATACAG AATTCACATA CACGATTTTA 300
 CAAGCTATTG ATCTCGGTCA TTTGAATAGA GAATTGAATT GTAAGATTCA AGTAGGTGGA 360

GTAGATAAGC AAATGATTAA TAGTTGAGGG GTATGTCGAT GAAGCG

466

(2) INFORMATION FOR SEQ ID NO: 940:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 940:

15 ATGAATCACC CATTGATACC AATCATTTAC ATCACTGTCA TACGAACATA TATTTAAATA 60
 GAAAAAAATT ATTTTAAAGA TTATAACTAC TCTTAATCAT TTTAGTGAAT TAAAAAAGT 120
 AGTGCAAAAA GCAAAATATA CTTTATACAC TACAAATCAT TTATTTATAA TAAAGTTTCA 180
 20 CCAAAAAATG TTCCAATAA TGAAACCGCT TGTTCAGCAG TATGATTATn ACTGTCAATC 240
 AATGGATTTA CTCAACTAA ATCCATTGAG GAAATTAAAT GTGATTGATG CAGTAATTCC 300
 AATGCnAAAT GGCTTTCTCT ATnACTAAG 329

25 (2) INFORMATION FOR SEQ ID NO: 941:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 941:

35 CGATATAGTA CCAATTTATT TGAAGAAAAA TCCGAAC TTC AAATTTCCGA TGAAGCAAGA 60
 TATACCGGTT ATTATGATTG GACCAGGTAC TGAATTGCT CCTTTTAGAG CATATTTACA 120
 40 AGAACGTGAA GAACTTGATA TGACTGGAAA AACATGGTTG TTCTTTGGTG ATCAACACCG 180
 TAGTTCTGAC TTTTATATG AAGAAGAAAT AGAAGATGG CnTGAAAATG GAACTAACA 240
 CGCGTAGATT AGCATTTCCA AGAGnCCAGA CACAAGATAT GACAGCCnCG ATATGGAGAA 300
 45 GTAACGTTCC ATGAT 315

(2) INFORMATION FOR SEQ ID NO: 942:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 699 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 942:

TACCAATAAT CAACTTGTTT TACATCATCG TGTGTTTCAA TCACTTTCCT TTTTATACCT 60
 5 TTCTTACCTT TAAAGAATGC ATCAACATCT TTTATTGAAG ATCCTTTTGA ATCTTTAGTA 120
 AATCTATAAT CTGCAAGTTC CACTTTACCC ATTAATTCTT TGTAATCTTT CCATCCTTGA 180
 ATCCCTTTAC TATTTCGTAA CGACTTTTCT GTCATTAATG GATCCAACTT ATCAAGAGAT 240
 10 GGCGCATCTT TAATTCCTTT CATTTTCTTC TCTATTTCTT CATATTTCTC TAAATCTGGA 300
 TCTTTCTCTT CTTCGGATTC TTTTTTTACA GTTCTTGTT TTGATTCTTC TGATTTCTTT 360
 GATGATAATT TATGATTCCC ACCAAAAGAA CAACCTGCTA CGACTAAAAG CATAATTAAA 420
 15 AGTAAACATC CCAGTGTCTT TTTCAATAAC TTTCTCCTCT TAAGTTATTT TGTTTGAATC 480
 AAATAACAT ACATAAATTT AAAAACTTA TTTATATTG_a TATTTTACAT TAACCATCAA 540
 20 TATTTTAAA TACTTTAAWT GaTAATTTAA GAAAATTGTT TTGTCTAATA ATTTAAGTAG 600
 TTAAACATA GATAGATATA AAATAGTTTA TAGCCATTAA TTTATAAGTT TAAAATTCGC 660
 ACTATTTCAA TTTGCCATTT AAAAATAGTT TGTTTAATC 699

25 (2) INFORMATION FOR SEQ ID NO: 943:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 943:

35 CGCTCCATAA ATCAACAATG TTCGAGTCTG TAATCTAGAT GATAAAACGC CAAGAATGAT 60
 CATAAATGGC ACTTCTAAAc CAGCACATAA ACTAGCTAAA TAACCGACAT GTTGTTTATT 120
 40 TTCTTTTAAA TAATCAGTAA CAAATAAAGG CATATTCATC GTATACATCC ATTGTCCAAT 180
 GTGTAATAAA ATAAATGCAA TAAATGGTAA TAAAAGCGTT TTGTCTTTAA ACATATTAGG 240
 AGCAATTTTT TCAACATGTT GTTGCGTACT AATAGGGTGT TTAATGTTTA AATCCTTATA 300
 45 GAnAAACACT TGAAGTACTA AAGTAAATAA AATGATACTT ATTGGGCCAC CAAACAATCC 360
 AGCATAGCCT TTTAATCCGA TTAATTGGGC ACCAATAAAT 400

(2) INFORMATION FOR SEQ ID NO: 944:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 570 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 944:

5 AAGATGACAA TACTTTGTTT CAAGAATTGA AAAAAGAATT AGAACAATGG GATTTTAATG 60
 TTGCTGGTAT TGAAGATTC GCCAAAGTAA TGCATACATT TGAAAGTTT AATCCTGAAA 120
 TTGTTATATT GGATGTTCAA TTACCTAmAT ATGATGGGTT TTATTGGTGC AGAAAAATGA 180
 10 GAGAAGTTTC CAACGTACCA ATATTATTTT TATCATCTCG TGATAATCCA ATGGATCAAG 240
 TGATGAGTAT GGAACCTGGC GCAGATGATT ATATGCAAAA ACCGTTCTAT ACCAATGTAT 300
 TAATTGCTAA ATTACAAGCG ATTTATCGTC GTGTCTATGA GTTTACAGCT GAAGAAAAAC 360
 15 GTACATTGAC TTGGCAAGAT GCTGTCGTTG ATCTATCAAA AGATAGTATA CAAAAAGGTG 420
 ATCAGACGAT TTTCTGTCC AAAACAGAAA TGATTATATT AGAAATTCTT ATTACCAAAA 480
 20 AAAATCAAAT CGTTTCGAGA GATACAATTA TCACTGCATT ATGGGATGAT GAAGCATTG 540
 TTAGTGATAA TACGTTAACA GTAAATGTGA 570

(2) INFORMATION FOR SEQ ID NO: 945:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 945:

CCGAGnCCAC CGTTCCAAAG TCCATTTTTA TCCCCATCCC TCTCTGAATT GAACTATAAT 60
 35 TTTTGAATTT ATTAATAATG CTATTTTThT TATTTTATCA AAAACTGATT ACAAATACAC 120
 ATAGAAAATG AAATATATTT TTCTTTGACT ATACATAACT GTTATTTCTT TGGATATTTA 180
 40 TATTAAATGC ATTGGTAGTA GTTGTAGCGC ATTAATGTTT GACGGTGTAT AGTATTAATT 240
 ATATTGAAAG TTAGTTGGAA GTTGATAGTA GGAGTGGGAG CATTGAAGCG ATTTGTGGCG 300
 ACGGTATTAT TATTACTAGT CTTTATATCA GGATGtGGTA ATGrTaAATA TGTGAAAGAA 360
 45 ATaGATGAAG CAGTTAAAaT TCAAAATCaA AAACAAGAAC ACTTGCCCAA AAAAGGCAAC 420
 GGTGATCGTG TTGATCATTT TGAACGCAAA GATGCTAATA TTTATGTCTA TGATAAGGAT 480
 AAAATTATCA TTTTAGCTTA TAAACCTTTG AGTAATGATG ATGAAGTGCA TTATTATGCA 540
 50 TATGATTTTA GTGATAAACG TGTATCATAT AAGCAAGATT TTGATTCGAG ACGATATTAT 600
 CAACAACATG ATGCGGATTA TCATGAAGAA AATATGACGA ACTAGATATG AATAGGAGTT 660

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GGTAAAAAAG AATCAGCAAC GACATCTTCG AAAAAACGGCA AACCATTAGT TGTCGTATAT 780
 GGCGACTATA AATGTCCTTA TTGTAAAGAA TTAGATGAAA AAGTCATGCC AAAGTTGCGT 840
 5 AAAAATTATA TAGATAATCA CAAAGTGGAA TACCAATTTG TCAATTTAGC TTTCTTAGGT 900
 AAAGACTCAA TTGTTGGTTC GCGTGCGAGT CATGCAGTAT TGATGTATGC ACCTAAATCA 960
 TTTTtagatt TTCAAAAGCA ATTATTTGCT GCCCAGCAAG ATGAAAATAA AGAATGGTTA 1020
 10 ACAAAGAAC TATTAGATAA ACATATTAAA CAACTGCATT TAGATAAAGA GACGGAAGAT 1080
 AAAATTATAA AAGATTACAA GACAAAAGAT AGCAAGTCTT GGAAAGCTGC AGAGAAAGAT 1140
 AAAAAATAG CGAAAGATAA TCATATAaa aCGACACCAA CTGCATTTAT TAATGGCGAG 1200
 15 AAAGTTGAGA TCCATATGAT TATGAAAGTT ATGAGAAGTT A 1241

(2) INFORMATION FOR SEQ ID NO: 946:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1057 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 946:

TAATACAATG ACACCATTTA GCATGACCGT TATCCCTGTA ATTCAGCTGA TATTATCTGT 60
 30 TGCAATTTTA TGTGACGAAC TGTGCACTT AATTTGATAA ATCAACAAAT ACAAAAAATC 120
 TAAGTTGAAC AATTATGATA CAACCGTGCA AACGATATGT AGTATAACTT GTCAACTTAG 180
 ACTTATTGAT AAATATATTA ATAGTGGTTT ACCATAGCAG GAGATTTTAC aTCAAAATTT 240
 35 TGAAGTAGCG TATCaATCTT TGaATCaTCa ATATATACct TATGTAAATT TTTCaTATAC 300
 ATCGAATGAG AAAGTGCTTC aTAATTTAAT GAAAAAGATA TATGATCTCC AACTTGATAG 360
 40 TGTCCCTGAC CATTAAATC AAGCATTAAA TGATCACTCG AAGCGCCTAA AATATTGATA 420
 TGCTGATCCA TAGGTGAAAT ATTATCGACT TTTGTayCTA AATAACCAAT ATCTACAATA 480
 GCTTGTAAGA ATGATTATG CGTTTGTGTA TTAACCTGAG GTTTAATTTT TAAAATCTCA 540
 45 GCCTCCAATG TAATCGCATC TTGATATAAC ATAGCGATCG CTTGATTTGT CGTTGTATCA 600
 ACACCTCTAA ACAACGTTTC ACCTATTGCG AATTCATTTA TTTTACCCAA ATCATTATAT 660
 AAAAGTTGTG GTAACATGCT CGAATTACCA CCTGAAATAA TTTTCAATCG ATATCCTATT 720
 50 TCTCTTTCAA CAGCTGAGAC GAATCGATTA ATCATAAAGA TATCATCATC ACTTGGCGCA 780
 TCAGATTTAA AACACATAAA ATTGAATGCT AAACCTACAA AATGGATATT TTTCAAGTGA 840

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CAATCTACCA TTAATAAAAT CTTATGTTTT TTCCTAAAA CTTCTGgCTA CTTCAITTTAT 960
 TTGATGTATG GGTAGATAAT TCCGGTTTGG GATACCTCCA TATCnAACCT TTTTTCCTAA 1020
 5 TCAATATCCT GGAAAAhCCC TTTTTTGGG CAGGGCG 1057

(2) INFORMATION FOR SEQ ID NO: 947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 649 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 947:

GATATCCGCT CGATGAATAT ACCTTTAAAG GTGTTGGTGC AAATTCTGAA CAATTAAGTG 60
 20 CTATGAATCA TGATTCTTTA AAAAAGGAGT ACATTTCAAA TGACTGTTAA ATATAATCAA 120
 AATGGCGAAT TAACAATGGA TGGTATTAGT TTAAAAACGA TTGCACAAAG CTTTGGTACA 180
 CCTACCATTG TTTATGATGA ACTACAAATT aGAGAACAGA TGCGCCGTTA CCATCGCGCA 240
 25 TTTAAAGATA GTGGATTAAA ATACAATATT TCATACGCCT CAAAGGCATT TACTTGCAIT 300
 CAAATGGTCA AACTTGTAGC TGAGGAAGAT TTACAGTTAG ATGTTGTTTC TGAAGGTGAA 360
 TTATATACAG CTTTAGAAGC AGGTTTTTGAA CCGAGTCGCA TCCATTTCCA TGGTAACAAT 420
 30 AAAACGAAAC ATGAAATTAG GTATGCTTTA GAaATAATA TCGGTTATTT TGTTATAGAT 480
 TCATTAGAAG AAATTGAATT rATAGACCGC TATGCTrATG ATACGGTTCA AGTTGTATtA 540
 CcGAGTTAAT CCcAGGTGgT TGrAAGCcAC mTrCaCaCgA aTTTATTCaA ACyGGGcaaG 600
 35 AAgGATAGGT TAAAGTTTTG GGATTAAhCC nntTTCCCAT TAATGGGCC 649

(2) INFORMATION FOR SEQ ID NO: 948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 948:

TACAAAGCTT AAAACAGAG CTTAGTyTCG TTGAACCATT AATTAGCCGC TTAGAATTAG 60
 50 AAGAAGCTAA TGATAAACTA GCTAATATCA ATGATAAGTT AGATGACATG TATGATTTAA 120
 TTGAACATGA AGTTAAAGCT AAAAATGATG TCGAAGAAAC AAAAGATATC aTTACGATA 180

EP 0 786 519 A2

AAAACTACTA TATAAATGAA TCTGATGCTC AGAGTGTTTCG TCAATTTGaa AATGrAATTC 300
aAAGTTTAAT TTCTGTATAT GATGATATTT TAAAAGAnAT GTCTAAATCT GCTGTGCGAT 360
5 ATAGCGAGGT TCAGGATAAT TTACAATATT TAGAAGATCA TGTCACAGTT ATTAATGACC 420
AACAAAGAAAA GCTACAAAAT CATCTGATTC AATTGCGTGA AGATGnGCAG AA 472

(2) INFORMATION FOR SEQ ID NO: 949:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 949:

AGAGGATCCC AGGCGTTTGT TGATCCAGCA GCCGATnCAG AATACATCTT CTATGCATAT 60
AAACGTTTCA ATTTGCAATT GAAAGATCCA AACTTCACTA GTGAAGAAAA TATGTTTAAA 120
GATGTATCAG ACAAACCATT AATACCTGCT CGTAAAGCTC AAATTACAAA TGCGAACTAT 180
25 AAACGACATG GTATGAAGTT GATGATTCTT GGAATGACG AACCATATAA CAATGAGTTC 240
AAGAAAGATG ATCGAAAATG CGAAGAATGA GAAATTTCAA AGGTGCGCAn GTCAAGCCAT 300
GTGTCAGGGG GGCATATGAT TTCnGGTCAT CAGTAAGGAC TGTGTCATGC CATGGCCATC 360
30 TGTGTACnG ATCTCTAATA GAATCTCAGA TGCCCGGCAA 400

(2) INFORMATION FOR SEQ ID NO: 950:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 556 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 950:

AAAATCTTCG ATGACAAAGA AATCTAATGA TGTTTCTTTA AAATGACCAA ACTGCAACGG 60
45 AATGATATAA CCACACTTGA GATATGGCGC TTCTTTTTTC AACTTAGTCA TCACATCATA 120
ATCCAAAGAC ATCACACGAT ATTGATGTTT AACACCATGC TTTTTCAAAA TATCAATAAC 180
ACGTTGTGTA TAATCTGCTG GTTCTTTACC ATGTGGCTTT AACTCTACTA GTAGCTTCAC 240
50 ATTTGATTGT TTAGCCGTTT CAATAAATTC GTCTAAGGAT ACAAATTTTG CTTCATGTCC 300
ATTTTGACGC ATTTTCAAAC CGACGATATC TTTGAAATTA GATTCAGAAA TATTTTTATT 360

CATAATTGTA TCTAACTCAA CGTATTCGAC ATTCGCTTTT GCAGCAGCTT TCAATGACGG 480
 AATAGAATTT TCAACACCTT TATCTTCGAA ACCACGTGGC CAATAATGGA GATATTGTAA 540
 5 TTGATAGTAT TATTGG 556

(2) INFORMATION FOR SEQ ID NO: 951:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 951:

TTGTGGTAAT GATGTTAATC AGTATATTTT TACTTTTGAC AATGACATCT AAAGGATTAA 60
 20 GCAATCTTAG AGTAATAGAT GATGAGGCAA ATATCATTTT TTTTATTACT GAATTGAATT 120
 ATATTAAGTC GCAAGCTATA GCAAATCAAG GATATATCAA TGTTAGATTT TATGAAAACA 180
 GTGACACTAT TAAAGTAATA GAGAATAATA AAATACGATT TCTAAAATTA AAAGTAGGCA 240
 25 AAATAATTAA TGTTGCAAAA GTTGATATTA TTGCCTTTGA TAAAAAAGGG AATATCAATA 300
 AATTTGGTAG CATAACAATT TACAATAACA ATTCAATTTA TAGgAATAAT ATTCCATATT 360
 GaaaaAGGcA AGAATTCGTT ATGAAAAGCT ATAAGTGTA AGGTTTCATTC TTAATAGATA 420
 30 GTATGGCTGG nTTTTTGCCA ATTGGGATTG nATTACATTA CTATTGATT 469

(2) INFORMATION FOR SEQ ID NO: 952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 952:

ACATnTATAA TnCTTATTTG CTTGCTCCTT TCACTTTTnTA AGAGTAAAAh ATAACCTGAA 60
 45 ACATAACTTT AACATCCAAG TTTCAGGTTA GTGTAATGTA AATGATTTAC TTTGTTnTAT 120
 TATGATTAAA CATCTAATTC TCTGCTTGTA AGTGCTTTAA TCATCTCTGG ATCAGCATGT 180
 GAGAAAAATT GGCTATTACT TTCTTCTAAT GTCGCAATTT GTTGTTTATC TTCTTCTGTA 240
 50 AGTTCAAAAT CAAATATATC TAAGTTTGA GCCATACGTT CTGGATTTAC TGATTTTGCG 300
 AGTACAACAA TGTCACGTTT TACTAACCAG CGTAAATAA CTTGTGCAAT TGATTTGTTG 360

AATGGTGCCC AAGCTTCTAC CACAACATTT TCTTGTTGAA GTGCTGCAAC TTGTTCTTCT 480
 TGTTGATGGA ATGGATTAAT TTCTATTGG TCACTTGTG GTTGAATTG ATTGTGAATA 540
 5 CCTAAATCTA CAATTCGATC AACGCCGAAG TTAGATACAC CGATTGCTTT AAaTTTTACC 600
 ATTTTctTTT AACTCCTCCA ATGCACGCC ATGGAGCCAT ATACnGCCAT TGGTAAAGGT 660
 TGGGTGGAAT nAAGCACCTA GGATCCAGGA TAGGTCCAA ATTTTAATCC GGTGGGnAAT 720
 10 GGATCGGTTT 730

(2) INFORMATION FOR SEQ ID NO: 953:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 953:

ACAAATGACA ACGTACAATG ACGTCTTCAC AAACATGCAT TTTAGGAGAT TGATTATTAC 60
 25 AAATATCCAG TTTTGTGTA CATCTATTG CAAATCTGCA CTTATTAACG TGAAATGCTT 120
 GGATTGATGG CACAATCCT TCTATCGTT CAAGTCGTT CTGCTCTTCT TTAAGTTTGG 180
 GAATTGTTGA TAATAATTTT TGGGTATAAG GATGTTTCGG ATTGTGTAGT ATTTCTTTTA 240
 30 TGCCTCCAAA TTCTACAATT TGACCTGCAT ACATAACTAA GACTTTATCG CAAAACCTCAG 300
 CAACTACACT CAAATCATGT GTAATCATCA TAATTGCCAT TTGCGTTTCC TTTTGCAATT 360
 CTTTTAATAA GTCTAATATT TGCGCTTGAA TCGTGACATC 400

(2) INFORMATION FOR SEQ ID NO: 954:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 954:

TAAATCTTGA GGACGTTTGG TCTGAAAGCG ATGCTCAACT GTTGATAAAT CCAATTCGAT 60
 AACATCTGTA TAATTAGGAT CTTCTTCTC AACATCAAAn ACATATGGTT TTGTTTCAA 120
 50 TATTCTTTTA CTAGCGCGAT ATGTTCTGCT GATCTACCAG TTAAC TTCAT ATATTTAAGA 180
 ATTCTCATCA ACTGGGAAG AATCCGCAAG TTGCTCCATA CTCTGGTGCC ATGTTTnCAA 240

55

(2) INFORMATION FOR SEQ ID NO: 955:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 955:

AAACATTTAC ACAAGTAGTA GAAGCAATTT ATGATGAAGA AGGTAACAGC TTaGamgCGG 60
 CGCGCCATCC aTTACAAATC GTTCAAATTA AAGTGGATCG CCCGATATAT CCAAACAACA 120
 TGATGAGAAA GGAAATTGGC TAATGAAAGC TACTACAATC ATTGGCATAG CTGGTGATC 180
 TGGCTCAGGA AAAACAACCTG TAACTAACGA AATTATGAAA AACTTAGAAG GTCATAGTGT 240
 CGCTTTACTT GcTCAAGATT ACTATTATAA AGATCAAAAG CACTTGACTT TCGACGAGCG 300
 CCTAGAAACC AATTATGACC ATCCATTTGC ATTCGATAAT GATTTATTAA TTGAAAATCT 360
 TAAAGACTTG AAAAATGGTA AAGCAGTAGA AGTACCGACA TATGATTATG CtAGTCATAC 420
 AAGAAGTGgA CATTACCATT GGATTTTtAA ACCTAAAGAT GtTTATTTAT CGTAGAAGGG 480
 CCTTTTTCGC CTTTAGGAAA ATAAGGGTAT TTAC 514

(2) INFORMATION FOR SEQ ID NO: 956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 956:

ATTTTAAACGA ATATCTTGCC GTACGATGCC CAAGCTGCAT CTGAAAAGGA TACTGAAATT 60
 ACAAAGAGA TATTATCTAA GCAAGATTTA TTAGACAAAG TTGACAAGGC AATTCGTCAA 120
 ATTGAGCAAT TAAACAGTT ATCGGCTTCA TCTAAAGAAC ATTATAAAGC ACAACTAAAT 180
 GAAGCGAAAA CAGCATCGCA AATAGATGAA ATCATAAAAC GAGCTAATGA GTTGGATAGC 240
 AAGCCATAAA GTCTCACCTG AATGACGGTC AAGTGTATAG CATAATAGTC ATGCTAAGTT 300
 AATGAGTCTC AATGTGTAGG GCACAAGTGC GGGCGTCTAT GCATGAATGT TGCCACGCTC 360
 ACAACTGGGA AGTGTAATG TGA CTGTA 388

(2) INFORMATION FOR SEQ ID NO: 957:

- (A) LENGTH: 394 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 957:

10 AACAAAGTAC ATCGCAGTTA CGAGAAGAAA TAAATGCATT GTATAATCAA GTTATAGAGG 60
 TTGGACAAGC GTTATCAAAG CAGCGTCGTA TAGTCGCTAG GGAGTTAAGw GACCACATTG 120
 TATCGGAAAT TCAAACTTA CAAATGAAAG ACGCAAATCT TGAGATTTCA TTTAAAAAAT 180
 15 TAGAAGAACC GAATATTGAT GGAATCGAAT TTGTAGAATT TTTAATCAGT CCAAATAAAG 240
 GGAACCATTT AAAAAGTTTA AATAAAATTG CGTCAGGTGG AGAACTTTCT AGAATTATGT 300
 TAGCGTTAAA AAGTATTTTT GTTAAATCGa GAGGTCAAAC TGCAATTtTr TTcGATGAGG 360
 20 TTGaCTCAGG TGTATCtGGr caAGCTGcAC CAnA 394

(2) INFORMATION FOR SEQ ID NO: 958:

- (i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 503 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 958:

CCGCCATTTT TTTGATTTT TTTTCAAGT TTTTCACGGT CTTTGAAGA TAGACTATTG 60
 35 AAATCTTTTG CACCACTATC ATCAAATCA ATATCTGCTT TCAATTTTGT GCTAGATTTT 120
 AAAATGAAAT TAATTGGTTC TTCAGcATAt TTGATGCCGA TATyTAACGT AGATTTCTGA 180
 GTGTTATTyT TTACGTCAGA ATCTATATTA TTTTCAAAG TGAATTCATT TTCGTCGCTA 240
 40 TATTTATCTA ATGCGACAGT GATTTTACCT TTATCTTGAC GTTTTGTGCC ATCTACTTTT 300
 TCTTGATTAT CTAATTTGAT TTTTGATTCA TCATATTCTG TCTTTTACC AAATTCGTAT 360
 TTATCATTAT ATTTATtATC TTTwCTTTA GAAGATACGC CTTTAATTGT ATATTTTCGCT 420
 45 TCAGCATACG TGTATTTATC TTGATCGAAA TCAAGTTCGT AATCTAGTTT TAACTTATCG 480
 TCTTCTAAAG TATTAGTACC TTT 503

50 (2) INFORMATION FOR SEQ ID NO: 959:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 959:

5 TCAAACGTAC AGAGCTTGTT AAGTGTTTAG ATTATTTACG AGAGAGCGAC ACATTAGTTG 60
 TCTATCAACT TGATCGGTGA GGTAGAACGA CAAACTATT AATTGAATTA TCACAATGAT 120
 TCGATGATAA CGGAATTGAC TTACCAATT AGTAACCTGA ACATTTCAC GAAAGACCCC 180
 10 ATGGGGCCAA AATGTTTTTA CCGATGATGA GTGCCTTTTT CCGGGTTAGA AGTTAATTTA 240
 CTATGTGAGT GTATAAAATA GACTnAGCAG CCACAAGnCG AGAGGCCGAA AAAAGCGGGC 300
 GCCCTCT 307

15 (2) INFORMATION FOR SEQ ID NO: 960:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 960:

ATAAGGACAT TTATAGTCGC CATATACGAC AACTAATGGT TTGCCGTTTT TCGAAGATGT 60
 CGTTGCTGAT TCTTTTTTAC CGCAAGCTGT TAAAATTAAC ATGCTCACTA TAAATAATGT 120
 30 TAGTAATTTT TAGTCCATAA TTACTCCTAA TCCTAACCAn GTCnGCnAAA TTTCTCCAT 180
 GATAATCCGC ATCATGTTGT TGATAATATC GTCTCGAATC AAAATCTTGC TTATATGATA 240
 CACGTTTATC ACTAAAATCA TATGCATAAT AATGCACTTC ATCATCATT CTCAAAGGTT 300
 35 TATAAGCTAA AATGATAATT TTATCCTTAT CATAGACATA AATATTAGCA TCTTTGCGTT 360
 CAAAATGATC AACACGATCA CCGTGCCTTT TTTGGCAAGT 400

40 (2) INFORMATION FOR SEQ ID NO: 961:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 961:

50 ACAATTAGTT ATACCCAAAA GAGTTATGTC AGTGAAGTAG ACAAGCAAAA CTCAAAATCT 60
 GTTAAATGGG GTGTAAAGC AAACGAATTT GTTACGCCTG ATGGAAAAAA ATCTGCGCAT 120

55

GCTCCTGATA ATCAATTGCC ACCTTTAGTT CAAAGTGGCT TTAATCCATC GTTTATCACT 240
 AACTATCAC ATGAAAAAGG TyCagTGATA CGAGTGaATT TGaAATTTCa TATGGTAAGA 300
 5 ACTTAGATAT TACCTATGCG ACTTTATTCC CTAGAACTGG TATTTACGCn GGAAGGAAGC 360
 ATAATGCATT TGGAAATAGG AACCTTGTAⁿ TTAnGTATGG 400

(2) INFORMATION FOR SEQ ID NO: 962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 962:

CTTTTACAAA GACAAATTAG CGGTAATCGG TAAⁿGATCGT TGTⁿGATCCA GTTGCACTAT 60
 TGAAAGAATT AGACGGATTA AATGAACGTG GCATTCCTAC AAGTAATTTA CGTATATCTA 120
 ATCGTGCGCA AGTGATTTTA CCATATCACT TAGCACAAGA TGAATATGAA GAACGTTTAC 180
 25 TGGTGACAAT AAGATTGGTA CACTAAAAA GGTATCGGTC CAGCATATGT AGCCAAGTCA 240
 CGTATCGGTA TCGTATGCAG ATTACTTGAA AAGAACATCG AAGATATTAA ATCAACATGA 300
 TATAACCAGC TATTCAAGGA TGTTACGAAC ATGⁿCACATT GATGAAnCTT GAGATATA 358

(2) INFORMATION FOR SEQ ID NO: 963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 963:

AGTGAGCAGG TTGAAGTAGT AGGGCCGATT CAAATGGAAA GAGATACACA TAAAGATGGT 60
 AAGGTAAAGT GGCAATTGCT TTATATAATG AATCAGGATG ATGATGAAAT TAAGCCACCA 120
 45 TTTTTTATTC AATGGGAGGA AAGTGATTCC ATTGCGTACT AAAAAATTGC AAAAATATTT 180
 TCAAAACCAT TTTCAATTGA AACTGTATTG TGAAAGTAAA ACCGTCACAA CAGTATCGAT 240
 50 TGGTTGAAnT GGTTGnAT 258

(2) INFORMATION FOR SEQ ID NO: 964:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 964:

	TTATCAAACC GCCATAGCCA CATCTCGATT CAAGGATAAA TTTGTTTTCT CATATCTTAT	60
10	CTCTCATGAC AGTGCACGAT ATATATCTTT TCCAAATATT CATCACTTTT TTCCTGTAA	120
	AATCATTTCT ATTATTAATG CTTTAATGAC AACTTATTTA ATTTATTGCA TTTAATGCCC	180
	TGCTTCATTT TCAAATATTA ACTTTAATCG ACTAGCTCAT CACACTATTT ACCCTTTCCA	240
15	CCTATCACTA CTGAATTCAA AACGATTTGT TTACAAATCC CCTTATGCCA ACGGTCGAAT	300
	TTTCATCATGT TTACATTTAA TTGCAAATGC CCTCTTGAAA TATTTTAAAA TTAATATTAT	360
	TCTTAGCATA CTAGTCGGAA TTATATTC	388

20

(2) INFORMATION FOR SEQ ID NO: 965:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 602 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 965:

	AAAGTGAGGT ATAGTCCGAC CATACTCTAA AAACGTAGCG AGATAAATAT ATTTCAATCC	60
	TAACTTTTAT GTTTTGAGGC ACTTGCCATT TAGGATATTG TCGTTCGTAA TACGACACTT	120
35	GTTGTATAAA TACACCTAGT CCAATGGCA GCATCATGAG TAAGATACTT CTAAATAAC	180
	TTAAACCAAT ATCATGCCAT ATGTGTCCAA TAATCAATTG AAAGACAATG ATAGATACTA	240
	TTAAAACGAT TATATTTATT GTCACCTGTT CAAACGCACT CCTTTTCCAA ATAATAGAAT	300
40	TGCTGCTTGC ATGACAACCA TAAACATAC AACATAGCA GTTTTAAGCG TTAGACTTTC	360
	TAGAATGTGa TTTAGAACAT GTAAGGGCTC ATTAAAGAAA TAAACGGaAT GTAAGCGTAA	420
	GAAACGACCA ATATAAATTC CGAATCCATT TAAAAACATT AGcACGaCAA CrATTAATCT	480
45	ATTaAGCCAA CGGTGaGaAG TCAATGtTAG TATTTCAAAA TAGATTnAAA TCATCACATA	540
	AACCGCTAAG AAGACACCAA GCAGTAAATA GGTAAAGTAT TTCCACTCAC TTAAATTTAG	600
50	TC	602

(2) INFORMATION FOR SEQ ID NO: 966:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 744 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 966:

	GTCCTAAGGT AGATTTATCT ACAACTGTTG TTATTTTAnC AATTATTGGA GCGATTTTAT	60
10	TAATGTTTGC TAGCATATAT TTTATnAAAA TTGTGACATC ATACTTTACT AAGAACTTT	120
	TAGAAATTAA ATTTAATTCG AAATAGTATT TTCAATGAAG TGCTTCAAAG CTAAACTTTC	180
	ATGACATTTT TTTGAACTA GAGAAAATGG CTCATCAACT TCTAGCtGAA TGCCTTCTTG	240
15	AAAATGTATT AATGTTGAAT TCTCTATGGC AGTCATACCA ACAATATAAT GTGCATTGAT	300
	ATAAATTTGT ATCGGTGCAC GTTTATGTTT TAACGGAAAA AGTATAGTTT TTGGGTTGAT	360
	GTAAATAGGA ACCAGTTTAT TAATATTTAG TATGTTTTTT GCAGTCTCAA TTAGCACACT	420
20	TTGTGATGAT AAATGCAATT TCGCATAATA TGraACGAGT TTGTTAATTG GAACTTTAAG	480
	AATGTAATCG CAATGTAAAA AGACACAATT TGTTTCGAGA TGGTTTGAAG TAGCAGTTTG	540
	GATATAAAGT AGATATTTAG TAGAATTGTC TTGCAAATAT AGTACTCCTC GTTTAATAAG	600
25	TTGTTAATTT AATGGTTAAA ATAAATTTAT ATGAAGATGT TAGGGTGTTC CAACATCATT	660
	AACACATCGA CCGAAATTTT ACAATAAACT AATTAAAATT ATGTTGGCAT TTACGCTTAA	720
30	CGGACATCTT AATTAATTTA ATCG	744

(2) INFORMATION FOR SEQ ID NO: 967:

(i) SEQUENCE CHARACTERISTICS:

35	(A) LENGTH: 503 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 967:

	TACTTTGCAG GAGCATTAGG TATTCTAGCA TTTATAATGT CAATTGTATT GATTCACGAT	60
45	CCGAAAAAGT CTACGACAAG TGGTTTCCAA AAGTTAGAGC CACAATTGCT AACGAAAATT	120
	AACTGGAAAG TGTTTATTAC ACCAGTTATT TTAACACTTG TATTATCGTT TGGTTTATCT	180
	GCATTTGAAA CATTGTATTC ACTATACACA GCTGACAAGG TAAATTATTC ACCTAAAGAT	240
50	ATTTGATTG CTATTACGGG TGGCGGTATA TTTGGGGCAC TTTTCmAAT CTATTTCTTC	300
	GATAAATTTA TGAAGTATTT CTCAGAGTTA ACaTTTATAG CyTGGkCaTT AwTATATTCA	360
55	GTTGTGTGTCy TAAwAwTAWT AgTTTTtGCT AATGGACTAT TGGGTCAATA ATGGTTAATC	420

TTTTCCnAA_n ATTGCnGGGG AAG

503

(2) INFORMATION FOR SEQ ID NO: 968:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 465 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 968:

15 TACAGGTAAA AAAGGTGGTC CGTTTATCGA TTCATTAAAC CATCGTAGTT ACACGAAAGC 60
 ATATGTTTCA TCAGAAACCG ATATTCCATT TTATGCTGAA GCATTGGAA TTAGAGAAGA 120
 AAATGTTGTA CCAACAGGTG TACCACGTAC TGaTGTAATA TTTGATGAAG CTTATGCAAC 180
 20 ACAAATTAATA CAAGAGATGG AAGATGAATT GCCAATTATA AAAGGTAAGA AAGTTATTCT 240
 ATTCGCACCG ACATTTAGAG GTAATGGTCA CGGTACGGCA CATTATCCAT TTTTAAAAAT 300
 TGATTTTGAA CGTTTAGCAA GATACTGCGA GAAGCATAAT GCAGTTGTGT TATTcMAAAT 360
 25 GCATCCGTTC GTAAAAAATa GmCTTAATAT TcaCgTGaAC CATAGACCAT ACCTTAATCC 420
 GATGTGGTCC AGATCCATCC GTGGAAAGTT AAACGGATAT TCCnC 465

30

(2) INFORMATION FOR SEQ ID NO: 969:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 969:

40 AATTCGGAAC AACGAGCTGG CAACAACATA AGATGACAGA GGCGAATGGT CAATCAATTC 60
 AAGTTAACTT AAATAATGCG CAAnGCGATT TGGGATATTT AACTGCTGGT AATTACTATG 120
 CAACAAGAGT GCCGATTTA CCAGTAGCGT TGAAAGTTAT GAGGGTATTT ATCGGTATTC 180
 45 GTAAAGATGA TACAACAACn ATTTACTCAC ACCTATACTC TAAAAGATTh CACACGTCAT 240
 CACAACGGCG ACTTGAGCAA CATGGACAGT TCCTAATGAA CATAATCAAC GGTATTGTTC 300

50

(2) INFORMATION FOR SEQ ID NO: 970:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 970:

5 ATACGCGAGC GAACGGTGAA GCGACTTGCT GCTGCAAAAC GTCTGCGACC TTGAGCAACA 60
 ACATGAATGG TCTTCGGTTT CCGTGTTTCG TAAAGTCTGG AAACGCGGAA GTCAGCGCCC 120
 TGCACCATTA TGTTCCGGAT CTGCATCGCA GGAATGCTGC TGGATTATCA TCCGATTTTT 180
 10 AAAACGTTAT TAGGCGTTGT CGTTGCAATT CAATTTACAG TACCTGCTTT GATTGGTGCA 240
 TTGGTTGCCA TGAAATTTGA CCTATCGCCA TTAGCAATTG CTGTTGTGGC AAGTGCAGCA 300
 TATGTAGGAA GCGGTGCAGC GCAGTTTAAA AATGGTGCTT GGATGATTAC GGGTATTGGT 360
 15 GATTTAATnA ATACAATGAT TACAGCAGCG ATTGCAGTTG 400

(2) INFORMATION FOR SEQ ID NO: 971:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 971:

AAGTGTAAGA TTAGAATAAA AAATTTATAA ACGAATTGAG AAAGACCAAA GCTAGCAATT 60
 30 ATTCAGAAAT TAAATCGAAG AGTCTACAG TTAATGACTT ACCTGAACGA GATTTATCnA 120
 ACAAATCTCA GTATGACCAA TATGGCAAAT GCCGTGTCCA TGTTAACTGA TGAAAAGTAC 180
 TTTGGTGGTA GTTTTGAAAG ATTACAAGCA TTGACGACAA AAACAACATT ACCCGTATTA 240
 35 TGCAAAGnCT T 251

(2) INFORMATION FOR SEQ ID NO: 972:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 414 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 972:

TGAAGCTCTT aATAAATCTT TTCTGAACA CACACCAACA AAATCGTTAT CTTCATTAAT 60
 50 AATAAATAAT GTACTTACAT CTTCTAAAAA AATTGTACAA ATAGCGTCAT AAAGTGTGTG 120
 ATTCTCTCTT AGCACAACAG GTTGAGACAT ATAGTCCTTA ACCTCAAATT GTCGAAGTTT 180

55

TTCTAAAAAA CCTGACATTG TTAATATCGC TAAATCTGGT CTAAGCGTTG CTCTTGTTAA 300
 ATTCAACTTA TCTGCTATTT GTTCACCAGw AATGGGTCCT TTAGTTTTAA CAATTCGAT 360
 5 GATTCGTTCT TGTCTTTGAC TGAGTTCTrw AGGkCTTCac CCCTTTtTAT GCnC 414

(2) INFORMATION FOR SEQ ID NO: 973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 747 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 973:

GAAATCGATA CTAATATCTT CTTTATTTAC ACCTGCTAGT TCAGCTTCTA AGTAATATAA 60
 20 TTCGTCTGTt CATAcATATt CGtTACAAaT GAAGGTGTtG AAAaGTAAaTT AAaTaCTTGT 120
 TTaCCTAAAT CTTTAAaTGT ATCACTTGGA TTACCGTTAA AAAAGTTTTG ATTCTCGAAT 180
 TGATTGAAGT TCAtATCATC ACTTCCATTA TAGAAATTTG TATTACAAAG CCATTATATG 240
 25 AGTAGTATTA AAAAAGTTAA AGTAAAAGGG GAGATAAAAA AGTAATAAAT GGGTAGATTT 300
 GTGCCTGATA AGGAATCAGG GCAAAAGAAC TGAGCATCGA GATTTATACA AGCAATAAAG 360
 ATAATGAATA AACATATCGA TGCATACTTC TGCCCATCAC CTTATGATAG GGAGTTATTT 420
 30 TTTGTGCGAA TAGTCAAaT TTTTAGAAAC AAAATTCCGC AAATTATTAA TTATATCTGA 480
 TGCTTCTCGT TCTGAAATGT TGAATTCATT AAAGACcTTA ACAGAAATTT CAGCAAGAGG 540
 GCTTTTTATT GCTTTACCTT GTTCTGTTAG AGAAATTTGT AGGTTTCTTT CATCTTTCTC 600
 35 TTCACGTGTT CGAACAACGT AATCTTTCTT TTCTAATTTT TTTAGTAATG GkGTCAGTGT 660
 TCCAGAATCT AAGAACACAC GTTCACCTAA TTTTTTGATG TTAAGTTTTT CATCATTTTC 720
 40 AATCGCCAAT TAAACCAngG TAnCnGG 747

(2) INFORMATION FOR SEQ ID NO: 974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 974:

TGCTTCCAAG TAATGTGGAC ATTTAATACG AGCTGGGATT GAGATACACC TTGCAATGCT 60

TCTTGGnCAT TTGCATTGCT TCTCCCAAGT GAATGCCTTT AACAGCTTGT GTCATCATCG 180
 ATGACTTGCC ATTGAAATCG ACAACCTTCA CCTTCAAAC TAGCATCTTT TATAATGCCG 240
 5 nCTTCTATAT CAAATGT 257

(2) INFORMATION FOR SEQ ID NO: 975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 975:

CAATGGAGCA TATTTTACGT TCGGCAATGG ACATTGATCA nACAACAAAA CATTATATAA 60
 20 mTAATAAAGT AGAAGTTATC AAAGAAATTA TTAaaaaAGT AAGAGGGGGA AATCACGTGA 120
 CATCACAAAA TCCAGAAGTT AATTACGAAG CATTAGCTAA ATATGGCCGC GACTTAGTAG 180
 AAGAAGTTAG ACAAGGTAAA ATGGATCCTG TTATAGGAAG AGATGAAGAA ATTCGAAATA 240
 25 CGATTTCGTAT TTTAAGTCGT AAAACTAAAA ACAACCCTGT GTCATTGGT GAACCAGGTG 300
 TTGGTAAAAC TGCAATTGTT GAAGGATTAG CGCAACGTAT AGTTAAGAAA GATGTGCCAG 360
 AATCATTATT AGATAAAACT GTTTTGTAGT TAGATTTAAG CGCATTAGTA GCGGGCGCTA 420
 30 AATATCGTGG TGAATTGAA GAGAGATTAA A 451

(2) INFORMATION FOR SEQ ID NO: 976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 571 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 976:

AACTATTAAT AATATTAAGT TCACTACAGA TGTTGCTAAT GGACCATAAG TTTTAAAGAC 60
 45 ATCTTCACTT TTATAACCAA CAATCGCATC TAAAAATTGA ACTAAGATCA TTGCAATGGA 120
 TATAGTTATC AAAAATATAG CACTATGAAT GACTAAAGAA AnAATAGCTA ATAAaAATAA 180
 AGGTAAGCTT CGACTAAGTG cATAATATGC ATTTATATTA TGGCTAGATG CACATGCTTG 240
 50 AATTGAATAA CCTAAACTTA CACTGGCACT GATTATTGTA AATATTGCTA AAACAAAATA 300
 CATGTTAATC CTTCTTTCTA TATTGGATA TAAACAAGTA CTTGTCTAAA GTTATTTAAA 360

TATAACTATG TCATAAACTG AATTTGTTGA AATTTTTCAT TATGCAAATT TATTAATAAC 480
 AACAGCTCG AACTATAGCA TCATTTTACT AATGAATGCA TTAAAGTAAC TATGACTAAA 540
 5 AATGCATATT AATTATCATT ATTAAGACTA T 571

(2) INFORMATION FOR SEQ ID NO: 977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 977:

CCCCAAAAA TTTAGACATT TTCAAACAGT AACATTTGAA GATTTGTCTA AGCTGGAAAA 60
 20 GAGTAGTATG CCATCAGGGG TCGGTATATT AGGCTATGCT GTTGACAAAG GTGTTGCTTT 120
 AAACAAGGGG CGCATTGGTG CAAAAGAAGG ACCAGATGCG ATTAAACAAG CATTTGCAGG 180
 TTTGCCGGAT TTGAATCCAT GTGnACTTTA GTcGATTAC CGGAATGTTT ATCCTGGTCA 240
 25 TGGGGGAATT AATTGGATAC CCCAAAAAGG AATT 274

(2) INFORMATION FOR SEQ ID NO: 978:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 877 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 978:

nTnTTACTTC TTCTTTTAAT ATTTCTCGTA TAGCTTCAAA TTTTTCAGTG TCAAACAGTG 60
 40 TTCTTAATAT CCCTTGCTTT TCACGACTGT TTGATATTAA AAAGCGTTTG AATTCACCTT 120
 GAGGCAAAAT AAACAATTGT CGGAATTGAT CTGCATTTAC TCCTAATAAT TCAATAATGA 180
 ATTGGGTACC TGAAATTACT TTACTTTCTC TAATTTCATA CTTGCCATCC ACCATCTCAA 240
 45 ATaCATCAAA TTTAGCGTTC GTTTTTGTTG TATTACCTTC TTTGATATAA GGGCCTTGTC 300
 TATGCACTTT ATAAATTGGA TGATTTAATT GAAATTCAAA TGTTACTGAC ATCGGCTGTT 360
 TACCATCAGC GAAATGACTT CTCAAATCAT TTTCTTCTCT TTGTTAGTTT GATGCTTTAC 420
 50 CAAACAAGGC ATAAGTCATT GCATCAAAAA TCATTGTTTT ACCCGATCCA GTCTTACCAC 480
 TTATTAATAA CAATTCATTA TTATCAATTT TAGAAAAATC AATTCTTCT TTTAAAAAGG 540

CGTTTTCTAA AATATTTTTT ATCTTTTATG ATTGGATATC CgATAATTCT TTATCAGTTA 660
 TATGTTTATA AAACATTTTCg ATAATTGACA TGTCaTCTTT TTCACTTATT TCyATAGCAT 720
 5 TATTTTCTTC ATnGTAATTA AAAGTTTCAT TCGTCAGCGC TAAAGTATTA GGATAAAATn 780
 GTTTTAAACT CATCATTGGA TCAGTAATAT GAGACATATT TTTAAGTTTA AAATGTAAAA 840
 TAATTATCGT TATnTTTCAC ATGAACTTnT TCATTAA 877

10 (2) INFORMATION FOR SEQ ID NO: 979:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 624 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 979:

ATTGGTACTA TACCATTTGT CCATTTTAGC GAAGACGTTA AACTATCGAT TAGCTAGTGA 60
 AGAAATTAAT CTCACTATAC CTTCTATACA TAAGCAAATT AAAAATTTAG AACAGCATCT 120
 25 CAATGTGAAA CTATTGAAA CTTATAAAAA TCAAATTATC TTGACTGAAG ATGGTCATAC 180
 ATTTCTTCCA ATTGCGCAAA GTTTTATTGA ACAATATGAA AGTGGCATCA AACATATCCA 240
 ACTTAAAAAA ACGATGTTTC AATCGAAATT AAATGTTGTC GTGTCTTCAT ATATCGCGAC 300
 30 ATTCATTATG CCCAAATTTT TAAATCTTT CTTTAACGAG CATCCTTTTA TCGATGTTTC 360
 TCTTCATGTC AAAAATGAAA ATATTGAAAA AGATATTAAT AATCATACGT ATGACATCGG 420
 GATTAGCAGA AATCAACCTA AACTAAGAGA AGTTCATTCT GAAAAAGTAT GCGAAGGTAA 480
 35 AATTGTATTG ATTGCTCCCA ATAAAGAGAA TAATCATCTT CTAACGAGG CATCTTTATT 540
 TGAAAAATAC AAAATAATAA GTGATAACCA TCCAGAATAT TGGGTCATCA CTTAAAAATA 600
 40 ATATTTTAAA TATTTATGAA AAAG 624

(2) INFORMATION FOR SEQ ID NO: 980:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 457 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 980:

TTTGTCTCTGT TGCATAAACT GCAGCTAGCA TAATGTTAAT TGTTGCACCT ACGCTAACCA 60
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TkGATTcATc AATTTCAGCA CCTAAAGCTT TAAATCCTTT AATATGTTGA TCAATTGGAC 180
 GTGGCCCAAG TGGACATCCT CCCGGTAAAC CAATCACACA TTTTTTAAAT CTACCTAACA 240
 5 TGGCACCcAT CATATAGTAT GAAGCACGTA ATGATTCAAC TTTATTATTT GGTAAATGCAG 300
 CATTTTGTAT TTCAGTTGTA TCAACTTCTA AwTCCGTACC ATTTaGTGaw GcCTTAAtAt 360
 TTAAAtCtkc tAatAAACTC aCTAAAGTTT TAACATCAGA GATTThGCGG TAACCCTTCT 420
 10 AATTTCACAT GTCCTTGAGC TAATAATGTT GCAGGAA 457

(2) INFORMATION FOR SEQ ID NO: 981:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 997 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 981:

ATTGCAGCAA CGCCCCCTGT AAAACTACGT ACTCTTACAT TTATGAAACC TGCTTCTTCA 60
 25 AACATGCGCT TCAACTCTTC TTTTCCAGGA AAATTAAACG TAGATTGCTG TAACCATTCA 120
 TATTCTTCTT TTGATTTTGC AAATAATTTT CCAAAAATAG GCATAACAAA TTAAAGTAT 180
 AGTGCATACA TTTGTTTAAA GACTGGCAAA GTTGGTTGGC TCGTTTCAAG ACATACCACC 240
 30 ATACCACCTG GTTTAAGTAC TCTATTcATT TyTTTTaCG CGACTAAATA GTCTGGCACA 300
 TTTCTTAATC CAAACCCAAT TGTTACATAA TCAAAAGAAT TGTCTTCAAA CGGCAATTCC 360
 ATTGCATCAC CATGAACAAG TTTAACATTT TCCATTGAAG CAGTTTTTTC TTTTCTACT 420
 35 TCTAACATAT TCTCACTAAA GTCAATACCA GTAACCTCAC CTGTTGGTCC TACAGCTTTG 480
 CTTAATGCGA TTGTCCAATC ACCAGTACCA CAACAAACAT CTAATGCTTT CGTCCCTTTT 540
 40 CTAACACCCA TGCTTTTCAT GACGCGTTTT CTCCATACTT TATGCTGCTC AAAACTAATA 600
 ATATTATTIA ATCTATCATA TTTTTTTGAA ATATTTTGAA AAACGCGATG TACTTGCTCT 660
 TTATTTGCTT TATTGTCAGC CATGCTTAAT TACCTCTACT TTTTAAATAA CTTTTTTGGA 720
 45 TATCGTGTAa GTAATGCTTT ACTTCACTTT GATTATATTT CTTGAAGTAT GATGGATAGT 780
 AATCAGACAT ATCTTCAAAT AAATAATTAT ATATTTCCGA CTCATCAATA TTGATACCGA 840
 AATGAGATAA CGTAAtATAT GGgAAAAGTG tTTCAATTTT TACTATTGCT TGAGAAATTT 900
 50 CATAATCATT TAAAGCTTGA TGATGTAATG AAGATTTCAA TTCATTAATT TCAACAATTG 960
 CTTTACTAAT TTCATTTTGA AATGATAAAT CATTGAT 997

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 982:

10 CATTCCCTTT ATCGGnACAA TTATTTTAAA TAATTGGTTA ATAAGTTTTT CTATTAATTG 60
 CTGTTTTACT TTCTAGAGCA ACAATAAATG TTTTCAGTTT AAAATAATTA AGATTGTCAT 120
 15 TTACTAATTT GCTTTTTCCA TTCTTTAACC ATAAATCAAC TTGTAATTGC CACTCAATAG 180
 GATGATTTTT AATATAAAT TGCTCTGGAA AAATATAACC ATAATTGTGC ACTACTTCTT 240
 GATCAGTTAA CTGTAATTGA TACATTGCAC TTAAAGTGGG TTCTAAAACA GAATTTTGCC 300
 20 AGCGACAATA TTTGATATAT TGATTAATTG CGAACTTTGA TAATTTATAA ACAGCATGAT 360
 AATCACAAGG CGCCTCATTA AACAACTCAC TAATTTTGGC ATTTCTTTTT TCAGCGACAT 420
 ATTTGTGCCC GCCTAAATAT TGTATTTGTT GAAACATCAT TATTTGTTTT TTCTCTAAAT 480
 25 TGAACGTATG AAGTTTTCGA GTGAATGGAT TAATAAACAT ACTTTGAAAA TGATTGAACT 540
 TCACTTTTATT ATGACAATAA TCAACATCAT TTAmTAACCA ACTTACTTTA TATCCCATTT 600
 TCTTKAAACC TTCCGTTTCGT TGAAGAATCT GTTTATAAGG AATTGGCGAA TACTGTAGCT 660
 30 CAATAACATA TTTATTATTA ATCAAAATAT CCGGAATTTG TTTTATTTCT TTTAAAAATG 720
 GCTCTATCTC TACTTTACAT CCTTGTGCT GTATCATCTG TGCTAAAATC AATTTACTTT 780
 TATAATGTTT AATCGTTTCA TTATTAAAAC ATTTTGTTC CGCTAAATGT TTATGTGCAA 840
 35 AATGACTAAT TACTTTGAGC CCACGCTTTA AAATAACTTG CTGCCACAC ACCGGACAAA 900
 AATATTGTGT CTTTCTCAAT GCAGTAGTTG CTAATACGCG TTCCTTTTCT TCATTTAAAG 960
 40 CTACTAACAT ATCTTCACCT CAAAATATTA CACGTAAGTT TAACTACTAT TACTTTTTCA 1020
 GCTTTGAAA TCCATTAAAA AAAAGGGACC CCCAAAGGAG GCCTCCTTTC ATAnGTGCGG 1080
 TGGCCTAATT AAATAATCCG TTAATTCCAG GTGGnCnC 1118

(2) INFORMATION FOR SEQ ID NO: 983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 269 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

CATCCCCTGT TAAAAATTGn TATTTGTGTA TTGATGCTTC TCAGnCATTa TTACGAGTCC 60
 ATATTCATTG CTTCAAGTGAA ATATCAGTAG CAATAACATT TAAATCCGGC TTTTCACATT 120
 5 TCAAGGTAAT TGCAGTACAC CACTACCCGT TTCCGATATC TACGGATTGT TGCATCATCT 180
 TCTAACTGTT GGTAAGAAAT GCAACCATTa CTGCTTCAGT TTCAGGTCTG GTATCAAACA 240
 ATTTGAGTTT ACATCAAACG GTCTACCTT 269

(2) INFORMATION FOR SEQ ID NO: 984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 984:

AACCCAAGTG GAAnnGGTTT TGGTGGA AAA ATTtTAGGTC CTTTATCTGT CGTGCGAATC 60
 ATTGTATTTT TTAAACTTTC CGCATAATCT TGATGGTCGA TTAACtttTC GCGATAACAA 120
 25 TATTCAATCA CTTCAGAAAT CGCTTGCTCT GATATCTCTT CTTTTTGTAa ATATTGTATA 180
 ACTTCTTTTT CAGTtCTCTT TTTATATGAT AAATATTGGA TTGCTTTATT TAAACCTATG 240
 CGATAATGAT CATACTTTTG AATCTCTGCC ATGTCAGCAG CnTCAAGTTG TnGCCCTT 298

(2) INFORMATION FOR SEQ ID NO: 985:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 985:

CCATGCGATT CCACCTATTA ATAGTAAGAC AATAATAATA GGAATTATAA TTTTAACTT 60
 TTTAGACATT TTGCTTCCTC CCAATTATTT ATGAGTTAAT CATATCAGAA CAATACATTT 120
 45 TATTAAATGG TTTATTTTAA ATTTTGTTTA AATTAATAGA ATTTTAGTTA TAATAATGTT 180
 TAATAAGTTA TTGGrAATCy AATAAACTAC mAAAAATAGT TTGATTACaT AATGATTCTtT 240
 50 GAAAAATGkT GGkTAACyTA ATAATATGCA TTTTTTtGGC GArGARgATT tATTtAACyT 300
 ATAAAAATAT kGAaGTAAAGa TtGGGGAGAT tATGAATTtA TGGrATtGAA AGTCGATGAT 360
 TTTGTAAAGA ATATAAAAAG ACCATACTTG ACTGTATTGG GAGTATTTGT AGTTGCAGTT 420

(2) INFORMATION FOR SEQ ID NO: 986:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 986:

AAGGTTAGGn TGGAGTACCC AAAGTAGGTT TTAAAGGTTG GAAATACnAG GAGGATGAAT 60
 AACATGAATC AGTCAGTCAA ATTACTTAAA CATTTAACAG ATGTAAACGG CATTGCTGGT 120
 TATGAAATGC AAGTTAAAGA AGCAATGCGT AACTATATAG AGCCTGTCAG TGATCAAATT 180
 ATTGAAGATA ACTTGGTGGC ATTTTTGGAA AGAAAAATGC TGAGAATGGT CAATACTCAT 240
 TATGATTTCT GGTCTATGGA TGAAGTGGTT ATGGTAACAA GATGTAAACT GTTATTCATT 300
 ACGCGTGGTG TGTGATCAGC nGCACTCAA 329

(2) INFORMATION FOR SEQ ID NO: 987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 987:

CATATTATTT nTATATGAGT TTACCACTGT CAAAAAACA ATTGCTTAAT GCCAACTATA 60
 TTACATGCAT TGTTTAAACA TTAATTGGAA CGCTTGTTAT TAGTTTATAT GCTTATGAAG 120
 CAGATGTGAT TGAACCAAAT TCAATCTATT TTTCAACTGC ATATGCATTT GTCATATCTA 180
 ACTTCTTGTC TATACCAATT GCATTTAGTC AATTACAGA ATTGCGTAGA GTCAAAGTGC 240
 CATATGGTAT ATACGTGTTT ACTATTATCA TTTTAGTTCC ATTTTATTT TCAATTGCAA 300
 TAGTATTGGT GAATTATTTT GTTCTAAGTC AATCATCATT CCCAGATTTA TATTCATATA 360
 TTTTAAATAT TGGTTTCTA ATTATAAGCA TTGTTATACT TATTGTTAAT TATTTTAAAC 420
 AGCTCAATAA AATAAATACT AGAAAATTTA AAGGAGGCAG TCGATGAAAT TAGAACATAT 480
 TACAAAAAAA TACGGCTCAA ATGTCGTTT AAATGATATT GATTTTGAAT TTGGCGAnAG 540
 TAGAA 545

(2) INFORMATION FOR SEQ ID NO: 988:

(A) LENGTH: 607 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 988:

10 ACCTAGCATG ACATAATCAA ATATATCAAA AACACCTTTC TGAAGTGAAT CAACCGTTCC 60
 AATAGTTAAT GGTCTTTCAG AATCAGATGT CTTCCACCT TGAACAGTCA GATGACTAAT 120
 TAAATATTG ACGGCATCTT CATCAATTTT CGGTGCTATT GTTTCATAC AGCGCGTAAT 180
 15 TCCCTGTTGA TGTGTTTCAA TGGTGTGATC TTCAAAGTAG TGTTCATTT CGCTCACAGT 240
 AGCATAAGGG AGTGATATAA AATTAACCCC ATTTATCTCT ATTGGTGAAT TAATCGATGT 300
 AAAATCTGTT CTTATAAATA ACTGATTATG TTCAAACCAA CTCGCCCCAT AGTTTAACCT 360
 20 CTCTTTACCA TCGTGATTTT CACTAATAAT AATTATTGGT ATACGCAGTT CTAAATTTAA 420
 CTTTCCAATC GCTTGTCTTA ATAACATGAT TGCATCTTTA CTTGGATATG TTGTGTCATA 480
 TAAATCCAG CTATCACAAT GTATCAGGT TCTTCTTCTT TCATTTTTTC TACGAACATA 540
 25 TCTAAATAT ACGCTTGATC TTCTAAAAGC TGTTGCCAT CTAATATTTT CCCTAAGTGC 600
 CAGTCTG 607

30 (2) INFORMATION FOR SEQ ID NO: 989:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 722 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 989:

40 ATCGCGTTAA GCAACAATTA CAACAATCAT CATATAAGCT AACGCCACAA CGCGAACTAC 60
 TGTTAGAGTT CTAATTGAAA ATGAAAAAGA TCATCTAAGT GCTGAAGACG TATATCTGAA 120
 AGTAAAAGAT AAAGCGCCTG AAATTGGCTT GGCGACAGTA TACAGAACGT TAGAGTTGTT 180
 45 AGCTGAACTA AAAGTTGTCG AAAAAATTAA CTTTGGTGAT GGCGTCGCTC GTTTTGATTT 240
 AAGAAAAGAA GGCGCAAAAC ATTTCCACCA TCATTTAGTA TGTATGGAAT GTGGTCGTGT 300
 AGATGAAATC GATGAAGATT TGTTACCAGA AGTTGAAAAT CGAGTTGAAA ATGAGTTCAA 360
 50 TTTTAAAATT TTAGATCATC GTTTAACTTT CCATGGTGTG TGTGAAACGT GCCAAGCTAA 420
 AGGTAAAGGA TAGTAAATTG CGTAGGTAA ATTAACCTTC GCTTTTMTTA GAGGTGTGGT 480

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TAACACAATT GGTGCTTATA GACGTGATTT GAAAAAGTAT CAAGATTATA TGA CTGAACA 600
 TCATATCTCG CATATTGATT TTATAGATCG ACAATTAATT CAAGAGTGTh TGGGGCATTT 660
 5 AATAGACCAA GGGCAATCTG CTAAATCTAT TGCGCGATTT ATTTCAACAA TCCGTAGTTT 720
 TC 722

(2) INFORMATION FOR SEQ ID NO: 990:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 990:

20 ATCCAAAAAA TACGAAAGCG CTTTCTATAT TGGTATGCAA GTATTTCAAA AAGAATAAAT 60
 TTAATTTTCC TACTTTTCTA AACATTTATC TTTATGTATA ATGTTTTCAA GTA ACTAAAT 120
 TATAAATTAA ATAAAGGGAG TGT TTATCAT GCTTACAATG GGGACAGCAT TAAGTCAACA 180
 25 AGTAGATGCC AATTGGCAAA CTTATATTAT GATTGCCGTC TACTTCTTGG GThATGACTC 240
 CAACTTATTG ATAGTGThT TATGTTTCAG ATAATGCCCG ATGACTTTGT CATGCCAGCT 300
 CCACCGATTT TGAGnAACGA CAGCGACTTC CGTCCCAGC CGTGCCAGGT GCTGCCTCCA 360
 30 GTATTC 366

(2) INFORMATION FOR SEQ ID NO: 991:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 991:

TGACTACAGT AACATTACCT GTAAATAATG ATTGAATGGC TTCATTTTCA TCATGAATAC 60
 45 CTGTAATAAA TTCTAATTCT TCATCTGAAA CTTTACAAT ATGCGCCAAT GGCAAAAAGG 120
 TATGAATAGT TTGTCTTAAA TCTTCAGCGT TATCCCATAA TGGCAATCTT ACATTAGGAT 180
 CAAATACGAC AGTACCATTT GCATTTAATG TTTTGGTAAT CAATTGATAA TGTGCATCTC 240
 50 TCATCGGACT ATCGACCAAA TCAACAGAAC AAAAATGTAC TACATCATTT TCATTACAT 300
 CaATATCATT CACAAAACtk GGkTCaAaTA aCATATCn 338

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 992:

10 AGTTCATCGT ATTCTTAATA CCTATATGCT ATCGTTCACA AACTTTTGTT CTTTCTTCC 60
 AACATACCGC CTATAATGCT CAAAAAGAAA TCAGCAGTGG AACCACTACG TTCCCTACCG 120
 15 CTTTATCATT TTCAGGCTTA AATATTTTAA AAATTTTGTT AGGAATCCGC TTAAAAAAC 180
 TCATATCTTC AAAAAAATG ACAAATTTA AATTTTGA TAACATCATT TTTAGTAA 240
 TGTATAATT TCTTTATAAT ACAAATATCG AAAGAAGGCG ACTGACTTTG AAAAAATTAT 300
 20 GTTCATTAAT TGTAGGTAGC ATTAGTTTGT ATCCTTGCCA TTATCAGCTT GTGGnAAAGA 360
 ACnAACnAA A 371

(2) INFORMATION FOR SEQ ID NO: 993:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 530 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 993:

35 ATAATGATTT ATCAATCGAT GTTAGATGCG GTTCAATTAT ATCCTAAGTC TATCGTGGTT 60
 GATTATACTG TGGATGGACA ATACaAAAAT GATTGTCACT ATTTCCGTCA ATCATCGATC 120
 AACATTGCCG ATTGGGCTCA AAACAATAAT TATTATCCTA ACCTGATATA TGCATTCAA 180
 40 CAGACTCTTG ATTTAATACA TTATTACTCT GTAGAAACGA TTTTCGATTT AGCTTTATTG 240
 ACACTTCTGA AAGGTGATTT ATCAATCGAT GGTCAATGTCG TTTTGTATTT TAAAGCCCCT 300
 ATAGCAACAA GTGCTTCAAT ATGGGAAACT ATTAAACTA TTGAAGATTT TGATATGATG 360
 45 TCcAGTTTTt TTGAtAAAtG GCTTATATtG ATCATCATCC TATACCTTTT CGCAACCTTT 420
 TTATCGAGGA TTCAGAACAA CTTAATTCGC CAGATAATTG GTTGTATTCT ACCAAGTTTA 480
 50 TGCTACCTAA ATGGGnTATA TAAATAAGC AAAGCAACGT GCTGATAACA 530

(2) INFORMATION FOR SEQ ID NO: 994:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 551 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 994:

	TATTGGATTn TThCCACCAA AGGCAACGGT TCCTTTTCTA ATTCTAATAA TCAAATCCCC	60
10	ATTAATATCA ATCCCACTCA AATTCTTTCA CATCATTGAG TATAAAATAA TATGGTGATA	120
	TACGTTGAAG TTGATTnTCT TATTTAAGTA TACTCCAACA GTATTTTATA AAATTATTTA	180
	GTCATCATCT TCAGTGTTTA ATTCAAAAAT ATAGAATCTA CTGTATTGCA TAATAAATTG	240
15	AAATGCCACA AATTGTGTAC AAGCAATAAT AATGATACTT ACCATTATGA CAAACTTGGA	300
	TTCTACGACA TTGGGCACCA ATATATATTC GATAATTCTT TCAATATATA TAAATGCGCT	360
	CAACGCGGTT AATAATAAAC CGAAATGTGT TTTaGTTTTA CCACCCCAAC GTTTTGTyAC	420
20	TTTAGGTAAT TTTAATAACG TGAACATTCC GCCAATTACT AATAACAAAT AACTAATTAT	480
	GATTGAAATC GTACCCATCA ACCAATAATT GAATAGGTCA TAATGATTTT GTACAGCAAC	540
25	AAAATAATAA A	551

(2) INFORMATION FOR SEQ ID NO: 995:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 729 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 995:

	ATTCGCCACC ATTAGGTAGT GGAACACGAA CTTCATCATC TAAACCTTTA CCAATTAACG	60
	CTTTAGCCAT TGGTGATTCA TTTGAAATCT TACCATTAAA TGCATCTGAT TCAGCTGAAC	120
40	CAACGATTG ATAACTTTCC TCTTCATCAC CTGGTAATTC TACAAACGTT ACTGTTTTAC	180
	CAATTTTAAC AACGTTGTTA TCTCCAGTAT CTCAATGAT TAATGCATTT CTTAACATAT	240
45	GCTCAATTCT TTGAATATCT TGTTGATGA ATCCTTGTTT ATCTTTTGCT GCATCATACT	300
	CAGAGTTCTC TGATAAGTCA CCAATGAAC GTGCAACTTT AATTTTCTCT ACAACTTCAG	360
	GACGCTTAAC TGTTTTTAAT TCTTCAAGTT CACGCTCTAA TTTTCAAAA CCTTCTTGAG	420
50	TCATTGGATA TTGCTTTTGA TTTTCCATAT TGTCATCTTC CTTTACTGAA TTATACTATT	480
	GCTTGCTAAC TAAAGACTGA ATTTTGTGTT TCATAATATC TATTGCAACT TTATTGCTCC	540
	CACCTTCAGG AATAATTATA TCAGCATATT TCTTAGTCGG TTCAATAAAT TGGTCATGCA	600

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TTAGTATCTC GTGTTGAAAC GCGTAATAT nCTCAAGTCT GGCATCTGTA TCAACATATA 720
TnTtnAACA 729

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(2) INFORMATION FOR SEQ ID NO: 996:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 996:

GACAAATATA CTGCTTCTAC TCAAATATTA GTGAACATGA AAAAGTCCTC AAGTGATTTA 60
GCTTTCCCAA AATGTTCAAA GTAGTTTGCA GTCTGTTAAT ACATATACGG AnATTATCAA 120
AAGTCCTAGA TTCTAGATAA AGTATCTAGA GAATTGATGG TCAGTATTCA ACAGCTGAGT 180
GAAATCATTT TAAAAGTAAC CATCCAACCA ACTCTCAAAT TATTACTGTA CAGTTACACT 240
GGGATAATCT GATCTGACAA ATGTATAAAT ACTAAGTTT GCCAGCAGCT AAATAGAGGT 300
GTATGTACGA CTTCCAnCTG TAGnG 325

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(2) INFORMATION FOR SEQ ID NO: 997:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 997:

CTTCAGTTGT CGGCAAATCT TCTATATTGG AAATACCama TACATTTAAA AATAAATCAG 60
TAGTAATTAA CTGTTGGCTA CGCTGTTTCAT TAACCACTTT AGCCTCAACT AGTCCTTTGG 120
CAATCAATGT CTTAACTGCA CCATCTGAAT TGaACTACG AATTAAATCA ATATCACTTC 180
TTGATAATGG CTGGTTATAA GCAATAATTG gATAGTACTT CCATTGCTGC TTGTGataAT 240
TTCATTGTG aCTTTTGTTT AATTGAATTG T 271

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(2) INFORMATION FOR SEQ ID NO: 998:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 498 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 998:

5 TTTATGTGCT AATTTGTAAT TGAGATTCAT AATGGTATTT AAATCATTAT GGTGCGGGAG 60
 TTATGGTATT GCCATAATAT GAGAGTGCAT CCACTTCTAT AAGTAATGCA TATTGCGAGT 120
 GCAGG~~a~~ATGA ATGAGTGCTT GATTAAAAATC CTTATGGGTG GTTGACATAA TTAAAAGAAA 180
 CCACATTTAA AATTTCTTAA TCACAAGCGG TTAAGTAGGT ATAGTTTAGT TTTGAGTAAA 240
 10 TCTTTTTTAAA GGTGTACTTG TGCATTTTAC TTAATTAAAG ACATAAGACA TTTAATCGGC 300
 CTAAAATAAA TAAAAAATA CCTGTTTAGG TAGTTTTTTT AATGTAATAG ATTA~~AA~~ACAC 360
 15 TAGTTCATTT CTTATTAAAG ATGGATAGTT ATTTTATAGA TAAATTTGTC CTTTAGTGTA 420
 GCGGTAATTT TTAGGACTTT TTGGTGG~~n~~AA AAATGTTCTT AATAAAAGTA ATAGTCCTAC 480
 TTTACCGCCA AAGCCATA 498

(2) INFORMATION FOR SEQ ID NO: 999:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 568 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 999:

30 TGAGCTGGTT GTTTATTATC ATCAGTTTTTCTTCTGATTAT CATCTGATTT ATCTTGAGAT 60
 GCTTTGTCAT CCTTATCTTT CGACTCATCC TTTGATGCTT TATCATCATT CTCTTCTTTA 120
 GCAGGACGTT GCTTTGTAGG TGCTTGTTGC TGAGGTGGCA CATATTGATA TTGATTCTGC 180
 35 TGTGGCAATT GCTGATATTG GTTTGCTTGT GAATCTAGCT CATTCTGCTC TTTTCTCTCT 240
 TGTGCTTTT TCTTTCTCTC TTTTCTGCA TTTTCTTTT GACGCTTTTC TTTTGTTC 300
 40 TGCTTTTGTT CGTTCAACAT ACGTTCTTTA GCTTTATTCG AATGATCTAC ATATGCAAAA 360
 ATTGCAAATA CTAATCCTCC GAGTAATAGC AATACCGTCG CAATGCTAAC TACTTTCGCT 420
 GTTGTACTCA TTTTCTTCTT ACTTCCATCT TCATTTTAT TGTAGTCGTA ATTTGATTC 480
 45 GACATACTCT CCCTCACTTC AACTAATTT AAATATAGAA ATTATCACGC AACCATTAAC 540
 ATTTTCACAA CTAATTTGCG ACC~~n~~AGTA 568

(2) INFORMATION FOR SEQ ID NO: 1000:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1441 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1000:

5	AGTGTCTTCTA ATTGCAAAAT TCCAAATACA GTGTCGTTAT TTACTTTTTT CATGCTAAAC	60
	ATCTCCCAAT TAATAATCAC ATATTAGCT ACTATACAAG TATTAACAAA CATCCCAACA	120
	ATCCCAAAAC TTGTATGTGC TAACTTATGC ATAAACTAC AAGTGTAAT AAACCTGCTT	180
10	TCTATTCAAT TGTCAAAGTT GAATAAAATT AAATAAGTAT AAAAACCAAT AATCAATAGA	240
	GTTAATATTT AGAAATAAGA TAATAGTACA TAAACAAAT CACTCTATTA CATATTAATT	300
	TTATAATTTA TATACAAAGA AAATATATCA ATATTACCAT TAAATTGCAA CAATTCTACA	360
15	TATATTTCTT CAAAAAGAT ACGCATTGAA TTTTATTAC ATATAACTCT CATGAAAATT	420
	GATTAACTA AATTAATTAG TTAGCCTTAA ATTTAACAAA TTAAATCAA CCGAATGAGG	480
	CTAAATTGGT TATTTTTCAA GATATGATT GTATAAATCA AAACATTTCT TACAAATCAA	540
20	ATGTGTATAA AATGTGATAT ACATTTTCAA CCTTAAAAA GTTCTAAAAA AAGATGAGCA	600
	TCTACTGTCT CATCTTTCAG TTCTTTTTTA CGGGTCTGTT TTCTAATTG AGCACAATCT	660
	TCGATTTCTT TATCTAAATG ACTACCAATT AAATCTATTT CTTCTATTGT TAAATCGCTA	720
25	TCTCCATCTT CTTTTATCTC TGGTATTATT TTTTCTTCAA CTAAGTCACG ATATAGTGTT	780
	TTTGAATTCT CGTTCAATTT CGATTCTGTA TTTTGAATAC TTTCTCCGC ACCAATGTAT	840
30	ATCTATTGGC ACTAGCTTCT ACTTTGTAC CATCAATAAA AATTGAATTA TCATCAATAA	900
	GATTTTGCTT TAAACATTGA CTATAGAACT GAATAAATAA AGATTCAATT AACGCATCAG	960
	TATTAGGATT CACTCTAAAA CGATTAATAG TTTTATAAGA AAGTGTGTA TCTTGGGCTA	1020
35	ACCACATCAT TCGAATACTG TCATGAAGTA ATTTCTCTAT TCTACGACCA GAAAATACAG	1080
	ATTGAGTATA TGCATATAAG ATGATTTTTA ACATCATTTT TGGaTGATAG GATGTTGCAC	1140
	CACGATGATG TCTGAATTCA TCGAATTCGC TATCAGGTAT CGTTTCAACA ATTTCAATTA	1200
40	CATATCGCGA AATATCATTT TGAGGAATTC TAACGAAGTT TCTATTGGTA GTGTAAGTTG	1260
	GGGTCATGTT ATAATTTTTA TACATAAGGC ACCTCTTTAA TTTAGTTTAG TAGTATTTAT	1320
	TAAATTATAC GaAGGGACCC AACACAGAAA ATTCATTTTA TTGAATTTTA CATTTATGTG	1380
45	CAAGTTGGGG AAAAATGTCT TATTTTTTCA AAGTATTTAA AAGTAAATT ACATGTTAAT	1440
	A	1441

(2) INFORMATION FOR SEQ ID NO: 1001:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 587 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1001:

	TAATAATATC TGTCATATTA AGTCTCCCTC ATTAGAACTC ATTATAAATG AAGTTATTGT	60
10	GTGTGTCGCC ACTGCCATAA ATTAAATATA AAGTAATAAA TATTGCCAAA TACAATAGTG	120
	TTAATAAATA TGGTTTGAAT GCTTCAACAT ATTTATTAGG TGGCTGTTTA CTTTITAGATT	180
	TCATATTGCA CCTCTTAAAG TTCTTAGTAA AAACGCCTTT ATAAAGACCG TTCAATATAA	240
15	AATACGTTTT AAAATTTGTT TTTTACAATT CATTATATCG ATATTCATAA TGAAATTCAA	300
	TTTTAATTTT ATAGATTCAA CATAGTAATT GGTGTGCATC ACTCAAKTAT TGTAATGAT	360
	ACACTTTGTT GAGACATCA TTCATTTTAA AGGTTATTTA AACATAAAC AATTACAGTC	420
20	TATATAACAA TTTTGTATA TACGTCAAAA TCAAATAAAC TCATCACATT AATATGACGA	480
	GTTTATAATG TTATTGAATT ATCATCAGCG CAAATATATA CATTGCAAG TCAAGCATAA	540
	CATATTTAAC AATTGCTTTG CTTGGTTTAA CCAATGGATT AAAAACC	587

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(2) INFORMATION FOR SEQ ID NO: 1002:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 522 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1002:

	CAATTGTGTC ATAATTTTGC TGATGATAAC TAATCGTTTT GGAGTAGCTA TTTGATGAAG	60
	TTCGTCCAAT ACCTTTTGTG GAATCGAATT TACCACCTGA GCGTATATGA AAATGTACTG	120
40	TCTACTTTTG CAGTTGAAAT TTTATTTTTC GGCAATTGGT CTAATATTTT AGTTTTACGA	180
	TTTCTTTTAA CTGAAAATC TACATGGTAC TCACTTGGAT ACTTTAACCA ATTTGAATTT	240
	TTTTCTTCTT TATGAGATT AAACTTTAAA TTTGAATGAA TTGAGCCTTG TTTTTAACA	300
45	AGTAATACAT TCTGTGATA AGTTGGATCA TCGATAAAGT CGAATTGTAA ATTTTGGAGT	360
	ATATTtGTWT TCTCATCATA TACTGTTTCA GTTCGTTTTG TGATTTTACC GTTTTTCCCA	420
	ATATCATCCG GTGCTGTTGA ATTTTATCT TTATTAGTAA CATTACGTTG CTTTGTGAn	480
50	CTTATCAACA TGTCTTCTAT TTGGCTGAnG CTTATGGnGA TT	522

(2) INFORMATION FOR SEQ ID NO: 1003:

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(A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1003:

10 TCITTGTTTG AGACATAATG TCATGTAAAG TTTTCACAAT GCGTTCTTCA ACTTGTTGCC 60
 TTGCCTCTCC TTTGAAAGGA ACAATTCGAT CTCCGAATAA GTCCTCAGGC TTGTATAGAT 120
 TATCAAATAG ATAGACTGAC TCACCTTCAA ATATTCCAAA ATGCCATTCC TTCAGTCCCT 180
 15 TAAAACGTTG ATACGATTGG WTAGGTGCAA CATTTTCAAG TGTGTCACTT GCGCGTTCTT 240
 GCGTTGATGA TGCATATAAA TCGAAGTTTA TCCCCTTAGT TTCATAATAA CTACGTGCCT 300
 TTnGAGCTTG AGCAATTCCA AGT 323

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(2) INFORMATION FOR SEQ ID NO: 1004:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1004:

30 TTCTAACTTG ACGTGACTGG GCATTTCTGT GnAAATnTTC TGACATTCTT TTTAATATCC 60
 GCAACGCAAT TGCTTCAGTT AAAGATTGnA ACTTGCAACA TTATTGGTA CGAAAAAGTC 120
 35 AGTTTTAATG TCGATATAAG ATTTATTTTT TTGTTATAT AGTTTCGCAA CTACATTG 180
 TTGTCTTACT TGATCATATT TTGCAACCGT ATCGAATGCC GTCTTTTCAA ACAGCTTTAC 240
 GAGATACGTA AACCATGACC CATCCATCGA AGTCCTTGGT AAAAACCAG GGTTCGAA 300
 40 GCCGTAGGGT TTGAAAGATA 320

(2) INFORMATION FOR SEQ ID NO: 1005:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1005:

50 nATTAATGCT AGCCAAAACA GAnTTGCAAn ATGTAAAGAC ATGTGAAACC CTCCTTATAT 60

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CGATATTTAT AAAAAATAAT ATTTCACTTA ACCAGTTTTT AGTTATCATT GCAATGGTAA 180
 AGGATACGAT GAGTATCACA CCACAAATGA TAATACCAGG CAGGAGCCAA CATAAATCAT 240
 5 CTAATCTTT ATTATATGTG ATTAAAATAT TAAAGATAAC AAAAGTGGTA GTAATAACTA 300
 TATTG 305

(2) INFORMATION FOR SEQ ID NO: 1006:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1006:

TTCAAGATAT CAGTATAAAT AAAAAGTTAA TATGCTCATT ATAGACAGCT ATAAGTATAT 60
 TTTCTCGTCC CACTCTATAG AAATCAATTT CATTTATTAC CATTTTCTCT ATTTAAAAAC 120
 ATATTTTTGG TATTAACAAT TAAAAGTGGG TATATATATT TAATGAACCA ATTTTTTAGG 180
 25 AAAGTAGGGC TAAACCTATG GAAAATAAAT TATACCACAT GGTGTCCTCT TTTACCATGA 240
 ACACAGTGAA TTAAAAATA TTAACAAGG TATTGGGGAA GTACACCAG CATTAGGTCC 300
 AATTGGTAGC CACCTTCCAA TCCATTGGGG GAAA 334

(2) INFORMATION FOR SEQ ID NO: 1007:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 565 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1007:

AGAAAATTTG TTATATTAGA AGCGAATAAT TTAAAACAT ATTATGAAAT GTAAGAAGAA 60
 ATATTATGAA ACTAGGAAAA GTAGATTGTT GAAAATTCCA TACAATAGGn GAnGTAAAGT 120
 45 GAATAAATTC TGGTATTACT AAAGCTATTG ATTGTCCTAA TTGTAATAAA AAGTTGGATA 180
 GTGTAGTTGA GGGGAGAAAA ACTAAAATGC AAAAATATAT TCTCAATGGA TCATTATAAA 240
 TACCAATTAG aTTAAAGTAT TGCGaACATT TACAATTAGa AATCAGTATT AATCTGCCAT 300
 50 AGATAATTGT ATTAATGTAA AAmATAAAAT AGAATGAGAA TATACGAAA TTTTTTATAC 360
 ATTTATAACC AATTCTGTTA AACTGTGAAG AGTAGAGTTA AAAACGAACT TTTTGTATTAT 420

AATGATTGAA CGCTATTCTA GAGAAGAAAT GTCTAATATT TGGACTGATC AAAATCGCTA 540

TGAAGCCATG GTTAGAAGTG GAAAT 565

5 (2) INFORMATION FOR SEQ ID NO: 1008:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1008:

CAACATTAGC GTCTAAACAA ATCTTTGACT AAACGTTTAC TTGAGCGACC ATCTTGATAT 60

TTAAATGTT TATCTAAGAA TGGCACAAC TTTTCAACCT CATAATCTTC ATTGTCCAAA 120

20 GCATCCATTA ATGCATCAAA GGACTGTACA ATTTTACCTG GAACAAATGA TTCAAATGGT 180

TCATAGAAAT CACGCGTCGT AATGTAATCT TCTAAGTCAA ATGCATAGAA AATCATCGGC 240

TTTTTAAATA CTGCATATTC ATATATTAAA GATGAATAAT CACTAATCAA CAAGTCTGTA 300

25 ACAAAGAGAA TATCGTTAAC TTCACGATGA TCTGACACAT CGATAAAGTA TyGTsTATGT 360

TCACGTGAAA TAYyAAGTCy ATTtTTTACG AaCGGATGCA 400

(2) INFORMATION FOR SEQ ID NO: 1009:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 454 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1009:

40 TATTGTAAAA ACTGTGGTTC TTACAATGGC GAAGAAGTAG CAGCTAAATA ATTTTAGTTA 60

CTCAATATAA AAaGTCCCGC TTAAATGAT TGTTTAAAGT GGGACTTTTT ATATTGCGAA 120

AAATAATTGG cGAACGAGGT AACTGGATAC CTCATCCGCC AATTAAAATT TGTTAATTTA 180

45 ATAATTAAAT ATAAAGACGA TTTATTAGTT TTTACGTTTT CTAGGTAATA CGAATGCAAC 240

GATGCTACTT AAAGCTAATA ATGCCATTAA TGGTAATGTC ATATCTnTAT TTGATTCTTC 300

ACCAGTTTGT GGTAATGATT TTGCTTTATT TTCTTGTGTA TTTGTATTGT TTTGGCTTTG 360

50 GAGTGTGTCC ATCATTTGTG TTTTAAATGT TTGCTTnTnG TAATGGAGCA CTAATCTTTT 420

GCCTCGCTAG AACCTGCCGG AGGTTTGGAA CCAC 454

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1010:

10	GGTACAACAA CTTTAGACAA TGAAATATTA AAAGATACGG ATGATAAAAA GTCGAGTAAA	60
	ACTTTTGTG GCGGAACAAA AGTTGATGAC CAACATGCTA GTATCGGAAT GGATTTTGAA	120
	AATCAGGACA AAACTTTAAC TGCCAAAAAA TCATATTTCA TATTAAACGA TAAAATTGTC	180
15	TTCTTAGGAA CTGGCATTAA AAGTACTGAT TCATCAAAGG ATCCCAGTTA CCAACCGATG	240
	AAAATCCGCA AGCCGATGGG GAATACGGTA TTTTCCGGCC GTTAACCAAC CACCCATTCC	300
20	GGTTATCCGG GAAACCATTC CATCCTTTTA GGAGnChCCG GTnChAAAAA GGACCTCGGG	360
	TATCCTTTTT TTAACCAACC CGAAATTACT GGTAAAAAAG	400

(2) INFORMATION FOR SEQ ID NO: 1011:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1011:

	TTAGGTATTC GCAAAAATGA TCTTCAATAT ATAGCTATGG CCAAAAGATG GGCTAAAGCT	60
35	TATACAATTA CTGTAGCAGT GGGAGTTGTT ACAGGTACAA TTATAGGACT TCAATTATCA	120
	TGATTTGGCC TACATTTATG GAAATGGGTG GACACGTATT GCACTTCCCT TATTATGGGA	180
	ACATTGCGGT CTCTTGAGC TATTTCTTAA GTATATATTA TATACTGGGA TCGTTTAAAA	240
40	TAATGGCACA TTCTTAATAG TATACCAGTA ATTATGGGGC CTTCTCAGCA TCTCATACTC	300
	AGGAATCATT ATGAATACGC CTGCAGGTTT GAGTGAAGAT GGAAGTGGCC ATGTCACChT	360
45	AGAGCGTGTT ACCCACGTTA AGTCGTCATT nCGAATACAC	400

(2) INFORMATION FOR SEQ ID NO: 1012:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1012:

CTTTATGGGA TACTACTACAA ATCGAGACTA TAAGGTTTTT TATTTTATTT ATTATTACAT 60
 5 TATCAATAGT TTTATAATCG AGCTTCAAAA CTTTAGAAAA TAGTAGAAAT AGCATTCAAT 120
 ATAGTGCAA AGTGCAAATT GATAACTTGA CACTTATCTC CTATAAACCG TACAATTAAT 180
 TTGTATGATT TATATATAAT TTCATAAAGT CATATTGAAT TTCATATAAA GAGCAAACCC 240
 10 TAGAAAAAGA GGTGTTGTGG AATTATTAAG CTCCTACTCA TTTGCGGGGT CATCTAGGGT 300
 GTGGAGGATG TGTGCCGAAT TGTGCTCAAA nATCCCAGCA GCAACGCGAG TTGAACAGCC 360
 TAAGACGCAA CAAAGGATCT GnnAAGGACC ATCAGGCACG 400

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(2) INFORMATION FOR SEQ ID NO: 1013:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 353 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1013:

25 TCGTTGCTG ATACCACGCC AGTATTGGTT TTAAATGATA AAAAAATCTG TGAGATTGCA 60
 TCATTGAGAC AAACATCGCT ATTTGAAATG GCCGAATATA TAGGGTTTAG CGAGCCACAG 120
 30 AAATTAGTAC AATTATTTAT TAACCATGAT AGGAAGGTGA GACGCCAATG AATCAATATA 180
 AIACTATAGG TTTTCACCCG GGAAATAGTC GTATTCATCA ATTAAATGCG ACTGTAAAC 240
 TTTTATnCTT ATTAGTTGTT CTATTCTGCA ATGGTnCTAT GCACAGGTAT TnATTTAATT 300
 35 AGGCTCACAT TTATGGGCAA TTCTCAATGA TGAACAGTCG TTGTGTAATC TCG 353

(2) INFORMATION FOR SEQ ID NO: 1014:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 627 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1014:

45 CAAAGCCTTC AACAAATAAT CTTTATTAG TACTGATTGG TTGCACAACA TAAGTTACAC 60
 CAGGTTTCATC TTAAATGTA ACTTCCTTAT AGAAGAGACC TTTTITAGCA CTATACTCTG 120
 50 TTTTITCTGA TTTAATTTTA TCTTTTAGAT TTTTCTCTC CAAGTAACTG TCAATTAGTT 180

55

ATGAAATAAA TAATATAATG ATAACCTTTAA TCGCGTTTTt TTTCTTCTTC ATTATGTAAC 300
 TCCTTTTTGC TTATCTATTC AGTATGAACG AATCAATTTA TTTAATAAAG AGTTTTTACC 360
 5 AGATTGTAAC AAATTTTTTT ATTCTCAATA TTATTATAGA AATCGAATTA CATACACGAT 420
 GCTTTTAAAA AATTTAATAA CAAATTTTAT TTTACTATCT ATCAAAATAA TTGACTACTT 480
 TTAACAATTA AGGATGATAC AATTACATTT TTTTCAATTT AAAAAATCAG TCATATCAGT 540
 10 AATTACCGAT GAAAATACTA AGATATCGAT ATATTTTGCA TTATTTAACA TTTAAATTCh 600
 ATTATAGACA ATTCAATAAT TGCGATG 627

(2) INFORMATION FOR SEQ ID NO: 1015:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 462 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1015:

25 TAGTGTGACA TTAACACTGG AACAAAAAGA AGCTGCAATT GCAGAAGTTA ATAAGCTTAA 60
 ACAACAAGCA ATTGATCATG TTAACAATGC ACCTGATGTT CATTCAAGTTG AAGAAATTCA 120
 ACAACAAGAA CAAGCGCATA TTGAACAATT TAATCCAGAA CAATTTACGA TTGAACAAGC 180
 30 AAAATCAAAT GCAATTAAAT CGATTGAAGA TGCAATTCAA CATATGATTG ATGAAATCAA 240
 AGCTCGTACT GATCTAACAG ATAAAGAGAA GCAAGAAGCT ATTGCTAAGT TAAATCAATT 300
 AAAAGAACAA GCAATTCAAG CGATTCAACG TCGCGAAAGC ATCGATGAAA TAAGTGAGCA 360
 35 ATTGGAACAA TTTAAAGCTC AAATGAAAGC AGCTAATCCA ACAGCAAAAG AACTAGCTAA 420
 ACGCAAGCAA GAAGCTATTA GTAGAATTAA AGACTTTTCA AA 462

(2) INFORMATION FOR SEQ ID NO: 1016:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1016:

50 TGATTGGTCC CATCGACTCG TTATAACAAA TTGAAGGTAC AAAAGTATCT TGTGATTTAA 60
 TAAATTCAAG TAAATTCGTA CCTGGTTCTA CAAGGTAATT CTTTCCATC AAGTGTAAAC 120

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ATAAATTGCG CATATCCACC nAAAATAACG ATGCCCCACA CATCTTTCAG ATAGG

235

(2) INFORMATION FOR SEQ ID NO: 1017:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1017:

15 GTTGAAACT ATAAGATCA nATAAAGGTAA AACAGTGGTT TGTGTCATTA GTGGTGGTAA 60
 TAATGATATT AATCGAATGA AAGAAATTGA AGAACGTTCA TTACTATACG AGGAAATGAA 120
 GCATTACTTT ATCTTAAATT TCCCTCAACG TCCAGGTGCA TTGAGAGAAT TTGTAAATGA 180
 20 CGTATTAGGA CCTCAAGACG ATATTACTAA ATTTGAATAC TTAAAT 227

(2) INFORMATION FOR SEQ ID NO: 1018:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 284 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1018:

GTCTTACTTG CACAAGGTAT TATTTCTATC TTACTCGTTG CTTTCGCAAT CATGCTATAT 60
 ATCATTAATA TTTTAGATGC ATATCGTAAT GCTGAACGAT TTAATCGCAA TGAGGAAATA 120
 35 AAGGATCCGA AGCGCGTATG GTGGCACATG GGACAAGACG TTCCCATACT TACTAATCTC 180
 ACCAGGTACA TnCTTATTGA TATTGTAGTG TAATTCCATT ATATTATGTT GGAGTAGCAT 240
 40 TACAATACAA TTATACACGC GCCTCGAGAC nACATAGATG GGTG 284

(2) INFORMATION FOR SEQ ID NO: 1019:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 779 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1019:

CAATCATCAC ACATAAATGT TCGAATAGGA TTGTTTTTAA GTCGTTTAGA CTCAGTTGTG 60

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CACCTCAATA TGAGTTACAT GGTGATTCTG ATATGAATAA CCATCTTCTT GATTGTAAAT 180
 AAAACTATCT ACACCATTAT CGCTGTAAAG TCGTTTACCG TCTTTTGCAA ATTGGAAAAA 240
 5 TAAATAGGGT AATAGATCTA TCGGTATATC TAAATGATCA TGCTCATTGT ATAATCGAAT 300
 AGTAGTTGCA GAGTCATGTG GTTCGGAATG TTTGAAAAAT GGTGTCATAT TAATGACAAA 360
 TGAACCTTCT AACATGGCAC GTTTTTTATA TTTTATTCTT GAATTTAAAG TAGGCGGATT 420
 10 AGTTTGTCCt TctAGGATAG CcCGATTCCa TTCaTGaTTA TcTTCAAAGT CGATTGGTTT 480
 TGAACCATCa AATACACCTT TTTCTAAATC TTCGATGCTA ACTTTTCTAT CATCGAAAAAT 540
 CCAAGTCGTA CTATCTAATG TTATAGGAAA CTTTACGGCT CCTTTAATTT GTATCATTTT 600
 15 CCCACTCCCT ATCAATGTAT ATAGCATTAT TTTAACACAA ATTGCTAACG ACACATTTTA 660
 AATCTACTTG CTTTTTAATA TTTAGTAAGA TAACTTTTA GTAAGACTTG AGAATTTATA 720
 20 TAGAGGGGGA GCGTGTCTATG GCGAAACAAG CAACAATGAA AAATGCAGCT TTGAAACAA 779

(2) INFORMATION FOR SEQ ID NO: 1020:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 950 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1020:

TTAATGGTCC ATTAAGAATA ATGGCAGAAA ACCGTTTGCA TAAATCAAAC CTTGATTCAC 60
 TAACTTAAGT AATACTCGCT TTTCTTAAAT CCTTTAGAAA GGAACTATnT ATCATGATTA 120
 35 CTTCAATTCAG ACATTCTGAA GATATAGATA AACATATTAT AAAAACACCA TTAGATCATA 180
 CAGCGTCATG GATTAATGTA GTAGAnCCAG ACCGAGAAGA AATTGAAAAT CTTATGGAAC 240
 40 AATATAATAT ACCTGAAGAC TTTATACGTG ACCCTTTGGA CTCAGAAGAA AGTTCCCGTA 300
 TTGAATATGA CGAAGATACT GGTACTCAT TAATCATTAT TGATTTACCT ATCGTCAATT 360
 CAACTAATCG TAGCGTTCTA TCTTTTGTA CGATTCCATT AGGCATTATT ATTGGCAACG 420
 45 GTATTATCGT AACAGTTTGT GACGCTGAAA ATGAATTTTT AGAAAATTTA CCTAAGCGTG 480
 ATATTAAATTT AAAATTTTAC AGCAGATTTG CATTAGAAAT TTAACTACT ATTGCCGACC 540
 ATTATAATCG TAACTTACGA TTACTIONAATA AAAGTAGAAT TCGTATTGAG AAAGAACFAA 600
 50 AAAATAACAT TACTAACAAA CAACTTTTCA AATTAATGGA AGTTGAAAAA AGTTTAGTAT 660
 ACTTTTTTAGC TGCCTtAAAA GGTAACGATA CAATTATTAA AAAGTTATTC CGTTTACCTG 720

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AAGCCATCGA AACAAACAGAA TTACATCAAC GTATCTTAGA AAGTATCACA ACATCATACG 840
 CTCCTTATT ATCTAATGAT ATGAATACGA TTATGAAGAC ATTAACACTT TTCACGGTAC 900
 5 TATTAACgTT ACCAAyACTc GTATTTAGTT TCTTCGGTAT GAATGTGTCTG 950

(2) INFORMATION FOR SEQ ID NO: 1021:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1021:

AATATATAAA ATGAATACAT TGTGAGGCAA TTATCAAATG AAATTTAATA AAGTAAAACT 60
 20 AGTTATACAT GCGTGTGTAC TATTATTTTAT CATTATTTCT ATAGCGTTAA TTTTTCATCG 120
 ATTACAGACG AAGACACATT CTATAGACCC AATACATAAG GAAACAAAAT TATCAGACAA 180
 TGAAAAATAT TTAGTGGATC GTAATAAGGA AAAGGTTGCG CCGTCTAAAC TAAAAGAGGT 240
 25 ATATAATAGC AAGGATCCTA AATATAAGAA AATTGACAAG TATTTACAAA GTTCATTATT 300
 TAACGGTTCA GTAGCTATAT ATGAAAATGG CAAATTGAAA aTGAGTAAaG GTtATGGaTA 360
 TCAAGaTTTT GAAAAAGGTa TTAAAAaCAC ACCGAaTACG aTGTTTTtAA TnGGTTCAGC 420
 30 TCAAAAATTT TCAACAGGGT TACTGTAAAA ACAGTTAGAA GAAGAACATA AAATAAATAT 480
 CAATGATCCA GTAAGTAAAT ACCTTCCATG GTTTAAACA TCTAAGCC 528

(2) INFORMATION FOR SEQ ID NO: 1022:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 713 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1022:

GCATTnCGGT TAAAgTakGt TTCAGCTTCT CTCaTTTTAG AAGTACCGaA AAaTGGTTGG 60
 TTAtCTGGAT TTAATrtCAC GATAAATATT GCTTACTTTG TTACTTTGTr AAATGTACCC 120
 ATTACGAGTC TCAATGTTAT TCCAATAAAT ATCACTTGTT GGTGCATGGT TTGGATATGC 180
 50 ACAATGATTT CTTGAAATTG TTTGAACGAT TTCTAATGGA TCACAGCCAA ATGTACTGTT 240
 TAATACTTCA GAGTCTCTGA ATAATGCACA AaNTGAAATA CAAGTTGTCC AGTTTGGTAA 300

AGTATCTTGC GTATAACCAG CCTCTATACG AACCATTTTA AATTTTGTTT GAATTAAATC 420
 TGTAAACTC TGTCTATCCA TTCTGTTATC TACCTTTCTG TTGGGGAAT TTTATCCGGA 480
 5 CACAAGAAAT TGCAATAATA CACATTTCTT GAAACACAGA TTACATCTTA ATATATTTT 540
 AATAAAATGA AAAGAGTCAA TTTCACATTT GTATTAAATT TTGATCAAGT CAACAAGAGT 600
 TAAGTTTACT TTATAATGAA GCGAAAGTAA ATGAAGTAAA ATTTTATGCA TAATCACTAG 660
 10 ATTTGATAAA ACTTACACTT TTATAATGAT ATCAAATTTA CAAaGGAAAA CTG 713

(2) INFORMATION FOR SEQ ID NO: 1023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1023:

AATAAAATAG AAATGATTAT GGGTACAATT ATCGCTATCA TATCCTTGTT ATTAATTATA 60
 25 TTACAAGCAT TTAATATTAC TTGGGGCGTT ATACCAATTA CAAATTTTGG ACATCAATTT 120
 TTCTTTTTCA TTGGTATTAT TTTAGTAATT GCCGGCATAT TTTwyAAGCG ACTtGAGTTT 180
 TCGGGaATcG GGTtATTATT TTGTcAAAAA ACCGTCGATG CAATGATTCA TAATCCACAA 240
 30 TCAGCCCAGA TTTTTTCATT AATTATATGG ATATTATTAG TAGTTCTAGT TATATATTTT 300
 ACAATTAGAT TATCTTCACG TACAAGATTA TAAATATGAT AAAACTATTC ACTTGaTTAA 360
 TTGTATTAAT TGaGATGaAT AGTTTTTTTA TTGTGGAAT AACTTTTGGT AATTTATAAA 420
 35 TAATTTAAAA AAATTGTTTA TAAAaGGAAG CGTATATAGA ATGAAGGTTG GGTATATAGT 480
 TTATTGAGGG AGGTGTCACA ATGAATAAAG TCACAaTTAA TCCTCAAATC CAATTAACCT 540
 40 ATCAAATTGA AGGTAAAGGG GATCCTATAn 570

(2) INFORMATION FOR SEQ ID NO: 1024:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1024:

CTTTGTTGTG CTTGAGCATT ATTAAAAAGA GTATTAAAT TTAGTTGTTG GTTTGTAATA 60

TCAGAATTAT TAACACTATA TTTCCCTTTA AATAATGGTG ATTcG_rAATA ATGCTTATCT 180
 TTATCTGCAG CTAAC_TGGAA TTkCCCTAAT GCAGAGTCTG CGATTGTTGG TTCAAGATTA 240
 5 ATCATTGATT TCTCTTTTTT AGGATCATGT CCATATGACA tGTaATTTTC GATGCATTAA 300
 CAACAGATTT AkGAATGCCA AGCCCTTTAA CAATTTCATC TGATGCATCT GCGCTTAATn 360
 CTAATGAAGA TAAAAACGat TAtCTTTCAT CkKtTCTTGG AACTTCACTT CATTTTCAAA 420
 10 ACGGTCATTA AAATAATCTT TATACATTTT TGCTGTTTGT TGTTCACTTT TTAGGTATGT 480
 ATTTTTC 487

15 (2) INFORMATION FOR SEQ ID NO: 1025:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 364 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1025:
 25 ATATGTTATA AACAA_TTTTTA CAGTTGTATC ATCTACTCGT TCTATTCTCA TATCATCTCA 60
 CTCCTTACAG TCGATGAATA GTATCCACAT TGTATTAAAG CATCAAACAA AATACAATTT 120
 ATTTGTTTGA TTTCTTTCTC TAAAmTATTT TGGTAACTTA TAATAACATA TTCGTTGTAG 180
 30 CAAAACTATT TAAATGATTT ATACAGTTAA AGCATTAAAG CACTTTCTTA ATTTAATTTT 240
 ACCTTATCAT AGCAAATGTT TCATCCAAAA CACTCTAATA TAGAGCTATA TTAACAATTG 300
 CAC_ATTTtGaT TTAAAAGATA CTAAGCAATT ATTGtAAAAT TAAAACCAAA AAaGCAACAC 360
 35 TATA 364

(2) INFORMATION FOR SEQ ID NO: 1026:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1026:
 TGCCCCAGGG GAGTAl_nAAA AAAAAGnGGG GTGGGGAATT GGAAACCGGA ATTAGTGGTT 60
 50 AAAGGGGTTT ATTGGATGTT GGGTCTAAAG TATTCCCAGA AATTTATCCA TChATGATTG 120
 CTTTAGCCAA GTTTTTTTCC AACCCATCTT TATGGAATTT AGTTATCTCA ATTACATTAA 180

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CTTATATAAA AATGGCACAA TTATTTTCATG TACCAACAAG AACAAATATTA ATACGTCATT 300
 TAACACCTAA AATTATACCG GCTATTATCG TTG 333

5 (2) INFORMATION FOR SEQ ID NO: 1027:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 450 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1027:

TGTTCCATTC GTTTTAATAA TGGTGATACT GTACCAGTAT CGAGTGCTAA TTCAGTTACG 60
 ACTTTCTTGA CGTTTACAGG AGATTCATCC CATAAAATTG TTAAGACAAG AAATTGTGGG 120
 20 TATGTTAGAT TGTACTTCTT AAAAAGTTT TTAGAGTAGT AGCGATTAAAC TTGTCTTTGA 180
 GCATTGTACA AACTAAAGCA TAGCTGTTCT TTAAATTAT GTTGATCAGA CATTAAAGTT 240
 CTCCTCCAGA CATACTATCC GTTTTTnTCT CTTTTCGGAT TGGTAATCAT TAAAAAGTTG 300
 25 ATTGTTTATT AATTCAACAAC TTTCTTTGAT TCAATGCCAT GCAAAAATTA AAGTATGTTT 360
 AAAGTTTAGA AGATATTTTT GATTAAATCA AGCAAAAAGA TAATTTAATA TATATGTGAT 420
 CATTTTTAAA AATAACTGTn ATAGAAAAGA 450

30 (2) INFORMATION FOR SEQ ID NO: 1028:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 535 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1028:

TGCATCTATA CCTAGAACTT TAATTTTCGGA TTTTATTGCG TCTGTAATAT CTTTAATACC 60
 ACTTTTCGATA GGGAAACTTT CGTCACCTTC AACATATTTA ATACCAAAGC CACCACCAAG 120
 45 GTTTAATAAT TCAACTTGAA TGCCTTGctC TTTaAGCCAA CGTAAAmCAA TTTTAGCaGT 180
 TTCAATAAAAt GCTTCTGTAC CTTCAAtCTG TGrACCaATA TGACAAATGTA CACCTTTTAA 240
 TTTTAAGTGT TTAGATTGTT GGACTTTGTC AATTGCTTTT TTAGCTAAGC CATATTGaAT 300
 50 TGaTAATCCA AACTTACTAT CTTCTTGCCC AGTTTGaATA AATTCgTGTG TATGTGCTTC 360
 aACACCTGGa TTAACTCGTA AtACAACCTG aACCGTATCA TTAGCATAGC GGTCTATTAA 420

55

AATTCATGT TTCGTTTTAT TGTTACCATG GAAATGGATG CGACTCGGTT CAAAA

535

(2) INFORMATION FOR SEQ ID NO: 1029:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1029:

GAAGATGATT GAATTATGGA ATTTTTTTTCG AGATATGTTA TTTCTGGGGAT CAGATTTTGC	60
GATTTTGCCT TGGATAGAGT AGTTGCGATT TGTAATACG TTTTTCAGGT TCGATTCAAT	120
TTCGTTGTTA AGATAATATG GATTAGTTTC ACTGACATGT TGATGCATGT CTTTTTTGTT	180
CTGATAAAGT ATAAAATGTT TACTTAACAT TACTTAGTAT GACACCTGCT AATTCAAACA	240
TTATTTGAGA CATTCTTTTC AAATTAATTA TAAATTTTTC CcATAGACT AGTTTGATAT	300
TTATCTACAT CTCAAATTC TCATCAACAA TCTGTCACAT CCAACATTTT TACTTnAGT	359

(2) INFORMATION FOR SEQ ID NO: 1030:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1030:

TACATTGGTA AATAATTCTC ATAGTTTATG TCTCGTTGAT TAATCCAATC ATTGTTTTTTA	60
TCGGGTAAAA CATTCAAAC TTTCAAATTC ACAATTGATT GATGTTTCAT TAAAGTATCT	120
AATTTTGTCT CTCTAGTTAA ATATTCACCA ATGTCATTAT AATAGATATC GTGATTGTAA	180
CTTCATCTT TAACTAAAAT AGATATAGCT ATCGGTGCTC TACTTCCTGA TCCAAATATT	240
TTTCCACCTT CTTTTCTTga TTTTTCACCC TGTGTTGTTT GGTCGCCTCT CAAATTAATT	300
ATGtACAGaT AGTTAAATTC ATCGaTAAAA CTTTTCTAAA T	341

(2) INFORMATION FOR SEQ ID NO: 1031:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1031:

5 GTCTAACTTT AATGTTTAAA AAnCTTAGAA ATTTTCTACT CATAAATGGA TGCTTTATGG 60
 AATATTATTA ACAGGCCAG CTTCAATGCT AGCTATAGAA TTTGGATGGT TCTTAACAGA 120
 GATGGGTAGA CAGCCTTGA TTGTCGTGG TTATATGCGC GTGGCAGAAG CAGCAACACA 180
 10 GCAGCGGAAT AACCTTCGTT ACAATTTTAT TTGGCATATG TACATCATTT AAGTATACAG 240
 TGCAACGTAT ATCGTAGTTA AAATAACCGC GTAGAGAGTA ACGTAGCAGA GCAGAGGAAT 300
 GAAAnATTAG CTTATGnAAC GGTAGG 326

(2) INFORMATION FOR SEQ ID NO: 1032:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1032:

25 ACAATCAGGC TTGTGAAGAA TGAATTGCAT GACGTTTGTG TAATTGAACT GCGAGGTTTA 60
 ATTTCTAAAA TGCTCCAGnC CTCCAATGTA ATCGCATCTT GATATAACAT AGCGATCGCT 120
 TGATTTGTCTG TTGTATCAAC ACCTCTAAAC AACGTTTCAC CTATTCGGCA ATTCATTTAT 180
 30 TTTACCCAAA TCATTATATA AAAGTTGTGG TAACATGCTC GAAATACCAC CTGAAATAAT 240
 nTCAATCGAT ATCCTATTTT TCT 263

(2) INFORMATION FOR SEQ ID NO: 1033:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 514 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1033:

45 TTTCTATAGA GGATCCTGTA GAGATGCAAA TTCCTGGTAT CGTCCAAATT AATGTGAATG 60
 ATAAAGCTGG CATAAACTAT GTAAATTCGT TTAAAGCTAT TTAAAGATGT GATCCTGATG 120
 TTATTTTAAT AGGTGAAATC AGAGATAAAG ATGTTGCCAA GTGTGTTATA CAGGCTAGTT 180
 50 TAAGTGGTCA CCTTGTTCTG ACTACATTGC ATGCAACTGA TTGTAAAGGT GCTATTTTAA 240
 GGCTATTAGA AATGGGCATT TCTGTACAAG AATTGATACA GGCAACTAAC TTAATTATAA 300

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AGCAACAACT CCGATATTTT TTTTCCCaTa ATCATtCATT ACCATCATCA TTTAAGAACT 420
 TAGAAGATAA ACTTGATGAT ATGACAAAAG CAGGTGTCAT TTGTGAAACT ACAATGCATA 480
 5 AATACATTTA AACTACATTC TAAGAAGCGA CAAT 514

(2) INFORMATION FOR SEQ ID NO: 1034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 598 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1034:

TTTTTCACGA ACATTTTTGT TTAAATTTTT CTTTCTTAA CGTATACTTT CTGGTGTAAC 60
 CTCAACAAGT TCATCATCAT TAATGAATTG TAACGCTTCT TCCAATGTTA GAATACGCGG 120
 TCTATTCATT GTTTGTGTTT GGTCTTTCGT TGCAGAACGT ACGTTAGTTT GATGTTTTGT 180
 TTTAGTGATG TTAACAGTTA AATCATTTTC ACGATTATGT TCACCAACAA TCATACCTTC 240
 25 ATAAACTTCA GTACCAGGTT CCATGAAGTT TACACCTCTA TCTTCAAGTC CCAAAATGGC 300
 ATAAGTACTT GCAGAACCTT GATCCATTGA AATTAATGCA CCATTACGAC GACCGCCAAT 360
 TTGTGCTTTA ATACGTGGTC TAAATTCyTC aAATGTATGG TTAATAATAC CGTAACCTCT 420
 30 TGTCATTGAC ATAAATTcAG TCGTATAACC AATCATACCA CGAGCCGGTA CATTAAAGAT 480
 TAAACGTGTA AGTCCATTAT CAGTTGTAGT CaTATCAACC ATTTCACCTT TaCGTGcACC 540
 TAAkGATTCa ATAACAGCAC CTGcATTtC TTGTGGCACT TCACATTGCA CAGTTTCA 598

(2) INFORMATION FOR SEQ ID NO: 1035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1035:

AAACAGTGCT TCATTATCGG TATTGATATT GATCCACAAG CCGTTGACCT AGGGCGCACA 60
 ATCGTTAACG TCTTAGCACC AAATGAAGAT ATAACAATTA CGGATCAAAA GGTATCTGAA 120
 50 CTTAAAGATA TCAAAGATGT GACGCATATC ATATTCAGCT CGACAATTCC TTAAAGTACC 180
 AGCATTTAGA AGGAATTATA TGAhTTAACC AATGAAAATG TCCGTAGTGC CATGCGCCTT 240

AAGTGGGCCA TGT

313

(2) INFORMATION FOR SEQ ID NO: 1036:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1036:

AATAATGAGT AGGTTTTGAT TACTTACGAG ATAACATGGT GAATTATTCT GAAGATAGAC 60
 TAATGCGTCC ATTACATTTT GCAATCATTG ATGAGGTTGA CTCAATTTTA AATCnACGAG 120
 GnCGACGCCA TTAATTATTT CTGGTGAAC TAAAAGTCAA CGTCACTTTA TACACAAGCA 180
 AATGTTTTTG CGAAAATGTT AAAACAGGAC GAAGATTATA AATACGATGA AAAAC 235

(2) INFORMATION FOR SEQ ID NO: 1037:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1037:

nCAATATACC TCCTATCATC ACACAAAATG CGTTGTTTCG TATGATTTTC TCAACATCGT 60
 AGACTAATGC AATCAGACAC AACACCATGC TCTATATCCA ATATTGCTT TATTGCCTAT 120
 CAATGAGCGT ACTGCGTGCT TTAAATAAT CATCATCAAT TAATGACTGT ACAGGCACCT 180
 CATGAAAATT ATCATCCGCC AAGTATTGCG CACGATCACT ATATGCTAAA TGCATCGCTT 240
 GTATCAnATG ATGCAAGTAA TCA 263

(2) INFORMATION FOR SEQ ID NO: 1038:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1038:

ATTGTACCTG GCACAATCTC ATTATGTATT GGATTATCAT CATTACGAGC GCCAAATATT 60

ACCGTTATGA CATGTTGATC ATTTTtAGTn AATGTTAAAG CTATAACGTG TGATATTGCG 180
 AGTCTGTCGG CATTCAATAT CTTCnAAATG CCCTACAT 218

5 (2) INFORMATION FOR SEQ ID NO: 1039:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1039:

GTtTAGACGC TAATGnTGGC ATATATTACT TGCCATGCAA ATGAGTCATA AGGCATAGTT 60
 TTCAAGAAGG GTTCTGACAA TGAAGTGAGC AACATGTCAT GATGAGAAGC AGGACTATAC 120
 20 AATGAGAATA ACCTTTTtGAT TTTTCATGCA TAAGGCGATT CAATCAAAAG CAATCACCTT 180
 CCAACTGAAT TGTCATTTTG TAAAATAAAA TAATCGATCC AATCGTTATC TAATTCATAA 240
 ATGTGTAAAC ACATACGTTA TGAATGGATA ACGATTTTTT GTTATGTAA AGTGGTACAT 300
 25 TAATCATGTA TTTCGTATGA TAATTAACGA CAAGTGTAAT GGTAAATGT ATTTTATGGA 360
 TGGAAATGCh ATAATAGGCC TGGGTTACCA TGGnGC 396

(2) INFORMATION FOR SEQ ID NO: 1040:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1040:

40 AGCATTTTGT TAAAAGCTG ATGAAGCAAT AATAAACTCT TCATATCCTC TGTCCATTAC 60
 AATTGACCT TGATATACAA TTTCTTTAAA GTTTTCGATT TCTTTAAATT CTCTGCTATC 120
 ATTTAAAATA GGTGCATTG TAATAACATT CGCTTCCTC TTATATCCTT TAGATTGATA 180
 45 ATATTCTTTT GCTGCATGAC TTA CTGTTAC GAAGGCATTA ACACGATGTT TTA CTATGTG 240
 TTTTCTATA CTTTCTACAA ACTTTGAAAT AAGTGGA ACT TTATTAATAA AGGCATTTTT 300
 CGCATATATt TCATGCGCAT CATAACAAT ATTAGCTTTT TtATAATTGC TTAAATAGAC 360
 50 CATTAATAAT ACGTCGAAAT CATTTCATG AATCACGTCA 400

(2) INFORMATION FOR SEQ ID NO: 1041:

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(A) LENGTH: 268 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1041:

10 ACTTGCGTTT CTATTTAGCT CAGACAGGAA AAATATTCGC TGGAAATATG TAGGAATTTT 60
 ACTTGCAATT CAGCTTATCT TTGCATTTAT CTTGCTTAAA ACTACAATGG GAATCAAGGT 120
 TATTGGTGGT ATTTCAAACG GTTTTAACTA CTTATTATTA AAAGCAGCAG ATGGTGTAA 180
 15 CTTGTATTTC GGTGGTATTC AATATATCGT CCCTAAGCAC CCACCCATTC CTCCTCCGGG 240
 GAATAATAAC CAACnGAATT AATTCCGn 268

(2) INFORMATION FOR SEQ ID NO: 1042:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 277 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1042:

30 GTGAAGATAA GAAATTAAAG TTAAGACAAG GTTAAAAATA AGCAAAAAAT ATTGAAATTA 60
 CAGATCATTG GANTGGTATT CCAGAGGAAG ATCAAGATTC ATTTTGTATC GCTTTTATCG 120
 ATGGATTAAA TCTCGTTCAA GAAGTCAAGC GGTAATGGAC TCGATTATCT ATTGCTCAAA 180
 35 AAATCATCAA TTAAACGGnG ATCGATTAAA ATTAAAGTGA ATTAACAAGG AGCAACGTTA 240
 AATCTATTTT AATCAGACTG AGACGTCATC AAGTCAT 277

(2) INFORMATION FOR SEQ ID NO: 1043:

40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1043:

50 TTATCATCAC AAGTGATTTT GAAAATAAAA AAATCGAAGA TGATGACAAT GATTCAGGTA 60
 GTGTGCCGAT ATTGCCGTTT ATTAAACGAG ACAAAGCATA TCAAATTATC CAGAATTTAG 120
 TACCAGATTT ATCTTATCAA CAAGTTAATG AAGGTATGCC TTTGTCAGGn TTCCACAGAC 180

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AACCATTATT ATTGTTATTA CCGATATAAC CATAGTCATA TGGTTATTGT GATCCAAGGT 300
 ACCTTATGTC AACAGCGGGT TAAAGCAGAG ACAATACATC AGATTTCGGCA TGAACGAAAT 360
 5 TATATTTAA_n GCT_nCTAAG 379

(2) INFORMATION FOR SEQ ID NO: 1044:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1044:

ATATTGAACT TGAAGACCAT GCAGATATAA ATGAAATAAC ATATCGATTA TCAAAAATTT 60
 20 TCGGTATTAA ATCTATTAGT CCAGTATTAA AAGTAGAAAA AACAAATAGAG GCAATAAGTG 120
 CAGGGACAAT TAAATTTGCG CCATT_nTGAA GAAAACAGCA CATTTAAAAT TGATGTGAAG 180
 CGTGCCGATA AAAATTTCCC AATGGATACG TATGAATTAC AGCGTGAATT GGGTGGTGCA 240
 25 GTATTGAAGC ACTTCGACAA TATTTTCAGTG aATGTCaAAC GTCCAGATCA TGgAAATTCg 300
 AGTGGGmAGT TtAGGmTTAG ATGCCAATTT TATATGGTAT GnAAGAAGTT GGTTCCGGGG 360
 30 TTCCAGGTGG GATTTACc_nG TTGGGTACTG GTGGGT_nAA 399

(2) INFORMATION FOR SEQ ID NO: 1045:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1045:

AnGATAAACA GAGGAGCACA AAAATGAAT_n nAAATATAAT CATCAAAAGT ATTGCGGCAT 60
 45 TGACGATTTT AACATCAATA ACTGGTGTCTG GCACAACAGT GGTGATGGT ATTCAACAAA 120
 CAGCCAAAGC AGAAAATAGT GTGAAATTAA TTACCAACAC GAATGTTGCA CCATACAGTG 180
 GTGTTACATG GATGGGCGCT GGAACAGGAT TTGTAGTTGG GAATCATACA ATCATTACCA 240
 50 ATAAACATGT TACTTATCAC A_tGAAAGTCG GTGATGAAAT CAAAGCACAT CCTAATGGTT 300
 TTTATAATAA CGGTGGTGGA CTTTATAAAG TTAATAAGAT TGTAAGATTAT CCTGGTAAAG 360
 AAGATATTGC GGTCTGACAA GTTGAAGAAA AATCAACGCA 400

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 626 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1046:

ATAAACTTCT ACACCATCAT CTTTACCTAC AACATTTGTA GCTTTAACTT TTAGTCCAAA 60
 GTTATCTTTA AAGAATTGTT CACCTACTTT TTCAAATTCT TTACGATGCT TCTTCACAAA 120
 TTCAATCGCA TCTTTTTCTG CAGGTGGTTG AAAGCCTTGT CCTACATATT TTGAAGCTTC 180
 CATTCTTCT GGTACTGATT TTGTTTCTGT ATTTGTTTCT GTATTTGTTT CTGTATTTGT 240
 GTCTTTTTTT GATTCATTAT TCATCGCTGA ACATCCTGAT AACAGTAGCG TTGCTATTAA 300
 GATTAATTTT GCCTTTTTAA ACATAGCTCA TCACCCATTT ATGTGkTTAT ATAGAATATT 360
 AAAAAGCATT TTAACAAAAA TTTATTCATC TTTACGATAC ACTCCATATT CTATTGGATC 420
 ATTATCATCA TAAAAGGCTT TTTTAGTATT AATAGTAGGC TTTCTATTT GAATTGTAAT 480
 TGTAGATTTT TCTGGCTTAT TTTTAAATTT ATATAGTTTA TCACTCAGTT CAATTACATC 540
 ATCAACTGTA TTGTCTTTAG TAAAATTTTC CTTTGTACTA AACAATGTTG TTACTGTATC 600
 TGTATTAGCA GCGnAATTCA CTTCTT 626

(2) INFORMATION FOR SEQ ID NO: 1047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1047:

GACGGCGTTC AAAATGCAAC GGTCAATTTA ACAACAGAGC AAGCTAAAGT TGA CTATTAT 60
 CCTGAAGAAA CAGATGCTGA TAACTTGTC ACTCGCATTC AAAAATTAGG TATGACGCGT 120
 CTATTAAAGA TAACAATAAA GTCAACGTCA CGCAACTGAA GCGTACAACA TAAATTGATA 180
 GnTATCATAT CAGCAGTATA TCTTACCACT ATAATGTAAT GTTGACACTT TCATATGCAT 240
 ATACAGACTA TTACGATCAT GTCCATTAT TAGCnCACTG TCATTATATG GTGGCATTAT 300
 GAGGGTATAA ACTTAGn 317

(2) INFORMATION FOR SEQ ID NO: 1048:

(A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1048:

10 ATACGnATTA TGCAAAAAAT AAAGTGAGAT TGGCATATGT GTAAATCTAA AATACTGTTG 60
 AAAAATATTT TTAGTGAAGT AATCAGAAGT TAAAGATTTA ACTGAAGTAA AAATATAATC 120
 AAGATTACGA GTCATTAACA TTTAGCTTTA AAGAGGGAAA CATATCAAAG TAGGTTAGCT 180
 15 AAGnAAAACA CCGACTAAAT CGGGGATATT TCGTGACATG TTG 223

(2) INFORMATION FOR SEQ ID NO: 1049:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 608 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1049:

AAATATGAAT AATGCAATTG ACCAACGTTC GATAACGTTC CCATACCCAT ATTAAATTTT 60
 30 GTATAACCTT GTTCTTTACT CCAAAGTAAC ATATGCAAGT ATAGACCATC CATTAAATGGT 120
 AAATCTAACT CTGGCAACCA TCTAATTAAA TCGACTGAAA TGGCATCATT AAAGTATGTT 180
 GGCATTAAAC TACAAAATGC AATTACTTCA TTTTCTTCAT TTCGCATTAC ACCAATTGGC 240
 35 GCTTTAGATA AGTATTCTTC ATTAAATnCA CCAACAGAGA AATGCATTTC CyGACGATTA 300
 TCTAGCCaTA AATcACTTAC ATGTTGAAGt TCATTTAtAA ATTcAGTTGr AAACGGtGGt 360
 TCAATAATTT CGAACGAAAT ATTAAGTTCA TCGAATTnAT TTAAAGTCGC TCTAAATCCC 420
 40 ACGGCGTTTT TTACCTGAAG TTGAAAATTG CGTTAAATCA ATAATTGCTT CTTCACCTAA 480
 TTTGAAAAAT TGGTTACCGG nATTATGATA TAAAGGCATG TGTTGATCTG TAACTTGATA 540
 45 GAATATAACA TCATAGCCTA AATACTCAGC GTAATTATAG AATGCTTCTA ACAATTCATC 600
 AAAGGCAT 608

(2) INFORMATION FOR SEQ ID NO: 1050:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1050:

5 TGTTTTCTA CGCTAAACTA TATGATAAAT TGCCTATGTA TTTACTGGTG TTTATGGCCT 60
 TTACAGCTGT AATTTTGATT ATGATGTACA TACAAGAGAA AAATGAAAAT TACAAAGTTG 120
 AAAAAAGATA TGTGGTTAGA TATCTCACAC TTAACGTTAT TGTGGGATAT ACTTTGCCAT 180
 10 TGCTTTTGT ATCTATTAC GTTTTGGTG TAGTCGGTTT TGGATTGAT GTTTCAATT 240
 ATTGTCTAGG TAKTATCTTG ATGTYATWTA TTTCTTGGTT TAGGTnTATT nT 292

(2) INFORMATION FOR SEQ ID NO: 1051:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 734 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1051:

TAAATChTCA AAGATTTCTT CTAAAACATT ATAATCTTCA ACGATACTCG AATAATAATA 60
 25 CAGCTCATCA TTTCTGGGCT TGGTATAATA AAATATAACT TGCCACCTC CATCGTCCAC 120
 ATATGCAATT ACATATACCT TTTCCCACTC TACTGGTATC ATTTCAATTGA TCTCATTGTC 180
 AATTTTATTG TACATTTTCA TTAATTTTTC TTCGAAATTC ATGTTATCGC CTCTATTGTT 240
 30 CAGCTTCTTC TTGCTCTTTA ACATATTGCT CGATTTCTTT AACTTTATTA ATTTTCATATT 300
 CCGTTTCTGG TAAAATTCCA AATTTTCTAT ACTTATAGTA ATTTTGTGCG CCTACTTGAC 360
 35 CAAATTCTGA ATTTATCCAA TCAATATAAT CAAATGAAAC TTTTAATTCA CCTTCTCTTG 420
 TAAAGTCAAA TTCGCATGAT GTCCATGGTT CATGTCCTTC TTCTTTAAAT AAATTCCTTA 480
 AATTTTGAAA TTGTTTATAC AACTCATACA CTGAATCCAT AAATCCGAT TCCGATATAT 540
 40 CATATTTATT TAATACACTA GTATAGTAGT ATAATTCATT ACTTCAGGT TCTGTGTAAT 600
 AGTAGAACAC TTCTCCTCCT CCGTCATCTA TATATGCCAT TGCATATACC TTTTCCCACT 660
 CTACCGGTAT CATGCTGCTA ATCTTATTCG CAATCTCGCT ATACATTTC ATTAATTTT 720
 45 CTTGAAAGT CATG 734

(2) INFORMATION FOR SEQ ID NO: 1052:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 775 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1052:

5 AATTTTAAACC AAAATTGCTT TTTTATCTGA AAAGAAAGGC AATGTTAATG TTTCTTCAAC 60
 AATTGGTGCA ATCTCTGTTT CGTATAAATT ATATTTTACA AAGTTAAAGT CATCTCTATC 120
 ACTTTTCAAA AATTGTGATA TGATTTCTGC ACTTTGTTTT TCAACCAATT CAGGCACATc 180
 10 TCCATAAAa GCTACAATAT TGTCGCTCAT TCATTACACC CTTTCATTCTG TTTGACACAT 240
 CAATAGATTA TATCATGTTT CTGTATCTAT AAACCACTTG CATTTCCATA AGAGCTTGAA 300
 TCAACTTTTa AATTATCATC TAAGTCAATT GTAACCTGAC CGTTTTtGTTG ACTATTGTAA 360
 15 ATGCGtACTG CGAATCCTTT GCAATCGTTt aACAACTTCT ATATTAGGaA GwTGATACAT 420
 ATTGTTCTTC CCAGAAGAAA TCAAACTTAT TTTAGGCTTA ATCATCTCTA TAAATTCTTT 480
 AGAACTACTT GTCTTGCTCC CATGATGTCC TACTTTTAAA ATATCAATCT CCGGCAAGTT 540
 20 ATATTTTTTT AGTAGTAAAG ATTCATTATT TTTACTAGCA TCGCCCATTA ATAAAACTTT 600
 TTTATTTTGA TATGTAATCA TAGTAATAAT CGAATACTCA TTTTATCTC GGCTATTTGG 660
 AATAAACTA TCAAAAAAAT AGAAACTAC TATCTCCAAG TTTAAACTA CTAACCTGTC 720
 25 TTACATCCAT AAGTTTAATG GTTGTACTTA TGGGCTTAAT TTCCGATAAT AACCA 775

(2) INFORMATION FOR SEQ ID NO: 1053:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1053:

GAGACCAATC ATCATAATGA ACGACAATCA TGTATTTAAT ATTTAATAAA ATACTGAATA 60
 40 ATGCTATAAC TGCCATTAAT TGAAGACCAA TCGCATCTAA TCGACAACA CGATCGGCAA 120
 GTGATGGGCC TAGCACAACG CGAATGAGCA TAGCTAACAT AGGAnGTGAC AACTATGATT 180
 AATGCAATAA CGATGAATAA CCTTGATGAn TCATTATAAT TCGCCACCT CTCT 234

45

(2) INFORMATION FOR SEQ ID NO: 1054:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

CTACTGGTAT CATCCACTGA TTTCATTTGC AATTTTCATTG TACATTTGAC TTAGCTTTTC 60
 TTCGAAAGTC ATGTTATCGC CCCTATAGTT CAGCTTCATC TTGCTCTTTA ATATATTGCT 120
 5 CGATTTCTTT AACTTCTTCC ATTTCGTATT CCATTTCTGG TAAAACACCA AACTTTTTTAT 180
 ACATATAATA GTTTTCACGG CCTAATTGAT CAAACTCTGT ATTTATCCAA TCAATATAAT 240
 CAAATGAAAC TTTTAATTTA CCTTCGCTTG TAAAGTCAAA TTCACTTGAT GTCCATGGTT 300
 10 CAAGCCCTTC TTCTTTAgAA AGTTTCTCTT AACTTCTTAA ACAATCTATA TAAATCCGTC 360
 CACAAATCAT AAAATACTTT TTCAGAGACA TTATACTCTC 400

(2) INFORMATION FOR SEQ ID NO: 1055:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1055:

25 GnGGCATATA TAGCGTTGGC GGTATAACAA AGAAAAATGT GAGATCAGTG TTTGGATTG 60
 TAAGTAATCC AAGTCTACAA GTTAAAAAAG TTGATGCTAA AAATGGCTTT TCGATAAACG 120
 AGTTGTTTTT TATTCAAAG GAAGAAGTAT CATTGAAGGA ACTGnACTTT AAAATAAGAA 180
 30 AACTCTTAAT CGAAAAATAT AGATTGTATA AAGGAACGTC TGATAAAGGT AGAATTGTTA 240
 TCAATATGAA AGACGAAAAG AAGCATGAAA TTGATTAAAG TGAAAAATTA AGTTTTGAAC 300
 35 GTATGTTTGA TGTAATGGaT AGTAAGCAAA TTA 333

(2) INFORMATION FOR SEQ ID NO: 1056:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 347 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1056:

TGGGCAGTTA CATTTATGAT TATCAGCACA TGTTTAGCTT ATAAATTTTT ACGAAAGTTT 60
 AGCCGTTTAT AAAGCACATG CATAATGAAA CGAGTATTTG CCACTTGATT AGTACTICAT 120
 50 TATTATGTCG AAAATAAAAA TAAGTGGTAT TTTTAATATA TTAAGAAGCA CTCATAATCG 180
 GCTGTTAATT AATAATATTT TTCATAAGTA TTGATTCATC ATTTTCTTTA TGTTAAATAT 240

55

TAATACAGAT ATCAATATGG CnAAAAGTGTT nnATGAATCA GAGGTAA

347

(2) INFORMATION FOR SEQ ID NO: 1057:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1057:

15 TCCAAAACGG AGAGCCAAGA GTTAACTCTA CTTATATAGG ATACGCGCCA ATTGATGATC 60
 CAAAATTAGC GTTTTCAATT GTATATACAA ATCAGCCTGT ACCACCACCA TGGTTAACAG 120
 GTGGAGACTT AGGTAGAGAT GTAATTAAC ACTACTTTAA GCAGTTAGGT AAAGATGATA 180
 20 AAAATAAGA CAAAGACAAA TAAAATTTAA CCTGACGATT GTGTAGCGCA TGGTTGTAA 240
 ATTTAACTT TGCMAATATT ATAGATGTTG GTATAATAAT AAAGTCGTAT TtAGaAATGA 300
 TwAGGaGGGA AT 312

25 (2) INFORMATION FOR SEQ ID NO: 1058:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 404 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1058:

35 GCCATTTTGC GATGCTAAAT CCATTGAAAA TGCAATACCT GAAAGTCCAC CAAACAAAGA 60
 ATTGTTATAT TGACCACTCT GTAAATATGG TGCTAATTC ATGATGTACT TATGCACAAT 120
 40 TTGCTCAGTA TTAATATCGA AACTTTTTtG AtAAGCATCT AAAACAAAA TGATACCTGG 180
 TATACCATGT GATAAAGTTG AAGGTTCAAA ATAATCGGTT TCAGTAGATG CTTTtGAAAT 240
 GAAATCATCT ACTTCTGAAA TCTCTTGAAA CTtCTTCTTC AATATTAGAT TCATATCAAT 300
 45 CATTTTtGTC ACCACACCAA TGCTTTTGAG TTTTAACAAT TTCTTTTACA ATAGATAAAA 360
 CAAATGTTTC TTGATCCTTA TCAATGCCAA ATATTGATT GnAG 404

(2) INFORMATION FOR SEQ ID NO: 1059:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1059:

5 ATGTACATAG GnatGACATA AGTGTGCCTT CTTTTTCAAG ACCCTCCATA GAAATAATAC 60
 ATGGATGTGC ACCACGnTAC TACCTCTTTA ACGTTACCAG AATTGATAAA TTAACCTTCT 120
 CTTGTGTGTC TAAACCTACA ACTGGTGTAC CTTCTTCGAT TAAGGCAATT GTACCATGTT 180
 10 TAAGTTCTCC ACCAGCAAAA CCTCGCTGAA TGTAGAAATT CTTAAGTTTA AGT 233

(2) INFORMATION FOR SEQ ID NO: 1060:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 295 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1060:

GCACCACTAC TGTTAATAAC ACACCTAAAA AAGTCGAAAT ATAAGGGTTA ATCGCTGTTT 60
 TAAATGTATA TCCTAGTGCG ATTGCCATTA ATTATCCGAT AGCTTTTTTCT GCTGCTTCCA 120
 25 TAGTCATCTC ACCTAATGTT GGATGTGCAT GGATTGTAA TGCGATATCT TCAGCATTCA 180
 TACCAGCTTC AATTGCTAAA CCTAATTCAG AGATAATATC TGATGCACCA GTACCAACTA 240
 30 CTTGAGCACC GATTAAAGTA TCATCTTCTT TAGTGTAAATA AGTTTAACAA ATCCG 295

(2) INFORMATION FOR SEQ ID NO: 1061:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 413 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1061:

CAATGCCTCT CGTGTTCAG CTTCTTCCGG TGAAAAACCA ATATTTTCAA GTGCAATAAT 60
 TTGATCTAAG TCCTGCATGA TTACTTTTCT TAATACCATA AAAACACTTC CTTAGCCCTA 120
 45 TATATCAAAA GTAATACCTT CATCTTTATA TTCATTATTT TCAAACCTACC TTTACTATAA 180
 AAAACGAGTC TTTTATTGA AAGCCATTCG CCTTAATCAA TTAGACAAGT TGTATKATAC 240
 50 GAATTAGTAA ATAATCATGA TTATAATTCA TTTTAAGCAT ACTCAAAAAG ACTGGTACAT 300
 GTATACCACT CTAATTCGAA AAAATATATT TAGTTAAAC CATTTCAAAA ACGACTTCAC 360

55

(2) INFORMATION FOR SEQ ID NO: 1062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1062:

AAGCTGCATA CTCTCCAAAC TTAGAACCAC CGAAGCGATT CACAAAATAT TTATTAGCTA 60
 AAAAGTCGGC ACATAAAATT AATATTGTTA GCAATGCCAT AGATACATAA AACACCCATG 120
 ATAAATGCTG ATTATGAAAG CCAAATTGAT AGATTAAAAA GCCAACCCAT AATACTAAAA 180
 CAGAAGGAAT AATCGGCTTA ATCAACCCAA CAAATGCTAA CATGAAGGCA GCGATGATAA 240
 GTAGCCATAA AATAATTGTC ATGTTGATAT CACATCCTCT TTTGTATTTT TTGATTTTTA 300
 GTAAAGAATA TAAGTATCAT ACCTAACATG GTTGATGCTG CTGGATACCA AAAAATACAT 360
 TTTCCCAAAC CTTACCCAGT GGAATCCTAG GCACCACCTT 400

(2) INFORMATION FOR SEQ ID NO: 1063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1063:

TGGATCAGAA GGAATCTGGA TGCCTATTGA TGACAAAGGA TACTTTAATT TTGACTTCAA 60
 AACGAAACGT TTCGATGATT TAGAGTTAAA GAAAAATGAT GAGATCTCAT TAACATTTGC 120
 ACCTGATGAC GAAGATGAGG CATTGAAGTC ATTAATTTTC AAAACTAAGG TAACGAGTTT 180
 AGAAGATATT GATAAAGCAG AACTAAATA TGACCATACT AAAGTGAAA AAGTAAAAGT 240
 ATTGAAAGAT GTTAAAGAAG ATTTACATGT AGATGAAATT TACGGAAGCT TATATCATAC 300
 AGAAAAAGGT AAAGGTATTC TTGATAAAGA AGGTACTAAA GTaATTaAG GTAAGACTAA 360
 ATTCGCAAAT GCAGTTGTGA AGGTAGACTC TGAAGTAGGT 400

(2) INFORMATION FOR SEQ ID NO: 1064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 434 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1064:

5 GTGGTCGTGA AGCAACTGAT TTCAAAGAAG AAGATATCGA GCTTTTCAAA GACATTGCCG 60
 ACAAAGTAAA ACAAACAAAT AGTTATGATC TAGCGTTTGA TGAATTAGAA AAAGAAAAAG 120
 ACTTCCTGCA AGTCATTGTC AAAAACGATG ACAAAAACCTT ACCTACTAAT CAAAATGTCTG 180
 10 CTCAACTAGT AGAAGATTTA CGCCTAGAAA TCCAGAAAAT GCGCGAAGAA CGTCACCTAC 240
 TTGGTCAAAT GATGAATCAA GTACATCAGC AACACAAGA ATTAAAAGAA CTTCAAAATC 300
 AACTTACATC TAAAATCGAT TCAAATAGCG AATCCTTAAA AGCCATCCAA ACATCACAAG 360
 15 AGGCTATCCA AGAAGCGCAA GCCTCTCAAG CAAAAGCATT AGCTGAATCC ACCAATAAAG 420
 TTGGAAAGAA TGCT 434

(2) INFORMATION FOR SEQ ID NO: 1065:

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1065:

30 TAAACATAT GGCTTGATAT TGCAGAAGAA TTGAAGTTAT CGTACCAGAA ACGGTACATA 60
 ATCATGATTA TATGGAAACG AAAAAAATAA AAATGGGTCA TTTAATATAG GAGGATTTAA 120
 CATTGAATTT TGAAGGTAAn TAATTGAAA AGATTTGAAG TTGCATCGTT ATTATCGTTT 180
 35 AATGATTTTA TCACTGGAAG ATTACTTGAA GGTGCAAAAG ATACnTTGAT TCGACATGA 239

(2) INFORMATION FOR SEQ ID NO: 1066:

- (i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1066:

AAATATCTAT AGACCTTTAT TCGGAAATGG TTCGTCTCCA GAATGGAAGG ATGAAGTACC 60
 50 GAGTATTGAA AGGTAGAAGG TCTCCAAACT TTACCTGnAC GTGCACGAnA TCTAACTGAA 120
 GATGATTTAG CAATTGAATT GAAACAGCCA ATTGTGCGTT GTAATAACTT AGGAGAGTTA 180

55

(2) INFORMATION FOR SEQ ID NO: 1067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 749 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1067:

CTACAATTCG ATCAACGCCG AAGTTAGATA CACCGATTGC TTAAATTTTA CCATTTTCTT	60
TTAACTCTTC TAATGCACGC CATGAGCCAT ATACGTCATT GTAAGGTTGG TGAATAAGCA	120
CTAGATCAAG ATAGTCCAAA TTTAATCGTT GTAATGATCG TTCGATTGAT TTGATAGTAT	180
CTTCATAGTT AACATTTTCA ATCCATACTT TAGTCGTAAT GAATAGTTCA CTTCTATCAA	240
TACCTGAAGC TTCAATACCT TGACCTACTT CAGTTTCATT TAAATAACTT TGTGCTGTAT	300
CAATATGTCT ATAACCCGCT TTAATTGCTT CTTTAACCGC TTCTGCnGTT TGTTCTTGAG	360
GAATTTGAAA TACTCCGAAA CCTAATACTG GTATCTTTAC ATCTTTACTT ATTTCAATAT	420
GATTCATAAA ATGAACCTCC TTTATCTtGT ATGTCCACTA TAAACCATGG AGCGAACTCT	480
ATAGCAAGCC ATAGGTTTAC TTTCTCTCCC AAAGACGTTT AACATTGTCA TCATAATTAT	540
CACTAGCATT GATTTTtagCA ATATGATTAT CATAATTATC AATTTTATAT TGTAGTAAAT	600
CTCTCGCATC ATGAATTGTC TTAAAGTTTt CATTTAATTC TTCGAGTTGC TTATTTAAAA	660
TTTGCTTTTG CTGTGCTTGA ATATTTTCAT TTTTAGGCAA nTGCGCTAAC CTGCAAAATT	720
CGATAAGCGA TTCAATACTG ACGCCTGCA	749

(2) INFORMATION FOR SEQ ID NO: 1068:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 436 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1068:

TCCTCGAGAT AGACAAGAAT GGTGGTACAA TGTTTTTTTAT GACGATGGCA AATATnATAA	60
GAAnATAA11: AAGAATGACA TGTCAAAAAT TAGGCGTAAT TTTTAGATTT ATCTATATAT	120
TTATGCCACC GCTCAAACCTT TTATnAAAAG TAAAAAGACA ATATTTATAT TGAACCTTGTG	180
ACGTGAATTT CTAAACACA ACCAACAATC CACAAGGAAA CTAGTAAATA AGTTTAAATA	240

TACTGACTAA AAAGATTTTG AAAGTGATTA AGTATTTAAA ACACGCCAAT CTTAAACCGC 360
 TATTGACAAA TATGAAGCGG AACCACCGTT GTnTTTCTTT TnCAGGTCCA ATTGAATAAA 420
 5 TGTTGATGAA TAGAAT 436

(2) INFORMATION FOR SEQ ID NO: 1069:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 551 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1069:

TTCTCAAGTA ACAGGTATTA TTGTTACTGG TACAATCAAT AGAGAAAAAT ATGGCATTAA 60
 CTTTAACCAA GCACTTGAAA CTGGTGGCGT AATGCTAGGC AAAGATGTTA AATTGGAAGC 120
 ATCAGCTGAA TTCTCAATCT CAGAATAATC TCATTACACA ATCCTCATTG TTTTAATATA 180
 TATACGAAAT GCCAACTATA TCATCCCTAG GTATAGTTGG CATTTTTCGT TTAACTCATG 240
 25 TGTAACAAGC ACTAACTGTT CACCCTAATT TTAGACGCCT TTCATTCAGG TAGGTCTTAT 300
 TGAAACTGAA AACTTTGatG ACCTTTTGcA AaGCCATTAA CTGTATAAAG CATAGATCCT 360
 CCGCCCATTT CTATATCATT GGAACAAATG ATGAGTTGAT TTGTTCCAGG TATAAATTGC 420
 30 GGATGAGTAG AACGTAACAT ATGCCCTTCA TCTCGGCCTG GTATCAATAT TTGTCCTATT 480
 GGATAACCCC TTTTATTAAA AACTAACACT CGACCTTGA CCATACATTG CTACGGATAA 540
 ATTATCGGCA C 551

(2) INFORMATION FOR SEQ ID NO: 1070:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1070:

TATnAtGGTA ACGCATGAnC CTGTTGCAGC ACGCTATGCA AATCGAGTAG TGATGCTAnA 60
 AGATGGTCAA ATTTTCACTG AATTATACCA AGGGGATGAC GATAAACATA CCTTTTCAA 120
 50 AGAAATAATA CGTGTACAAA GTGTTTTAGG TGGCGTTAAT TATGACCTTT AACGAGATAA 180
 TATTTAAAAA TTTCCGTCAA AATTATCAC ATTATGCCAT CTATCTTTT TCGTTAATTA 240

CAGAGTCATA TCCAATTATA CnGGC

325

(2) INFORMATION FOR SEQ ID NO: 1071:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 771 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1071:

15 TAAATGCCGC AATTGGATAG CTTTAATATA ATTAATAGTC AAGGTATTnC CAACAAnAAT 60
 ATATTATCCA CCCGAAGGAA GCGGGGTATn TTTGTTACTG ACGTCCCACA AGAAGCACAn 120
 ATATTAGATA GTGCTTACTC TGAAATTAAA AAATTAAGAG ATTATGATGA AAAACTAATT 180
 20 ATCCCAGGAT TTTTGGCGT ATCTCATGAA GGATATATAG TTACATTTCC ACGTGGCGGA 240
 TCAGATATAA CTGGCGCCAT CATATCAAGT GGTGTTAGAG CCACAATTTA TGAAAATTTT 300
 ACCGATGTGT CTGGTATTTA TAAAGCTAAT CCAAATATCA TCAAAGATCC TGAATTAATC 360
 25 GAAGAAATCA CTTATCGAGA AATGCGTGAA TTATCTTATG CTGGTTTTAG TGTTTTCCAT 420
 GATGAAGCCT TACAACCACT TTATAAAGAT CGCATCCCTG TGGTGATTAA AAATACGAAC 480
 CGCCCTCAAG ATAAGGTAC ATTTATAGTG CATGATAGAG AAATAAATGC GAAAAATGTG 540
 30 ATTAGCGGTA TAAGTTGTGA TAAAGATTTT ACCGTTATTA ATATCAAAAA GTATTTAATG 600
 AATAGACAAG TCGGCTTTAC TAGAAAGATA TTAGGTGTCT TAGAGGATAA TAATATTTCA 660
 TTTGATCATA TGCCTTCAGG TATTGATACT ATCAGTATCG TTATGCGTTC AAAACAAATT 720
 35 CAAAATAAAG AAACAAAAGT ATTAAATGAA ATTCGTCAAA AATGTGATGT T 771

(2) INFORMATION FOR SEQ ID NO: 1072:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1072:

CGGTGGATCC GTTTGATCTT GAGTGAGGIG CCAATGAAAG TTATGAGCCA CGTTGTCGCG 60
 50 CGCACCATAT CGTAGCACCT AGTGATAATA ATAAGGAGGA ATTATAAGTG TTTGATCAAT 120
 TAGATATTGT AGAAGAAAGA TACGAACAGT TAAATGAACT GTTAATGACC CAGATGTTGn 180

55

(2) INFORMATION FOR SEQ ID NO: 1073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 733 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1073:

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CTTCTTGTA GGGCGTTACA TCACCGGATG GATGATTATG AACTGCGATG ATTGCATTGG      60
CATTCTCTCT CACCGCAATA CTAAAAATTT CACGTGGATG TACAATCGAA CTATTTAATG      120
TACCTTTAAA AACACAGGTT TCTTTAATCA CTACATTTTT TGAATTAAAC AATAAAATGA      180
CAAAATGTTT TTGTGTTAAA TCTTTCATTG TTGGAATCAT ATAATCAGCA ACATCACTTG      240
GTGCGTTTAT TTkTATACGA TTATTTTCAG CTCTTCTCCC CATCCTTTCC CCTAACTCAA      300
ATGCTGCTTT TAAAGTAATT GCTTTTTGTA ATCCAATCCC TTAACTTTT ATCAAATCGT      360
TAATTGAAGA TTTTTTCAAT TCATTCAGAT TcGAAGCAGA TTTAAGCAGT TCATTACTAA      420
TGTCTATGCT CGAGAATCCT TTTCTTCCGG TGTTAATTAA TATAGCTAAT AATTCTGTAT      480
TCGAAAGACT TTTTGCACCA TGGCTTAACA AACGTTCTCT TGGCATTCTT GAAGTTACCA      540
TTTCTTTAAT TTTCAAAAAT ATACGCCTCC TAAAAATTGA TGGATATCAT TATAAAAAAG      600
TGAATTGATA AAAAAGGAra TAAATATAAA TGGAACAAGG GGTAATAGTT TAATCGGCTT      660
AAATATCATG GTAATTAAAG CAACTAAACC AGCAATGACA AATGTAAATA AnATGACATA      720
AATAGTGAAT TGG                                                    733

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(2) INFORMATION FOR SEQ ID NO: 1074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 768 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1074:

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ATGGTTATTT TTTATGCTCT AAATCGTATG TGTTTATAAG GTTCAATTTT TTGCCATTAT      60
TAATTTTGCC GAGCAGTAAT GGGTTGTTAA AGTATCCATC AATTATGCTT AGCAATATTG      120
AAAAATTTAA ATGAAAAAGC GGTTCaATTC TTGAAAAATA GTGTATATTT ACATTTTGGT      180
AATAACTAAC TATAATTTAC ATAAGGAGGT TGTCATTGGG TAGTATTGTT ATCTTATAGT      240

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TATTTACATA GAAGATCGAA ATGTGATTAT TGTAATTCGT CACTCAAAGW GTATGAATTA 360
 ATGCCGATTA TTAGTTTTTT ATTATTAAAA GGGCGATGTC GAAACTGTCG AAAGCGTATT 420
 5 TCCCTAACAC ATTTCTTAGG GGAAACCTTT GCTTTAATAC CTATCGTCTT TATTAAGTAT 480
 GATTTACAT ACGTAAATGt ACGCTATTTA TAACTACATA TGTtTTCTG CTTATTTTA 540
 CTATGACCGA TATCACTTCT TTAATGTTAG ATTGTCGCTT AATTATAATT TATTGTATCG 600
 10 TTTCTCTCTC GTTAAGTATG ATTTATCCAG TAGCTTTTAT CATTATTAGT ATGACCACGC 660
 ATATATTCTA CTTTTTATTT CGGGCATATA TTGGTTATGG TGACGTTTA CTAATATCTG 720
 CACTTTCTTT GTTTTTCCCC TCTCCAATTC ACTATTTATG TCATTTTA 768
 15

(2) INFORMATION FOR SEQ ID NO: 1075:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1075:

TCATATTCAT TTAAATACC ATTCATCTCA GCTTTTCTCA TTTTCTCTT ATAAAGTTGT 60
 ATTCGTGTC TTAATTCTGG CTCAGACATC TCACTCAATT TCTTCTGTTC CATCGGCAAT 120
 30 ACCACTTTCT TCTAATTTAG CTTTAATTTT ATCATATTTA TATCCTTTTC TCATAAGGCC 180
 TTCGATAGTT TTGAAATTA ATTTCTGTTG CGTGTACTTC TTTCGATTTT TATTATAAAT 240
 TTTTCTAAA TCTCGTTGTA ATAAATCGTC TAAAACCGCT TCATCTTGTG TAAAATCCAT 300
 35 TTCATTCAAT ACAGCATGAA TGGTTTCCAT TTCAAACCCT TTTTGAATTA AAGATTGCAT 360
 TACTTTTGCh TnAACTnTAT TTTGTGGCCC nTTTTTTGTT 400

40 (2) INFORMATION FOR SEQ ID NO: 1076:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 753 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1076:

TTAGGTCAAA ATATGTTTTA TCCAAAAGGC ATTTATCTC AATCTGCTGA AGCAAAGAGT 60
 ACAACATATA ATGCAACTAT AGGTATGGCG ACAAACAAAG ACGGAAAAAT GTTTCATCA 120

55

CAAGGCATCG AAGAATTACG TGATTTATGG CAACAAAAAA TGTTGCGTGA CAATCCAGAG 240
 CTATCAATCG ACAACATGTC ACTACCAATT GTTACGAATG CATTAAACACA TGGTTTATCT 300
 5 TTAGTTGGCG ATTTATTTGT AAATCAAGGT GACACTATCT TGTTACCAGA GCATAATTGG 360
 GGTAATTACA AACTTGTTTT CAATACGAGA AATGGTGCAA ACCTTCAAAC ATATCCTATC 420
 TTTGATAAAG ACGGGCATT TACTACTGAT TCACTTGTAG AAGCTTTACA ATCATACAAT 480
 10 AAAGATAAAG TCATTATGAT TTAAATTAT CTAATAATC CGACAGGTTA CACACCTACG 540
 CATAAGAAG TGACTACCAT CGTCGATGCA ATTAAGCAT TAGCTGATAA AGGTACAAAA 600
 15 GTTATAGCTG TTGTGGATGA CGCATACTAT GGTTTATTCT ATGAAGATGT GTATACTCAA 660
 TCATTATTTA CTGCATTATC TAATTTAAAT TCAAATGCAA TATTACCTGT TCGTTTAGAT 720
 GGTGCAACAA AAGAATTTTT CGCATGGGGA TTC 753

20 (2) INFORMATION FOR SEQ ID NO: 1077:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 405 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1077:

AGAAGCGATT TGACaATAAA ACAATTGAAA AACTTTTGGA AAGCAAGTGG TGGGAGAAAA 60
 CGCCTGACAA ACTAAAAGGA TTTTCGGTTG AATATTTAAA TAAAAAGGAT ACTTAATGAT 120
 35 ATGAGAATTT TAAATATGT ATCGAGTAAT ATTGTTCAAG ACCCAAGGGT ACTTAAACAA 180
 ATAGAAACAA TTAAAGGCGT TACGGATGAT TATAAAATTG TTGGAATGAA TAATTCACAA 240
 rCTACTAATA AGCGATTGGA AAATTTAGAT TGTAATTATC GTTTGTTAGG TAGCAAGGTA 300
 40 GATCCAAAAA ATATTCTTTC TAAATTAATT AAGCGTATAA GATTGCaAC AGGTGtTATC 360
 CGAGAAATTA AAGCTTATAA AcCTGACGTG AtTCATGCaA ATGAT 405

45 (2) INFORMATION FOR SEQ ID NO: 1078:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 504 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1078:

CATATTCACA CCTCAATATT CCATAACTTT TACTTTAATA TCAATCCACT TAAATCCATT 120
 CACATCATTG AGTATAAAAT AATATGGTGA TATACGTTGA AGTTGATTAT CTTATATATA 180
 5 AGTATACTTC ACAGAATTTA TAAAATTGTT TAGTCATCAT CTTCAAGTGT TAATTCAAAA 240
 ATATAGAATC TACTGTATTG CATmATAaAT TGAAATGCCA CAAATTGTGC TCCAGCGATA 300
 ACCAACATGC TCACAATAAT TATAAACTTA GATTCTACGA CATTAGGmAC CaAtATATATT 360
 10 CGATAATTTT TTCAATATAT ATAAATGAGC TCAACGCAGT TAATAATAAA CCGAAATGTG 420
 TTTTAGTTTT ACCACCCCAA CGTTTTGTGA CTTTAGGTAA TTTTAATAAC GTGAACATTC 480
 CGCCAATTAC TAATAACAAA TAAC 504
 15

(2) INFORMATION FOR SEQ ID NO: 1079:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 645 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1079:

CATTCTTAAT CAACTTCTTC ATAATGGGAA TTTGGCATGG TAnCGAAGTG TATTACATTG 60
 TTTATGGTTT ATACCATGCA GCATTGTTTA TAGGTTATGG CTATTATGAA CGTTGGCGTA 120
 30 AGAmACATCC GCCACGTTGG CAAATGGTT TCACAACAGC ACTTAGCATT GTGATTACAT 180
 TCCACTTTGT AACATTTGGC TTTTAAATCT TCTCAGGTAA ACTTATATAA TAAAGGAGAA 240
 TTTAATTATG GAATTTAGAG AACAAGTATT AAATTTATTA GCAGAAGTAG CAGAAAATGA 300
 35 TATTGTAAAA GAAAATCCAG ACGTAGAAAT TTTGAAGAA GGTATTATTG ATTCTTTCCa 360
 AACAGTTGGA TTATTATTAG AGATTCAAAA TAACTTGaT ATCGAAGTAT CTATTATGGa 420
 40 CTTTGaTAGA GATGAGTGGG caACACCAAA TAAATCGTT GAAGCATTAG AAGAGTTACG 480
 ATGAAATTAA AACCTTTTTT ACCCATTTTA ATTAGTGGAG CGGTATTCAT TGTCTTTCTA 540
 TTATTACCTG CTAGTTGGTT TACAGGATTA GTAAATGAAA AGACTGTAGA AGATAATAGA 600
 45 ACTTCATTGA CAGATCAAGT ACTAAAAGGC AACTCATTc AAGAT 645

(2) INFORMATION FOR SEQ ID NO: 1080:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1080:

5 AGATGCCAAA ATCAAAACCA ATAATTTGGC AACACATAT AAGTCCACTT TACCGGACCT 60
 nTAAACTTAT CGTACTGTTA AGAACCAAAC GACTGCCATT ATTTGGTCCT AAAGCCACGA 120
 TGGTGGTAGC CnTTGTAATA ATGCTGGCGT AGAAATTAAC CGCCACCCCT AACACCGAAC 180
 10 TATAACGCGG ATAAACCAAT AAAATTATGA TATAATCATC CGTTAAGTCA ATCCATAGTT 240
 TAACATCCCT TATGTTTAAAT TTACTCT 267

(2) INFORMATION FOR SEQ ID NO: 1081:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 441 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1081:

25 ATATTTGTCC ACTATTAGAA GATTGTAGAG AAGGACAAAA ACGTTATAAA GCTAGTTTGA 60
 AAGAAGCGTG ATAACATGAC AAATATTACA AAAGAGGTAT TTGATAATTT AGAACAAGAG 120
 ATTGATTTAT TTGCCAAAAA TAAGACATTA GGTTCCTAGTG AAGCAAAGCC CTACTTGGAT 180
 30 GAATACCATA GTAAAATTAT TGATTATTTT AAGCAGGTTA ATGACATAAC TGGCAATATT 240
 GATTTTGATA AATTAAATCA ATATCCTGTT GTGCCAATGA ATTTTAAAGA AAGATATGAT 300
 TATATGATTG AACGTAAATA TCATTTTATG GGCTATCGAC AAATGAAGAC CTTTAAACT 360
 35 GAATTGATTA AAATGnATGC TAGTTATCAA ACAAGGTTAA AGAATAAGCA GGTATnGACA 420
 AGATTGATCA TTTCTAGTG T 441

(2) INFORMATION FOR SEQ ID NO: 1082:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 410 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1082:

50 AAAATTTCCTT AGtTGATGGT TATTGTTGTT GATTTGAATA ATTTGTAGCG AATATTTTGT 60
 AACAGGGCTA CTAAGAATTT TTATAACAAG AAGTGATTTT AATCGTACTA ATTTTCAGCG 120
 TTTGATGACA AAAGTGATG TCCAACTTA AATAATGGCG ATAAAATTTA AGTCATGGGT 180

GTTGAATATC AATAAAAGAT TAGCAAGTTA GTTCAAAATG GCTATGTATT GTTTTTTGAA 300
 ATACATAGGT TTGAAATCTA TATTAATTAT GCACCAAATA ATTTAATTAG ACTCTATCGA 360
 5 AAATTTCCAA ATTTTGCTTA CTATCTTTCT AATTTTACTT TTATATTGTG 410

(2) INFORMATION FOR SEQ ID NO: 1083:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 586 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1083:

CAGATATTCC CTTCTATTTA CAAGTTGGTA ACCCATATTT ATCAGACAGC GTAGATAATC 60
 20 ATACCGAAAA GTTGTTAGAA CGCTACGAGC AGTTGGTGGA TTTAGTTATG yAAAGTAATG 120
 ATATGAATCA CGTTTTATGTG TTACCACAAC TTCATACATT ACTTTGGAGC AATAAAAAAG 180
 GTGTATAAAG GATAACTTAT TTTACTTTTT GCAAGTCATA TCTAATGAAT AACAATATAT 240
 25 TAATTGATAT AATAGTTGAT TGAAGTATAA CGAACAGGAG TCCATCATGA TTGTATATAT 300
 ATTAATTAAT ATTGCTATCG TCGTACTTAT AACTGGATTC AATTTATATA GGCATCAAAT 360
 GCAACATTTA TCATTAAGTG CAATGTTGTT ATCTATTACG ATaAACGCCT TTATAAATAC 420
 30 ATTCATAATT GATAAATATA ACTTTATTAC TCTGTGTACT ATAACGATGT TTATCATTTG 480
 GACGATACTA CAGTTTTACA TTGATAAAAA ATTAAACCT GTATACATTA CAGACCAAAA 540
 ATTTATTGCT ATCATATTAA CGATTGTTGT CAGTTTAACG CAACGT 586
 35

(2) INFORMATION FOR SEQ ID NO: 1084:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1084:

AACACAAGGT AGCGTCATTA GCATTTAGAT TTTATTGCCA AATTATATAA CGATTTATAC 60
 ATCAATAAGA AAACAATAGA TGATGTATCT GCAGTTTCTG AAGTGAAATA TGATATTAAA 120
 50 TCACAAATGA GTGATGATGA GATTAAGCGT TTAGAGGAAC AAGGACTTCA AGCTATTAAA 180
 GAAGGACAAT TTGCAGTACT TTTGATGGCA GGTGGTCAAG GAACAAGACT TGGTTACAAG 240

TTAAAAACAT TGAATCATCA ATCTGGACAT ACGATTCAAT GGTATATTAT GACAAGTGAT 360
 ATCAATCATG AAGAACTTT AGCTTATTTT GAAGCACATA GTTATTTTGG ATATGATCAA 420
 5 GAAGCAATCC ATTTCTTTAA ACAAGATAAT ATTGTGGCGC TTAGTGAAGA AGGGAAGTTA 480
 ATTTTAAATC AACAGGGTCG TATTATGGAA ACGCCGAATG GTAATGGTGG CGTGTTTAAA 540
 TCTTTAGACA AGGCAGGATA CTTAGAAGAA ATGTCTAATA ATGGCGTTAA GTCATATTTT 600
 10 CTTGAATAAT CATCGACAAT GTTTTCAGTA ACATGTTG 638

(2) INFORMATION FOR SEQ ID NO: 1085:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 618 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1085:

ATTGCAATAT TATCCGCTTG GTTCAACACG TCATCTTTaT tAaTACcATT TATTGgAAaT 60
 25 tCcACCCcATT TCCcGGgCTt CTtACTTCCc TTTATAAAAC TGcCCATTtA ATGAATACTG 120
 TTTAGCTTCA TCTATTCGTA CTTCCACTAG TTTACCAATC ATTTCTTTAG GCGCTTTGAA 180
 ATTAACTAGC TTATTTTTAT CAGTGTAGCC AGCAAGAACC TGATCATCTT TTTTACTACT 240
 30 TCCTTCACAA AGTACTGTTA CAGTTTGTC TCGTACTTA CTcATAGCTA TTTGTGAATA 300
 ATGACCAACT TTTTATTCA AACGTTGCAA TCGTTCCTT TTGACATTtA AAGGTACATT 360
 ATCTTTCATT TTAGCAGCAG GCGTACCATC ACGTTGTGAA TACAAGTACG TATATGCATG 420
 35 TTCAAAACCA ACTTCATCAT ACAGAGTTAA AGTTTCTTCA AATTGTTCCCT CTGATTCATT 480
 TGGATACCCT ACAATAATAT CTGTAGTTAA TGCTACATTa GGAATTCTAT CTTTGATTcG 540
 40 TTTTACTAAA TCCAAATAAC TTTCTCGTGT ATATTTTCTA CCCATTATnT TTAATACTGC 600
 ATTATTTCCA GATTGAAC 618

(2) INFORMATION FOR SEQ ID NO: 1086:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 502 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1086:

55

CAGCAATATC ATGATCAGTT TAATTCATCA AGAAAGTCTA TCTATACTTT TACAGAAACA 120
 GTTCAACCAA ATCGTGTTAT TTATGATTTT TATGATTATG ATCCGTATCA ATTAGCAGCA 180
 5 AATAATGCGA AAGCATTAAA GGATCATATT GAACAAAAC TTAACTTTAA AGTCCAAAGT 240
 ACCGGTGTTA KTTACTTTAG TGATGGTACA GTTAATATCA TTCAAGGTTT TGAAGAAAGA 300
 GATAAATATG TTGATACAGT TTCAACAAAA TCTTCGTTAC GACGTATTAT TAGCGAACCA 360
 10 nAGAGCTATC TAAACACCCT TTAAATAAAG AACAGGTTGA nCAAATCACA GCTATATTCA 420
 AGTAAATCA AAGGCATAAT AATCCATTAC GCTCGATACG CACTATGGTT ATTATGCCTT 480
 TAAATTATTT CTATATATAA nT 502

(2) INFORMATION FOR SEQ ID NO: 1087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 429 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1087:

TTGCCTGATG GACGATGGCC ATCAGAGACT GAGTTTAGAT TGTCTTTAAT GCAACAACTT 60
 GCTGTAAACC AAATTACGAG TGGTAATGAA AGAATAAGTT CAGTTAATGG GCCACCAGGT 120
 30 ACAGGTAAGA CTACTTTATT AAAAGATATA TTTGCTCATC TAGTAGTTGA mAGAGGTAAA 180
 GAGTTAGCTA AACTAAATAA TCCTAAAGAT GCATTTGTCA ArACAAAAAT TCATGAAACG 240
 GATGATAAAT ACGTATACTT ACTAAAGGAn nTATTGCCAA ATATAAGATG GTAGTCGCAT 300
 35 CTAGTAATAA TGGAGCTGTT GAAAATATAT CTAAAGATTT ACCGAAAATT GAAGAAATTA 360
 TAAGAnATCC CGAAAAATGT AAATCCCTA AATATGAACA GAATTATGCA AATTAGCAC 420
 ATGAATTAA 429

(2) INFORMATION FOR SEQ ID NO: 1088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 611 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1088:

TAAGACCTAA TATTTTGGnC CAATACTATG GTGCAGGTnA TTTATATATG ACACCAACAG 60

ATCCATTATT ACATGAGTTT GGTACGAAAA AGTATCCAGA TGAATATCGA TATGGTTTCT 180
 ATGCTAAGCC AACATTGAAT AGACTTAACG GGGGATTCTT TGGACAAGTC TTTACTGTTT 240
 5 ACTATAATGA TAAGTATGTA GTTGTACTTG CATTAATGT AAAAGGAAAC AATGAAGTTC 300
 GAATCAAACA TATTTATAAT GATATTTTAA AACAAAATAA ACCTTACAAT ACGAAGGGTG 360
 TTATTGTTCA ATAATTAATA TAGAAGATAT AACATGTATA TGGCATTAAAG GCATCGACCT 420
 10 TATCTGACCA GTATACGAGT TATATCTTCT TTTTATAGT GGTAAAAAGT TTAAAGTATA 480
 AGGTTGAAGA AGGATGAGTT TAAAAATATG TGTTAACTGA TAAAAGGGGA nATCATTTCG 540
 15 TGAGTTGGCA TCAGnCTAAA nTGAATGAAG ACGAATACGT TGGTCCATGC GTGGTGTGAn 600
 TGTTTTCTAA A 611

(2) INFORMATION FOR SEQ ID NO: 1089:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 644 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1089:

CTGGATAATC GCTTTAATAT GATCAATTTG CTTTTCACTC ATATTAAGCT TATCTAGCCC 60
 30 TTTCATTTTA TTCATACCTG GAATCATTTT CATAATATCA TCCAGTGGTC CTAGATTTTT 120
 CACCyGwTCA AGTTGTTCTA AAAAATCATC TAAAGTAAAC GATGACTCAC GCATCTTTTT 180
 CTCTAAATCT TTTGCTTTTT CTGATCCAC ATCTTGTTGC GCTTTTTCAA TTAAACTTAA 240
 35 CACATCACCC ATACCTAAAA TACGTGATGC CATACGTTCA GGATGGAATA GCTCTAAACC 300
 ATCTAACTTT TCACTCATAC CAACAAATTT AATTGGTTTT TGTGTCACCG AACGAATAGA 360
 40 TAAAGCTGcA CCACCACGTG tATCACCATC TAATTTAGTT AAGGtAACAC CTGTGACATC 420
 AAGTTGATCG TCAAAAGATT CTGCAACATT GACAGCATCT TGACCCGTCA TTGAATCGAC 480
 AACTAACATA ATTCGTTTG GTTTAGCAAT GTCTTTTACT TCTTTTAATT CGTTCATCAA 540
 45 TGCTTCATCG ATGTGTAATC GACCTGCTGG TATCAATGGA TTACAAAGTC TAAATGTTCT 600
 TCTTTAGCAn GTTTTAATGC ATTAGTTACA ATTTGGTGTG GGCC 644

(2) INFORMATION FOR SEQ ID NO: 1090:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1090:

5 GATCCTATCG TTTTAGTGCA TGGTTTCAAT GGGTTTACAG ATGATATTAA TCCTTCAGTG 60
 TTAACCTCATT ATTAGGGCGG TAATAAAATG AACATTTCGCC AAGATTTAGA AAAAATGGTT 120
 ACAAAGCTAT GAAGCAAGTA TAAGTGCTTT TGGAAGTAAC TATGACCGCG CATTGAACTT 180
 10 TATTATTATA TCAAAGGCnG TCGnGTA 207

(2) INFORMATION FOR SEQ ID NO: 1091:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1091:

20 GACTCTAGAG GATCCCCGCT CAAATGCCAT TTGGTGATAT TCGTGAAGCT GCTGGCGAAA 60
 AAACATTTAA TCCAGTGGA GATCGTTTCG TAATAAAAAA ATAATCAATA TATTGTTAGG 120
 25 AATGGGACAG AAATGATAAA GATTTCATTAG TTATTCATTA TGTGTAGTT CTTACACATT 180
 AGCCCGCTGCT AATnGCAACT TAAGAnTAGG TT 212

(2) INFORMATION FOR SEQ ID NO: 1092:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1092:

40 TGGACCTGCA ATTGGTTGCC AGCAGCAACT TTAGCTTCAT AGCTAGCTTT GTGAGCAAGT 60
 GGTAACCTG GAACGATATC ACCAATTGCA TAGATATTGC TGATAGACGT ACGGCTTTGT 120
 TTATCAACnn CTAATAATCC ACGTCAGCGA ATTTAACACC TAATTCTTCT AGGCCTAATT 180
 45 CGTCGTGTTT GGACGACGAC CTACATTA 208

(2) INFORMATION FOR SEQ ID NO: 1093:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 902 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1093:

5 CTTAAAAGTT GTnTCAATAA TGATTGTATT AGTTGCATGC TTATTATATA TGAATCATAG 60
 TATTGATTTA CCTACCCTTA TTATGATTTT AATTTTTTCA TTTGTGATAT TTGATAGTGT 120
 TGAAAATATT AATAGTGCTG CACACGTACT TGAAATGATA GATATGACGA TAGATGATAT 180
 10 TGmAAAGATA AAAAATGCTC CAGAACTGGA TGAGAATGGA AAAAATTGA CGATTAAAAA 240
 TGAAAATATC GCTTTTCAAA ACGTGAACCT TTCATATGAT GATAACAAG TGATAAGAA 300
 TGTGAATTTT GAGATACCTA CACAAACATC AACAGCAATA ATTGGACCTT CAGGAAGTGG 360
 15 GAAATCTACA TTATGTCACT TACTCTTGCG CTTTATGAT ATCGATGATG GAAATATTCTG 420
 CATCGATGGT GTTGATATTA AAGATATGAC ATTAAGTACG TTAATGTCGA AAATTAGTGC 480
 AGTATTTCAA AAGGTGTATT TATTTAATGA TACGATTGAA AATAACATAT TGTTTGGCAA 540
 20 TCCAGGTGCA ACGAAAGAAG AAATTATTCTG TGCCGCGAAG CAAGCATGTT GCCACGACTT 600
 CATCATGTCA TTACCTGAGG GATATCAAAC AATGCTAAAT GAAAAAGGTA GTAATTTATC 660
 TGGCGGAGAA AAGCAAAGGA TTCTATTGCG TAGGGCGATA TTAAAAGATG CACCAATAAT 720
 25 TATTTTAGAT GAAGCAACTG cAAGTATTGA CCCTGAAAAT GAACAGCTGA TTCAAACGGC 780
 AATTAATGAA TTAAGTAAAG GCAAAACAGT AATTACAATT GCACATAAAC TTGAAACTAT 840
 30 TAAAnATGCA GATCAGATTA TAGTGCTCAA TGnAGGTGAA ATAATTCAA AAGGTAGTCC 900
 TG 902

(2) INFORMATION FOR SEQ ID NO: 1094:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 632 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1094:

45 ACGCAAGGGA TATGATTAAA CACCATAATA TACAATCACC TTTTATATAC ATGAAAGCAC 60
 TAATAGAATC GATTCATTTA AACATAAAAC ATGATTTTAA CCAGCAAGAT TTGATTGAAA 120
 TACCAATTGT GTATGGTTCTG AAATATGGTC CGGATTTAGA ATCACTTTTA AAACATTACA 180
 50 AAATCAAGCT AGAAACTTTT ATTGAATTAC ATTCTAAGGC GCAATATTTT GTTTCGATGA 240
 TGGGATATTC ACCTGGGTTt CCTTATTTAA CTGGATTAAA TAAGAAATTG TATATTAATC 300

55

GCGGTATTGT AACTACGGAT ACAATTAATG ATTGGTTAGT TATTGGTTAT ACACCATTAT 420
 CACTTTTAA TCCGAAAGAA TCAGATTTTCG CACGCTTAAA GTTAGGCGAT AATATTAAAT 480
 5 TTAGACCTAT CAATGAAAAT GAATTAGAAG TAGGAGCGTT TAAAGATGTC AATCATAATT 540
 GAAAAAAGTG GCTTATTCAG TAGCTTTCAG aCTTTGGCAG AAGGGGATAT GAACATGATG 600
 GTGTAATTCC ATGTGGTGCA CTTGATACTT TA 632

10 (2) INFORMATION FOR SEQ ID NO: 1095:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1095:

GCAACACGAT TGCTAAAAAA TGATATACTT ATTAATTGTT GCAACACTTG TTTATGTGAT 60
 ATACTGATCA TGGCATTGTG GCGGATTGAT GACCATACAC ATGACGTGAC AATGATAAAT 120
 25 CATTGCCACT ACTTGTTAAA ACAGCAATTT CTCAAGTGGA AGCTGGTGCh ATATATTnCG 180
 CCAATAATAT GATGGATGGT TTGTTGCTGA AA 212

(2) INFORMATION FOR SEQ ID NO: 1096:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 466 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1096:

40 AATGAACTGG GTATTnCTTT TGCCATGCTT GCCCACTGCC ATGCATTTCG TGAAGAATGT 60
 TTTTGTAGAA CCGgCTTAAG AATTTGAAGT TTGTAGTAGT ATCTAAAAAG ATTACTTGGT 120
 GATACTCAGG ATGAATTCCT TGTTcATTAT TTTCAGCTCC TTTGCCCTGA ACCATCTGGA 180
 45 ACAGAGTTAT TTGTGAGTTT TTACCCAATA CTGTGTAATT ATAAAGGTAA TTAATTCAAA 240
 ACGCAAGCCC CTATATAATG TTTATTAAAT TATAGGTCGA CCCGTTTTAG TACTTTCTTC 300
 TGCACTTTT TGAGCTGCT TGAAGAAATC TtcATTATTC TTAGACCTTT TAAGTTTGCG 360
 50 AATAAATCTT TCAGTAAAGT CAGTTGAGTC AGTGAATAGA TTTCTTAATT GCCATAATGT 420
 GTCTAATTCA GATTTACTTA TCAACAATnC TnCTTTACGC GTTGAA 466

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1097:

TTTTGATTCA ATAGGCGGTT CCGTGTTATC ACTGACAACT TTAGTTGTAG CTTTCATCTTT 60
 ATGTATTCTT TCGTTAAATC CTTCAAGTTT TTAGTCGTGG GATTTTAACC TCAGGATGTT 120
 CCATCATGTC TTGACTATCA AGTCCTTnTA CACGTGTCTT TATGTGATGC TTGATTGCGT 180
 nCCCTTACTT TTTGAATAGG GGTAGTAA 208

(2) INFORMATION FOR SEQ ID NO: 1098:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 571 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1098:

CCTTCAACGA AAATAGCATA TTGACCATAA ATATTATGAA TTGTTTGTTT AACATCTTCA 60
 GTTATTGGAT CTTGACTCAA AAATACATTA AATACITCAA TACCAAATTT ACGTGACATT 120
 TCTACAGCTT CATACTATC AATAATACCA TCTTGACTAT AATTAAATGC AGACGGTTCG 180
 CCGTCTGAAA ATAnGATTAA AAATCGTTGA TGTGTATTTC GACGCATTAA TCGTTCACTT 240
 GCAACTCTAA TAGCAACACC ATCAGGATTA TCATCTTGAG GTTCAAGTGC CATAATACGT 300
 GGGCCATCTT TTTCAAAGGT TGAGTAATCA TAGTTAATAA TTTCATTAAAT GATATTTGGT 360
 TGTGCATGCT CGTCTGAATC AAAGGCATCC TCACTGAATG ATAAAATTTT ATGTTTAATG 420
 TTCAATGCTT TTAACGCTC GTGGAATAAC ACTACACCTT TCTTCGTTTC AGCCATTTTA 480
 TCATGCATAC TTGCTGgACG CATCAATTAA CAATGTAAAT GTnCGCATCA AATGATTnAC 540
 TTAAATCTTG TTTTTTGTA AACAATTTAT A 571

(2) INFORMATION FOR SEQ ID NO: 1099:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 214 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1099:

5 TGCAAGTGAA CAAGTCATTA ACTTGTTTAA TACACGTGGG GCACAAGTCG AAGAAGTTTG 60
 GGTGAAGGGC CATGAAATTA CAGAACTGG ATTAACGGCT GGTCAACAAA TACTTGGGAA 120
 ATAACAGTTC TATTAAGAAG CGGACAGATG GAAAAGATTT TACCTTTCAT CTGCCGCTTT 180
 10 TTGATTTGAA GGCCGGACCh AATTTACCAh GGAA 214

(2) INFORMATION FOR SEQ ID NO: 1100:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 1158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1100:

20 CACCGTATTG TACAAAGAAT TTAAAGTTTT CGATTTCTTn TCTTAATTTA TCATCAGCTA 60
 TCGGTTTGGT TGGGATAATT TTATTATGTT CCATTTTAC TGGATATTCT TTTCTTTAC 120
 25 TACGTGAGTA TCCTnTTTTA TCTTCCATA ATTCCCTCAC AATAAATTCA CCTTTGTCTG 180
 TTCTGGTATT GCGGTCTACA TACAGGACCA ATCCTCTGGA TTCCaTATTc TTTCCATTTG 240
 30 TTTCTATTGT CATTTTAGAG TGAATTATCC aAGTGCCTTT GTCGCCCTTT TCAAACCTCTT 300
 GATCTCGAAA GCCTTCCTTA TCATAAAAGT CTTCAAGATT TTTAGTTGGA TACAGGCTCA 360
 ACGTTTGTGTT GAAGTTTTCT TTAATTTGTT TATCTTTACT GCTTTCTTCC TTTTTCATTC 420
 35 CGCAAGCCCC TATAAAAACA GCTAATAATA CTAAATACAG CCAGAGCCTC AACCTTTTTG 480
 AGTGAATCAT CATTCACAT CCCCATTTTT ATTTTTGATG CAAAGTTAAG TtCAAATTCC 540
 AATATTAATA ATATTAGAGG aAAtTTtATG ATTAaATCCT CGTGGATTtT AATTGTTAGT 600
 40 TGTATTTTTC ACATATCAAC ATCACAAATT ATTTAAAAAG CGCAAATATC TTTATAATTT 660
 TTATTGGCCT AACCAACTAA TTAATTAAGA TAAATTGCGC TTATATTTAA AATAATAACA 720
 CTGAACTCA ATGTATTTAC TTATTAAAAT TGATGTTTAA ATACAACTTT ACTAACATTC 780
 45 ATTTTTCGGT TTACATTAAT TkGTTAGATA ACGATATATA TCAtCTCTTA CAGCTTTATC 840
 CAGTGCTAAA TCCATCGTTA CTACGTTTGA ACCATTCGGC ATTTTATCTT GCTTTTCTGA 900
 50 ACCTTCTATA TATCCAGCAG TTCCTAAATA ATAAAAATAT ATACCATCAT CATCTTTTTT 960
 CTGTACAAAA ATATACATTT TAATTCCTTT TGCTCTATGG GACAAAATTT TCTGAACCTC 1020
 TTTTGATTCT AGCGTTCTAT TAGATTAGT AAACCATTTT AATTCATCTT GACTTAAAAA 1080

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TGGCATTCTCT TGGCTTTT

1158

(2) INFORMATION FOR SEQ ID NO: 1101:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 353 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1101:

CCAAATGCTA TAAATGCAAA AATnGCTAAT GCGATATTTT TATAGAAAAT ATCTGGTCCT 60
 AAATTTTGTA AATACGTGGT AAACGTTGCG TATGACAATA AGCCAATCAC TACAGCGTAA 120
 ATATGTGAAA TAATTAAACC GAACCGTCTC GCTCTTTCAA AAACAAGTGT TGCTAAAATA 180
 ATAATCAGTA ATCCAAATGA CAAGGGTTGT CGCCAACTTA ATGGTAAAAA CTGACCTAGA 240
 TAGCATCCTA TGCCAAATAT AATCCAATAA TACATAAAAT AAAGCCACAC TTTACTTAtT 300
 GATTGAGCAT GCTGGTTTTG ATGATAATAT GAATGATTTG TATTTTGCGA CAA 353

(2) INFORMATION FOR SEQ ID NO: 1102:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 194 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1102:

CCCACACGTC TTCCACCGGA TAGGTTTCGA GCTCGGGCGA ACCGGGCAGG GCGGTGACCA 60
 CCCCCTGCGG TGTCTTCTTG GCCAGCTTGT TTGCGAGCTT GGCCAGCGTC TTCGTGGGGC 120
 CAATGCCCCAC GCAACACGGG ATGCCCCACCC ATTGGAGGAT CTGGGCACGG ACCTGGCGGG 180
 CCATCGCTTC GntG 194

(2) INFORMATION FOR SEQ ID NO: 1103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 220 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1103:

TCGCTTTTGC TTTTGCATCA GGTATTGCTG CTATTCAGC ATACTTTTGG ACTTTCAAAT 120
 CTGGTGATCA TGTCATCTTA CCCGATGGAT GTATATGGGC GGTTACTTTT CGTCTCACTG 180
 5 TGGCAAATTT TGGATCGATT TAATATTGAA TTTTACAACC 220

(2) INFORMATION FOR SEQ ID NO: 1104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1104:

GGACATTGTA TCGACATTTT AAAGATAAAA GCGATTTATG CTACTACGTC ATACAAAGAG 60
 20 ACCTTGATAT TTTTATCACT CATTTTAAAGC AAATTAAAGA TGAATATCAT TCTAATTATG 120
 AGGTTATGCA AGTGTCGTCA TCGCTTTTAA ATAAGTCATA ATAAAAATCA AATAATTCTT 180
 GATAAAATGC GCTTTGGTAA AAACGTAATT TATTGTTGCC TGCTTCAATA CATTG 235

(2) INFORMATION FOR SEQ ID NO: 1105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1105:

GCGGGGGCAG GTAAATCCAC TTTGACACAT CTTATTGCAG GTGTTTATCA GCCAACAATA 60
 GGTACTATAA GTACAAACCA GCGTGATTTT AATATTGGGA TACTTAGTCC AaAGCCCTAT 120
 40 ATTCAGGCT CTATAAAGA GGATATTACG ATGTTTAAAG nTATAGAAAA TAATACTAAT 180
 GAAGAAGTGC TAGACGAAGT AGGGTTTATT AGACCAAGTG CCATCCTTC 229

(2) INFORMATION FOR SEQ ID NO: 1106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 596 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1106:

1 rAATTAAAAT CAAAATTTGA TGAAGTAAAT GTAATCGCGT CAACAAACGG TAGAAAGTTT 120
 ATTAATGGTG AAATATTAAA GCAATTTTGC GATAACTATT ATGACGAATT TGaAGACCCT 180
 5 TTTTAAATC ATGTAGATAT AGCAAATAAA CATGACAAGA TTATTATTTT ACCTGCGACT 240
 TCTAATACGA TTAATAAAAT TGCmAATGGT ATATGTGaCA ATTTATTATT AACTATTTGT 300
 CATACAGCTT TTGrAAAAC TCTATATTT CCAAATATGA ATTTACGAAT GTGGGAAAAT 360
 10 CCAGTTACTC AAAATAATAT TCGATTATTA AAAGATTATG GTGTATCAAT ATATCCAGCA 420
 AATATTTTCAg AAAGTTATGA ATTAGCGTCA AAAACATTTA AAAAGAATGT TGTCGCACCT 480
 15 GGAACCATAT AAAGTTCTGG gAATTCATTT GaGATTAGAA TATGGAAAAT CaTAAAGCGC 540
 GCKATTGATT AGTTTAATGA ATGATTGGAG TcTTTTGAAG ATnCGATTTA CAATGG 596

(2) INFORMATION FOR SEQ ID NO: 1107:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 673 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1107:

30 ACTAGCTAAA AATAATATTC TATTCTTTTT AACATGGGCA GTTCCAGCGG CAATTAGTGG 60
 TATTTATATT AAATATATAA ACAAGGCTAC GGTAGAAAGA TTTTAAAT TAGTATTTTT 120
 CATATTTTCT GTTTCATTTA TTTTGTAAAT TTTAATACCA AAACCTACAG GTGAGATACC 180
 35 TAGCTATATC AATTTTGGAC TTATGAAC TAACAAACGCT TCGTACCTTT CAGCATTTAC 240
 TGCCGGATTA GGCATTTATT TCATTATGAA AGGTTCAAGT AAACATAAGT GGATATATGT 300
 TCTATTTACA ATAATTGATA TCCCTATTGT GTTTATACCA GGAGGGCGTG GAGGTGCTAT 360
 40 TTTATTAATT CTTTACGGCT TATTTGCATT TATACTTATT ACGTTTAAAA GAGGAATACC 420
 TATCGCAGTA AAAAGCATTA TGTATATTTT TGCATTAAGC ATATCTAGTG TATTGATTTA 480
 CTTTCTTTTT ACAAAGGTT CGAATACTAG AACATTTTCA TATCTACAAG GTGGAACACT 540
 45 TAATTTAGAA GGTACTTCTG GgAAGAGGAC CGATTTATGA AAAAGGTATT TACTTtATTC 600
 AACAAAGTTC GTTATTAGGC TATGGGCCAT TTAACATtA TAACTAATC GGAAATATAC 660
 50 CACATAACAG CAT 673

(2) INFORMATION FOR SEQ ID NO: 1108:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 506 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1108:

	TCACAGTGGC GGCACAAAAA GTAAGTGGAG ATTATTTTAA TTTAATTGAC CATAACGATG	60
10	GCACAAATGAG CTTTGCTGTT GCAGATGTCA TTGGAAAAGG TATACCAGCT GCTTTAGCAA	120
	TGAGTATGAT AAAGTTTGGC ATGGATTCTT ATGGACACTC ACAATTACCG AGTGATGGTT	180
	TAAAACGTTT AAATCGTGTT GTTGAAAAGA ATATTAATCA AAATATGTTT GTCACAATGT	240
15	TTTATGGTTT ATATGAAGAA ATGAACCATT TATTGTATTG TAGTTCAGCT GGCATGAGC	300
	CTGGATATAT TTATCGCGCT GAAAAAGAAG AATTTGAAGA AATTCAGTT AGAGGTAGAG	360
	TGTTAGGAAT CAGTTCACAA ACACGATATC AACAACAAGA AATCCAATA TACCTTGATG	420
20	ATTTAATTAT CATTTTAACG GATGGTGTGA CTGAAGCTAG AAAAGTGAAG GTACCTTTAT	480
	AGATAAACAA AAACTTTGTAG AATATA	506

(2) INFORMATION FOR SEQ ID NO: 1109:

25

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 552 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1109:

35	TGATATTGAA AAAGATGTCA TTGTTAAAGC ACAAGAAAGT AAAATTGCTC AAGTTATCAC	60
	GAATTTGTGA ACGAATGCAA TTAATATTC TTATGAAGAT GGAGATATTA ACGTTCGTGT	120
	GTATCGAGAT GACTTTCGTG TCATTTTCGA AGTACAAGAT TTTGGTATAG GTATTAAATT	180
40	AGAAGACCAA CAACGTATTT TTGAAAGATT TTATAGAGTA GATAAAGCAC GAAGTAGnAG	240
	ATTCTGGTGG GACAGGTCTT GGATTATCAA TTACAAAGCA TATAGTAGAs GCCCACCAAG	300
	GCAATATTGA AGTGAATAGT CAAGTTGGCA AAGGCTCAAC GTTCAAAGTT ATTCTAAAAG	360
45	ATTATAAAGA ATAAdAATTA AAGTGGTAAC AGCGCGTGTA TTTTTCACGA AGTTGTTGCT	420
	GCTTTTTTAT TTCGTTCAAA TCTCTATTGG TATTAAATTA GAGTTAATGA AGTGGAATAA	480
50	ATTCGGTTGT CAATTTTGTC ATTTGTATAT GTCGATTGT AAGTTATAAG TAATAGATTG	540
	TTGTGAATCA nG	552

(2) INFORMATION FOR SEQ ID NO: 1110:

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(A) LENGTH: 244 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1110:

10 AACAGATCAA CAATTGCAGA TCAATTACTC GTCATATTGA TCAATTATCT CTGACAACGA 60
 GTGATGATTT ATTACGTCAT TGATTGATCA TCACAAGATA AGTCGCTATT GATTTCTCAA 120
 TTTTACAACG AnATTAGGAA AGCTGnAGCA GATAATTGGC TAAGTTGGAC GATAAAGGTT 180
 15 ATCAATCGCC AATCGTTGCC ATTGAAGAAC TTTTGCTCAC TGGCGCACGC TTCAGATGAT 240
 ATTT 244

(2) INFORMATION FOR SEQ ID NO: 1111:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 825 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1111:

30 AGTATTGAGT GTTTGGATTT AAGAGACTTG GAAAGTGAGT CAATAATCAA AATCTTACTC 60
 AATACTTTTA TTTTGGTACT CGCAATTTAG ATTGTTAAC TAATTTTTTC GCTTATTATA 120
 AAACGAAACA ATCAAGTAAA CGATAAAGCC TACAAAGATA CCAATAAAA TAGATAGTAC 180
 35 TGCCGTCACT ATTAATGGTA ATTTGAAAAA TATTGTAGG AAAATmCCAA TGATAATTGC 240
 GATAATTACT GCAAtTaATG TGA CTGTATT TTCATTTGAA ATGTTCAttT AtttTCACTC 300
 CttAACAAATA ACATTATATC ATGCTATAGC TTTCCAAAAT ATTGAAATAT GTAGATATGG 360
 40 CTATTGACGA TATTTCTTAA CTTTTATATG ATTAATCGGA ATGAAAAAAG AGAAGTAGGT 420
 GGCAATATGA AGTCAAATAA ATCGCTTGCT ATGATTGTGG TAGCCATCAT TATTGTAGGT 480
 GTATTAGCAT TTCAATTTAT GAATCATACG GGTCCTTTCA AAAAGGGGAC GAATCATGAA 540
 45 ACTGTACAAG ATTTAAATGG TAAAGATAAA GTACATGTTT AAAGAGTTGT GGATGGTGAT 600
 ACATTTATTG CAAATCAAAA TGGTAAAGAA ATTAAAGTTA GGCTTATAGG GGTGATACG 660
 CCAGAAACGG TGAAACCGAA TACGCCTGTA CAACCATTTG GCAAAGAAGC ATCAAATTAT 720
 50 AGTAAGAAGA CATTAACAAA TCAAGATGTT TATTAGAAT ATGATAAAGA AAACCAAnTC 780
 GCTATGGTAG ACCATTGGCG TATGTATGGA TAAGTAAAGA TCGTA 825

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 621 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1112:

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10 TCCCTATAAA TCCCCACAAA AAAAGGGTAA ATCCGAACGT CAAATTTTCAT CTCTTTATGC      60
   CAATCAACGA TCGATTACC TTTTAAAATT TAAAATGTAT CTGTAATACT CTTAGCAATA      120
   TTTGTATATG CTGCATCTTC CATAGGTGGA TTGTGTAATC CTGCACGCAT GTCACGATAG      180
15 TAACGTTGTA ATGGTCGATT CATTCTAAG CTTTTCAGCAC CAACTATTCT CATCGCTAAA      240
   TCAATCACTT CAAGCCCTTG ATTCATTACC ATCACTTTAC TCGCACTTGT TGGATTTCTT      300
   ATCTGACTGT CATCTTTATA TTGTTGATAC CCTTTTGCTG TACTCCATAA AAATTGTCTC      360
   GCACATAACA ATAGCGTTTC CATTTCCTT AAATTTTGTT GCACAGTTGG CAATGTTGCA      420
   ATCGTTCCTT CAATACTATT AGGGCTATGT TGGATTGCAA AGTCTACAGC ATAATTTCTA      480
25 GCAGCTTG TG CTATACCTAA ATAACAGCTT GGTATATGCA ATATCCAACC ATTTGGCGCT      540
   TTACTTTTCT CTGTTTCCAC TAAATGTTTT AATGGTACTT TTACATCATT TAATATTAAA      600
   TCATGACTTT CTGTCGCTCG C                                          621

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(2) INFORMATION FOR SEQ ID NO: 1113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 619 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1113:

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40 GTACCTTGTT TTTCAGTGT AATTTCCCAA ATATAACCTG GTGTAATACC GTATTGTTTT      60
   GAGAAGTACT TGAAGGCACC TTCACTTGTA ATCATGGCAC GTTGTTCTTC TGGAATGTCA      120
   TTAAATTTGT CTTTACTGTC TTTACTGTCA TTATTTAATT TTTCCAATTG AGCAATGTAT      180
   TTGTTACCTT GCTTTTCATA ATCTGCTTTA TGTTTTTTGT CGTTATCGAT AAATGTTTGT      240
   TGAATTGTTT TTACGTATTT AATACCGTTA TCTAACTTA ACCATGCGTG TGGATCTTGT      300
50 TTATCTTTGT TGCCTTCTTC ACCGTTTAAA TAGATAGGTT TAACATCTTT TGATACTGCG      360
   ATAACTTTTT TATCTTTTAA TGATTTACCA GCCTGTCTA AGGCTTTTTC AAACCAACCG      420

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ATATCyTTAG GTTtAACyTC aTAWTCaTGA GGATCTkGAC CAACAGGTAC AATACnATGA 540
 ATATCGACGT TGTCTCCACC AACATTTTtA GCCATATCAG ATAGAATTGA ATTCGTCGnT 600
 5 ACTACTTTnA ATTTGCCAT 619

(2) INFORMATION FOR SEQ ID NO: 1114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1114:

GAAAACCGCA CGACAATGAA AAAAGATATC CGGTTAAAAT GGTGATAAT AAAATCATTTC 60
 20 CAACAAAAGA AATTAAAGAT GAAAAAATAA AAAAAGAAAT CGAAAACCTTT AAGTTCTTTG 120
 TTCAATATGG TGACTTTAAA AATTTGAAAA ATTATAAGA CGGAGATATT TCATATAATC 180
 CAGAGGTGCC GAGTTATTCG GCTAAATATC AATTAATAA TGATGATTAT AATGTAAAC 240
 25 AATTACGCAA AAGATATGAT ATACCGACGA GTAAAGCTCC AAAGTTATTG TTAAAAGGTT 300
 CAGGGAATTT AAAAGGCTCA TCAGTTGGAT ATAAAGATAT TGAATTTACG TTTGTAGAGA 360
 AAAAAGAgGA AAATATATAC TTTAGTGaTA GCTTAGATTA TAAAAAAGC GGAGATGTAT 420
 30 AATCATGGCT CAATCAGAAT ATGAAATCAA TCCCGGAAAA AGAGAGTGAT GAAATGATAA 480
 AACGTGTAAA TAAATTAGTG CTTGGTATTA GTCTTCTGTT TTTAGTCATT AGTATGCACT 540
 35 GCTGGTTGT 549

(2) INFORMATION FOR SEQ ID NO: 1115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1115:

TGTTATTGCA ACTATTAAAA ATATnAAAAA CAAAGACTTA ATTGATTATT CTTTATATAT 60
 TAAAAAAGGT TTAGTGGAGC CATTATTGT ATTCTATAAT CAAGAAAATA TATTCTACAT 120
 50 TAGCAATGCT GTTATAGATA TCATCAGTGT ATCCAAAGAT ACTCTTGATT ATATAAAGTC 180
 AGAATTCAAT GATCACTGTG tTCGCCATAC TGATTTTATA GCACAGAGAA AAGCCGTAGT 240

TTATCATCTT CGATGAA

317

(2) INFORMATION FOR SEQ ID NO: 1116:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1116:

15	ACTATGACTG CAATGCCAAC AATGAATGTT ATTGCATAAA GCATATGCAT TTAATCAAGC	60
	TTATGTTATT TAGCAAGGGC AAGCCACTTC TCGATTCATG GCTTGCCTTA TTTTATTGTA	120
	TATTTTAAAT TATCGTTGCT GGGCCCTTGA TTGACAATCG TATTAAAATG GCCTTATTAA	180
20	GTCAACTTTG TCTATACGGT TTGGAATCTT CTACCCAATG TCTTATAAAA GACAATCCCG	240
	CACCTGAAAC ATAACTCATG AATAATAAGAA nATGGTATAC CATTAATnTG AATCCATTTC	300
	CA nTTTATAA CGTTGTAAAT GACACATAAT TAGAATCATA AAGTTTTTCG TGGGATATTG	360
25	AAACTTTACC CATACGAGAC ATCATGGATA AAAGCGAGGC	400

(2) INFORMATION FOR SEQ ID NO: 1117:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 696 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1117:

	TGCATATAAT GTTCAAACGG CAATGATTCC ACTGTATAAA CCTCTTGTCG TGGATGATCT	60
40	TTAATTGTT GTTTTAATAA CTGAACTCTT TTTTCATGTT CATAATGAAC ATAAATAAAT	120
	GCACTAAGAT ATATCACAGC TAAACTAGT GATGCACCTT TAATAAAATT AACATTGATT	180
	GACTTATATT TCCGAAATTC TTTTAATAAA ATAATTAAAA TGATTACATG TATCGTATAA	240
45	ACAATCAAAA AATTACCTGG TTCTATTGGA GTAACAATGA CTAGTGTCGA CGCCGAAACA	300
	CATATTGCAA TAAGTAAGGA ATATAAAGTG ATTTGTGTTT TACGATCATT AATAGACAAA	360
	TAAATACCTA CAAATATCGA AAACGCAAAG TAACCACATA CAATTACGTT CACAAAACCA	420
50	ACCAATCCAA TATCTGTATT TTTATTTAAT AAAAAGTGAT TGTAATAATAG TAAATAATAA	480
	AGCGGTAAAG TGATAAATCC TATCATAATG ATACGACGCT TTAATATTGT TAAATGTACA	540

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ATCTGACTGA AAATGACACC ATATGGAAGT GACGTTGATA TCATTTCTGC AAATTTTGAA 660
 AAGATACCTT GATTATTTGA AACTTGTTGA TATTCT 696

5 (2) INFORMATION FOR SEQ ID NO: 1118:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1118:

GCAGTGACAA TCAATAATTT GTAAC TAGAA GATAATAAAG AGAACGCTCT ATAGAGACGA 60
 ATTGAAGGTT TGATTTTAAT GTCTGTTAGT AAGAATCATA TCAATGAGAT GCCTATAGTA 120
 20 CTCAGANTAT ATTAAATTAA AACCGTCATT AATTGTTTTT CCGAAAACCA TTTGTAACCA 180
 TTTnAATGTA GTTGGACCTA CCTACGTTCT CCAATAATCC ATT 223

(2) INFORMATION FOR SEQ ID NO: 1119:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1119:

35 CTGCTTTACC TTTTCCAAC TTAGAAATTG CTACATAGGG GCCTTCTGCT TTACCGCCCC 60
 AATTCCAATT CCACATTTTC AAGAAATAAG GAGGCAAAAA TGTT CATATA TGAATTGGAA 120
 TTATTTGTTT TCTTATTAGG CCGAGATGCG CCGCGTGCGG CTGCTGGAGA TGGCGGACGC 180
 40 GATGGATATG TTCTGCCAAG GGTGTTTGG CGCATT CACA GTTCTCCGCA AGAATTGATT 240
 GGCTCCAATT CTTGGAGTGG TGAAT 265

(2) INFORMATION FOR SEQ ID NO: 1120:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1120:

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CATGACATTA CATGCTTATT TAGGTAGAGC GGAACAGGT AAGTCTACGA AAATGTTGAC 120
 CGAAATAAAA CAAAAaATGa AAGCAGATCC GCTTGGAGAT CCAATCATTT TAATTGCGCa 180
 5 ACTCAAAGTA CATTTCAATT AGAAcAAGCC TTTGTCaATG ATCCGGAATT AAATGGTAGT 240
 TTAAGAACAG AAGTGTGCA TTTTGAACGA TTAAGTCATC GTATTTTcCA AGAAGTTGGT 300
 AGTTATAGCG AACAAAAGTh ATCTAAAGC 329

10 (2) INFORMATION FOR SEQ ID NO: 1121:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1121:

ACACCTCTTT TTTAATATAT GTGAACATA TATAGTGTAT AGAGAGGTTA CTTGTTACTC 60
 AATATAACA AAAATCAACT TTGTCAAAT AAATGTGACA AAATTAAATA AAGTGTATC 120
 25 AATGTGACAG TATAGATCAT TTTGCAAAAA GTCAAAACAA AAAAAATTGTT TTAGGGATTT 180
 TTCAAATTT TCATTGTGGA AAATGATTTG nCAAAACAAA ACAACACnTT GTGAGCAATG 240
 AAGCTTCAAT GG 252

30 (2) INFORMATION FOR SEQ ID NO: 1122:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1122:

nAATAATAGG CGCCACCTAA TAAACCAGCT GGAATGCCTA TCATTGGTGT TGTGAATGAG 60
 CTTAATACAA TAACAAGTAT TGTTAAAGCA ATGACGTTAT ACCAAGTTAC AGTCAAATTT 120
 45 TTCAAATCCT CATATGATTG TTTTACTAAT TCTCTAAATT TCATGATTCA ATCTCTCCTT 180
 TTCTTAAATC AATTAATAGT TATACTGCAT TGCTTAAAT CAAnATATCT AATGAAGCAT 240
 CTTTAAATCG TAAGTGTTAA ATGGTTTTCT TAATCAATTT GTTTGAATGT ATAAAnAGCAA 300
 50 TTAAAGCAAA AGTAATGTAA ATGAGGGTGT ATACAACAAT TACTACAATA ACCGGCATGA 360
 AGGAAATATT ACCCATCAAT TTCATAAATG CGATTGCGGC 400

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 270 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1123:

```

10 AATACAACCT TTTATCATAG TGTAATGTA TTCTACCACT ATTGAGAAGT TTTCATATTA      60
   TTCAATACCT GAAATCGCCA TAGTAATATT ACTAAATGCA CACTGCATAT GTTGTTTAAAC    120
   AACACAACCT TAAAAATATA TTCTAACTCT ATCTACGAAT GTACTTAAAT ATCATAACAA    180
15 TCTATTCCAA ATCAATTAC ATTATTAGCT ACCTTAAAAA CCAAACCGAG GCCTTAGGCC      240
   TCGGTTTAAA TATATATAAC GnGCGACATG                                     270

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(2) INFORMATION FOR SEQ ID NO: 1124:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1124:

```

30 GGTCTTCTGT ATCAAATTAT ATTATGAGAG TTAGACTCAG TATTAATGAA ATCGTTGATA      60
   AAGATCAAGT GCTTGCATCA CAAATAGGTG GATTACTATG ATGTTTAATC AAATTAATAA    120
35 TAAAAATGAA TTAGAAGAAT CATATGAATC TGAGAAAAAA CGTATAGAGA ATGAACTGCA      180
   AAATTTAAAT GAAGTTAGGC ATAGAAGTCG AAAAGAAAAT GAACGTAGTT ATGATGTTTT    240
   TCAATATTTG AAGCACGAAA TGAATTATAG TGAAGATGCC CAAAGGAAAA TGACGAGAAA    300
40 TATAGAAGCG TATGAGCAAG AAATCAATGA GATAATTAGA AAGCAAGAAT GGAAATTAGG      360
   AAGAATATAA AGAAGACTTA AAAAAGTCTT ATGAAAAGCA                             400

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(2) INFORMATION FOR SEQ ID NO: 1125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1125:

AAATATATyTC GATCATTGAT AATATGTGCT TTACTATTCC AAATAACTTT CAAATTTTGA 120
 TAATATTCAT CAATACTCTC AATATAACTA ACCAGTTTAT ACAACCATTG GCCATCGACT 180
 5 TTCACATATT TTTGAATACT ATTTCCAyT TtAAGACGTG TTGGTTCAAT TACAAAATGC 240
 CCCAAATTAA TACCACTTAA TAATCCAAAT GGAGTTGGAC GTGTTGACAT TCTAATTAAA 300
 TATTTTAATA AACTTTCTTT AGCATCTCTA ACCTTCTTGT TATCGCCATC AAAATTTATT 360
 10 nCnTGTAAG TACAATA 377

(2) INFORMATION FOR SEQ ID NO: 1126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1126:

GTTACATTAC TGTTTCATGTC CACAACGTTT GTCAGCGATT ATCATCATTG TGTATATCT 60
 25 TATTTATAGC AAGTGCATGG TCTGGATAAG TAAAGGTATT CATACTTAAG TAACTTGAAC 120
 ATTGGTTTAG GACTATTTTA ATGGTnCTGC TThAATTGTT GGCCAACTGG TTCTTATTTT 180
 30 AAATATGTAA CTAGCTCTAC GGGTAGTTAC TAAACACATC CTGGTTT 227

(2) INFORMATION FOR SEQ ID NO: 1127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 717 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1127:

CCAATGATAC CGTTATAGCA TGTTAATGTT TTTGTACGAA TATAATCTAA AACTTCGAGT 60
 TCATCACTTA ATTTCCACGT TTCTGCTTTG TTAAACCACA TTAAAGGAGT ATGAATGnCA 120
 45 AAATCTTTGT CCATAGCTAG GCTTAATGTT ACGTTCATTG ATTTTATAAA ACTATCGCGA 180
 CAGTCTGGGT AGCCTGAAAA GTCTGTtTCA CATA CGCCTG TAATAATATG CTTAGCCCCA 240
 50 ATTTGATAAG CTAGAGCGCC TGCAAACGAC AAGAAAAGTA AATTTCTAGC TGGAACAAAT 300
 GTATTAGGTA TACCATCTTC ATTATTAGTA ATTTCCATAT CATGTTGTGT TAATGCGTTT 360
 GGAGTAAGTT GTGATAATAA TGACATATCT AAAACGTGAT GTTTCATTCC TTGATCTTGT 420

AGTTCAACTT CTTTGAAATG TTTTMTGCA TAAAAGAGAC ATGTTGTACT GTCTTGACCA 540
 CCACTAAAGA CAACGATGGC TTTTTCATTA TTTAATACAC TTTCCATTTT GTAATTGCTC 600
 5 CTATCATTA TAATATTAAT AAAGAGGTTA ATGGCATTGA TAAGCCCGTT TTTAATTTAT 660
 AAAATAAAAA AAGCCnATCT CCATAAAAGA TAGACGAnAG AAATGGGTTG CTCCTAT 717

(2) INFORMATION FOR SEQ ID NO: 1128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 595 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1128:

20 GATTATTGCA TTGACAACTT ATATCTATCT AACGTTAGTA GCATTTAATT TCATTTCCGG 60
 GGTTCCTAACT TTACCAGGAT TAGCGGCGTT GGTATTAGGT GTAGGTATGG CTGTAGATGC 120
 CAATATTATC ATGTATGAGC GTATTAAGGA TGAACCTCGA ATAGGTAGAA CGATAAAGCA 180
 25 AGCCTTTTCT AAAGCAAACA AAAGTTCATT CCTAACAAAT TTTGATTCTA ACTTAACAAC 240
 AGTTATCGCC GCAGCAGTAT TATTCTTCTT CCGTGAAAGT TCAGTTAAAG GTTTCGCGAC 300
 AATGTTATTA TTAGGTATTC TAATGATCTT TGTTACAGCC GTGTTCTTAT CAAGATTCTT 360
 30 ATTATCATT CTTGTTTCAT CAAATATATT CAAAATCAA TTTTGGTTAT nTGGTGTAA 420
 AAAGAATAAA CGACATGATA TTAATGAAGG TGTAGATGTT CATGACCTTA AAACCTTCATT 480
 35 CGAGAAATGG AATTTTGTGA AATTAGCTAA GCCATTAATT GGAGTAAGTA TTTTAATTGT 540
 AGTGTGCGTT AGTTATTCnT TATATCTCAA GTAAACTTAG GAnTGAnTCT CAAGT 595

(2) INFORMATION FOR SEQ ID NO: 1129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1129:

50 ATTTTAACTT TCTAAGAACA AGTTGTCAAG ATTTTTCTT AACATATCAT GTTCTGTTAC 60
 AATATTAATA ATGAATACCG AAAGGACGAA TTGCAATGA AAAGCGTTGG CTTAATCACA 120
 GAATATAATC CCTTTCATAA TGGGCATCAA TATCATATTA ATCAATCTAA AAAACTTACA 180

ATCTATAATA AGTTACTCGT GCAAAATGGC TTTCCACCGC TGTTTAGTTT CGGACTACCA 300
 GCAACTGCAG TTATCACTGG CGnCATTTGC GACTGCCGTT AAGCGCGGTT TTGGTGCGTA 360
 5 CATGCnTGGn G 371

(2) INFORMATION FOR SEQ ID NO: 1130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1130:

ATGATGATGA GATTATGACT TTGCGAAAGA TATCGGTGCG CCTTATGAAT TTAAAACAnA 60
 nTAAAGACCA TGGTCGTTAC CGGTAGTTAA CTTTGCAGCT GGTGGCGTTG CGACTCCTCC 120
 AAGATGCTGC TTTAATGATG GAATTAGGTG CTGACGGTGT ATCCGTTGGA TCCGGGAATT 180
 TTAAAACCAG AAGATCCCGG 200

(2) INFORMATION FOR SEQ ID NO: 1131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1131:

ATGAGCTAGT CGATTAAAGT TAATATTTGA AAATGAAGCA GGGCATTAAA TGCAATAAAT 60
 TAAATAAGTT GTCATTAAAG CATTAATAAT AGAAATGATT TTAACAGGAA AAAAGTGATG 120
 AATATTTGGA AAAGATATAT ATCGTGCACT GTCCTGAGAG ATTAGATTTG GGAAACCAAT 180
 TTATCCnTGA ATCGAGATGT nGC 203

(2) INFORMATION FOR SEQ ID NO: 1132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1132:

ATCTAACAGT ATTGAAATCT TTGTTAGCGT CAATCGACCA TGTATTTTAA AGTATTGTCT 120
 CTAACAACCTT AGCACGACGT CTTAACCCCTT TAGTAAACAA TCCTTCTTTA GntTTAGTAC 180
 5 GT 182

(2) INFORMATION FOR SEQ ID NO: 1133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1133:

CAAATTTAGC CAGGnATACA AATACATATA ATAAAACTGT TTGTAAGCTT ACGTTGACAA 60
 20 TCTGGCGTAA TTGGAAAACT AATGAATTTT CTCCAAGTAG GTTTTACCCT GTAAACmAAA 120
 TAACAATTcm AATAATATGr AATCACAAAg CGACTAGAAA TCCGTAATA TGACTAATCA 180
 TATATTCAAT GTGTaaTAAT TTTAACAGCA ATAAATAGAC AACATAATAA TTTAACGTAT 240
 25 TAATGCCGCC AACAAATGATA AATTTTAAAA TTTcAGCATG CGTTTGTGTT AGTTTCATAT 300
 GTGTACTCCT CAACATCana ATATATGCAT AACTACGTTT TCGAACATAC TCGAATATGC 360
 GAGCCAATCC GCTTCACTTC AAATATGCTT ATTTCAATCT TTATACCCTT TCACAGCAAT 420
 30 TTAGTCTCTT ThCCCTCATC CTTATAGGCC nTATATGTAA CCGATTATCG GGTGGACTCA 480
 TTGGC 485

(2) INFORMATION FOR SEQ ID NO: 1134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1134:

CTTGTTTTAT CGACAGATGC TGAACACGCA GTCaAAATAA ATAAATTACA TAATAAAATT 60
 CCAATTAATC TTTTCATAAT ATCATCCTTT TGTTTTCAA TTGATATTCA TTTTCAATTA 120
 50 TAAATATTA rAAGAATTAG TCAACGCCTG TGAGTAATAC ACATCAGTAA CATTtCTATt 180
 TTCATTATG ATATTATCTA ATTATTAATT TAT 213

(2) INFORMATION FOR SEQ ID NO: 1135:

(A) LENGTH: 526 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1135:

10 TGTGACTCCA TGTATTCATG TATCATTTGTA CATTGTGTGAA TTGGTTGAAA ACTGATAGTG 60
 CCCGTTTAAAT TACAGGTACT GAGGATGCTT TCAGGACATG GATTGTGTCG AAAATATGAC 120
 AATATTTTAC TATGGCTCTT CACTTCTCTA GGGAAATTGC TATCTTGATT AATCCAATCA 180
 15 ACCAATTCAC CTAATGGTGT GTCATCACCA AGAAAACCTT GCATAAATTC GTAAAAGCTC 240
 AATACCTCAC CTCGATTaAT ATACTTGAGC CATTaATATA ATACCATAAA AGAATGTGTA 300
 TTTTaCATAA AACTTTTTTaT AAAGCAATTT TATAAATCTA AATTTATTGA ATGTTTAAGA 360
 20 AGTTGTGTAT AATGAAATAA ACGTGTGTA ATAGTTAGGA TGATGTTAGT GGATATCAAA 420
 CATATGAAAT ATTTnATTGA AGTCGTTAAG CAnGGAGGCA TGAATAATGC TTCCAAATCA 480
 TTATATATTG CACAACCTAC AATTAGGAAA GChATTAAAG ATATTG 526

25

(2) INFORMATION FOR SEQ ID NO: 1136:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1136:

35 AGCAAAAGCA ATGATGACAA AAGAACAAGC TATGTTAGCA GATGGAAGTA TTAAACAAGA 60
 TCAATATGAT AAACAACTGT TATCGAnAAT CGGAAATCA CAATTAGATG AATTGTCTTC 120
 40 TAAAGATTTA CAAGTTTTAG CTATTTTTCC GAGAGATGAA TGCAGGAACA GTTTTAGATC 180
 CACAAATGAT AAAAnATGGA AGATGTTTCA TGCAAAAAGA GTATGGCAGC AGTTTTCTCC 240
 45 AGCAACTTTT CCAAnATTAC CCAGGTGTTT AACACGTCCT ATTGGATTTG GGCTTAGGAC 300
 AATTATTCCA TATGGGCGGA T 321

45

(2) INFORMATION FOR SEQ ID NO: 1137:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1137:

5 ATAAATCCTT ATAAAATCAT GAGTTGGACG ACTTATCCAC ACAATTATAC TTTTCAGTT 60
 CTCTATATGT CAAATACCTG TGAATATGTT GCTAAAAATA GTATAACTTT GTGTGTAATT 120
 TCTAATTATC CACAATTCTG AAAACTATAA ATGTGCATAA GTGGATAmCT TTcCTTCTAT 180
 AGAGTATCTG TTAGTGAGTG TATCAAAaCA GTTTGGGAAa TAATTtATAA AGTnTGTATA 240
 10 AGAnCTGTAT AAGGTGTTTC AACATTGTAA ACACTCATGC TTCGGACCAA ACTCATGGTG 300
 ATGTTATGAA ATTTGATTGC TCGCATCGnG 330

(2) INFORMATION FOR SEQ ID NO: 1138:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 459 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1138:

25 CTTGATAAGG GAAGATTTGC CAGCACCATT CGGGCCCATG ATACCAATTA TTTCGCCGCG 60
 TACTGGTATC GATAAGGAAA TGTTTTTAAG TACATGCTTA TTACCTAAAA ACAGATTTAA 120
 ATCTTTTGTT TCTAACAAAC GTTTATACCT CCTAATTAAA AGTTTAGGCT AACCTAATTA 180
 30 ATTGTATAAT AAAGTGAAG TATTTATCAT GTCAAGTAAA TTCGTGATAT AATATAGACA 240
 ATGTATGTGA GGTGAAAGTA TGTTAACTGA AGAAAAAGAG GACTATTTAA AGGCAATCCT 300
 TACGAATAAT GGCATAAAA ACTTTGTGAC AAATAAAATC TTATCTCAAT TTTTAAATAT 360
 35 TAAGCCTCCA TCTGTAAGTG AAATGGTAGG ACGTCTTGAA AAAGCAGGCT aTGTTGAAAC 420
 AAAACCATAC AAAGGTGTGA GATTAACAGA GGATGGTTT 459

(2) INFORMATION FOR SEQ ID NO: 1139:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1139:

50 TAAATACTCT CGCCGGTTAT TTCGCTTCCT CTATACGGAT TGGCGAAAGA TACGGTGCAT 60
 CGGTTTCAAC TAGCAAACGC TCCATTGACA CATGCTTAGC AACTTCTTTA GGCTGTTTAG 120

55

(2) INFORMATION FOR SEQ ID NO: 1140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1140:

ACCTGAATGC CCATCAATGA CAGACTGGAT AAAGAAAATA TGGTACATAT aCACTATGGA 60
 ATACTATGCA GCCAGAAAAA AATGAGGTCA TATCTTTTGT GGGACATAGA TGCAGCTGGA 120
 GGCCATTATA TTTAGTAAAC TAATGCAGGA ACAGAAAAAC AAATACTGCA TGTTCACACA 180
 GCAGGAGCTG AATGATGACA ATTCATGAAC ATAA 214

(2) INFORMATION FOR SEQ ID NO: 1141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1141:

GTTTCTAGTT GTTTATAGTT ATCGCATCTC TTGATGTAAA ATCTAAGATG TTTATGCATT 60
 TCTAGATGTT AATTCTTCGC TGCTTAAGAA TTATCTTGAT GGTAATCTA GTTGTGCCAT 120
 GCATTTTCTC ATGATGAATC TAAGGTGTTA ATTCATTGAT GTGTGCTGTT TCTTGnnGCT 180
 TCATTATCTT GATGGTGAAT TTCGTTGTCT AATGCACTTT TTCAAATGA 229

(2) INFORMATION FOR SEQ ID NO: 1142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1142:

TTATGAATCG TAAACACTAT TATGAAATTG CGAGAGTAGT ATGGACAATT AGAATGATGG 60
 TTTGAGATnA ATGAGTGTTA TTAACCAAGTG CGTCATTTTC AAAATTAGAT GCCATTGCT 120
 GTTTATAATA AGAAGATTG ATAATTAAGT ATGATAAGAA AAAATAATAA TCCCCTAAAT 180

GGTAAATGTG TGAATAGGAA TATCGTTaAA CTAGTTGTGT TCATGCTAAT TTTAGTTGTA 300
GCAGTAGCGG G 311

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(2) INFORMATION FOR SEQ ID NO: 1143:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 403 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1143:

15

GATCATGCTG CTTATGAATT ATTAAAAGAG CAATTAGAAG ATGTGCTTGA TACATTAACT 60

GATAGAGrAG AAAATGTATT ACGATTAGA TTTGGTCTTG ATGACGGCAG AACAAGAACA 120

20

CTTGAAGAAG TTGGTAAAGT TTTCGGTGTT ACACGTGAAC GTATTGACA AATTGAAGCA 180

AAAGCACTTA GAAAATTAAG ACATCCAAGT CGTAGTAAAC GTTTGAAAGA CTTTATGGAT 240

TAATTTATAT CAATTTTAAT GATTGATACC AAGACATGAA TAAGCGCTTA TTTATTTTAA 300

25

GATTAAGATT TAACTTGAGT GAGGTTGGTA CATTGAATAA TGTTCAACCT CTTTTTTCAT 360

AAAGGAGAAT AAAATGATTT CGTTAAATAA CCGATTAAACG ACn 403

(2) INFORMATION FOR SEQ ID NO: 1144:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 612 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1144:

40

nTTTTTATTG ACGAATnGAT TTGGATGCCA GTGGTTTGGT CCTAAATCTT GAATGGTAAT 60

CGGTATTTTG AAGTTGTCAT GTGCTACACG GTAACCGATA CChATAAGTA CGAGTGCGAT 120

GACAATGGTT GTTACGAGCA AGATGTATTG TAACCATTGC TTGAACACAA CAAGTTGTAT 180

45

ATAAGGCTTC ATTGACGATA CCTCCAAACC AATACAGCTA AATTAATTAT CAAAAGTGCG 240

ATGAAsCTAA GATAGAAACT AGGGTGCAGT TCTAAAATGT AGTTGTTTAA AATAATTTCT 300

50

AACAATTGAT TTGTTACAAC TGCGAACGGT TGAATATTGA AAACACCATT TGCTATATGT 360

TGTAAAAAAA TCGTAGGTAT TGTTAAACCA GATAACACCA GGATGACAAT AGCTAATATG 420

ACTTTACTAA TACTATTCAA CAAGCCTGTT GTTAAAAGTT CGATGAGTAA TAACCACAGT 480

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AAGATATTCG GAATACTGAA CACAATCCAA ACTACACCAA CGATACTCCA TAACATAGTA 600
TAAAACCATG Tn 612

5 (2) INFORMATION FOR SEQ ID NO: 1145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1145:

GAATTAATTA CGCAATATCC GCATCTTAAA TCAGTAATCG AAAAATATGC TTAAAAATAA 60
 AAGTGATCAA TGAAGTGGTT TGAAGGTTGT nAATAAACCT TTGAGTCACT TCCATTTTTTA 120
 20 AAnGTATCCT GGATGGAACC AGAATAGATT TGAAGCTTCA GCGGTTTTTA ATGAAAATAG 180
 CCATTAAATG ATTTGGAAAC GGTAAGAGGG GGTATTTAAA ATG 223

(2) INFORMATION FOR SEQ ID NO: 1146:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 598 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1146:

CGCTACGGTT GTCACGTAGA GATTAAAGAC ATTCGTTTTA GCAGTCTTTT TTATTGAAGT 60
 35 AGACAATGCA AGATTAAATG GTAGTGT CAT TTCATTTTAT TCAACTGCTA GTAATACAAT 120
 ACTCAGTGTT ATTTCTGAAG ACTGGTTGAT AATGAGACAT GCATATTTAC AAAACTGTGT 180
 40 ATATTGTGTA TATTGTATAT ATACAGAAGT TGATAGGGGG ACGTTGATGA AAATAATTTT 240
 AAAAAACAAT AGTGATTTTC CGATTATGA ACAGATTAAG CAACAAGTAA AACAAAATAT 300
 TTTAAAGGGA CATGTTGCTC CTGGAGAGCA TTTGCCGTCA ATGAGAGAAC TTGCCAAAGA 360
 45 TCTTCAAGTA AGTTTGATTA CTACCAAACG TGCTTATGAA GATTTAGAGA AAGACGGTTT 420
 TGTTACAACA ATTAGAGGAA AAGGGACCTT TGTTAAGGAG CAAGATAGTT CTATTTTAAA 480
 AGAGAAACAA TTTTTTACCA TGAAAAATTG GGTAAAGGA ATTGGGTAA TTAAGCnCAA 540
 50 GCCCATCCGA ATTGCCACTT GAGGGAnTTC CAGGATATTT nACCGTCATT TATTGAGG 598

(2) INFORMATION FOR SEQ ID NO: 1147:

55

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1147:

10 CAAATCCAAG TGCAACAGCT TTATCAACCG CTAAAGCTAA ATCCGTATCA GCTTTTTCAG 60
 CTTGAACTGG TTTGATTGT AACTGTTCTG TTAGAAGTTG GCGTTCCTCT TTAGTGACTG 120
 AATCAAAGTC TCCCACTGAG AAAAAAGGGA TAATTTGATG CTTCAATAAA ATCAAAGCAC 180
 15 CTCTATCAAC GCCGCCCAT TTACCTTCAT TACTTTTGGC CCAAATATCT TCGGCAAGT 240
 GTCGATCAGA ACATAATAAA TTTATATGCA TATACTCA ACCTTTCAAT GCTTGTGTGA 300
 CTTTTTAAAA TCCCCTGGT AAAGGAAAAT GAACnGGTTA CCAGCATTGT AGGCACCATT 360
 20 TCAACACCAA CTTGGCGGA TcngGATTAC GCCTCCATCC 400

(2) INFORMATION FOR SEQ ID NO: 1148:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1148:

TTTTATGGGT CGTATTTTTT AAAGAACAGT CATCTCAATC AAAAGAATAG AATTATGATT 60
 35 AAAATTGATG TrGTGTAATT AAAGTAAGAA ATrrkAAATT TCCTAGATAC TAGATAAATC 120
 GTTCAATATT TTATTAATAA GGAGGCCAAT GAYTGTGAAT TATCTTAAAC ATAAGTTTAA 180
 TAACTTGTTA ACTACAATGA TTGTTCTCTT TATTTTTGTA CTTTCTGGTG CGATTTTTTT 240
 40 AACATTTCTA GGGTTTGGTT TATATGGATT AAGTAGAATA CTTATTTATT TTAGGTTGGG 300
 TGACTTTACA TATAATAGAA GTATGTACGA TAACCTATnA TATTATGGCA GT 352

(2) INFORMATION FOR SEQ ID NO: 1149:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 916 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1149:

55

GGCAAGTGTC GATCAGAACA TAATAAATTT ATATGCATAT AACTCAACC TTTCAATGCT 120
 TGTGTGACTT TTTTATAATC CTCTTGTTTA AAGAAAAATG AACCTGTTAC TAGCATTGTA 180
 5 GCACCATTTT CAACACAAAC TTTCGCTGTA TCGGTATTTA CGCCTCCATC AACTTCAATA 240
 TCAAAGTTTA ATTGACGTTT CATTTTAATA GCATTAAGAC CCGCTATTTT TTCTACGCAT 300
 TGATCAATAA ATGATTGACC ACCAAACCCCT GGGkTAACTG TCATCACTAG TACATAATCA 360
 10 ACAATGTCTA AAATAGGkTC AATTTGTGAT ATkGGkGTAC CAGGATTAAT TACTACACCA 420
 GCTTTTTTAT CTAAATGTTT AATCATTTGA ATAGCAGCAT GAATATGAGG CGTTGATTGG 480
 ACATGAATTG AAATCATATC GGCACCATGT TCTGCAAATG ATGCAATATA CTTTTCTGGA 540
 15 TTTTCAATCA TCAAATGTAC GTCTATAGGT AATGTTGTGC CTTTTCTTAC TGCATCTAAT 600
 ATTGGTAAAC CAATAGATAT ATTAGGCACA AATTGACCAT CCATAACATC AAAATGAACT 660
 20 CCGTCGACGC CTGCTTCTTC AAGTCGTTTT AATTCATGTT GTAAATCCAA AAAATCAACA 720
 GATAATAATG ATGGATATAG TTTTGTCAAT TAATATCTAA CCTTTCTATT TGAAATTTCA 780
 TTAAATAGTT GTAAATAATG GTCGTATCTA AATTGCGCAA TATTCCCTAT CTCTAATTGA 840
 25 TGChTAACCA TTACCATTAG GGTCTTGGn AAGGnTACCA ATCCCAAACC TTACCATGGT 900
 TCCCCCATAA CGGTTT 916

(2) INFORMATION FOR SEQ ID NO: 1150:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1150:

40 AATTGGTTGT GGCTTCATAA TGTGCAGTTG CTAGACTGAC AACACATCG TTTTCTAAGC 60
 CTACGATAAA GACATAATCG TTTTCGGTTT TGTGTTTTTC TAATGAGCGT TTGATGATAC 120
 GTTTATCTTC AGTTAAAGAT AAATTTAACT TAGTATCGTA AAGTTTAAGT GCTTCGTTGT 180
 45 AATGTGGATC TTTGACAGAT TGAATGGTTT TAAATCCAT AAGAACACCT CCCCAATTTA 240
 AATAATATTA TAGCATAATC GCCTGCTGTA AAAGACTGTT CATAAACTTT TAAATGGTAT 300
 AAAAaACTGT ACTATCTTAA ATTAGACAGT ACAGTAATCT CATTTTGAAT TCAGTGTGAT 360
 50 AACTAAGCtT TGGGACCTTT AGATGChTTC ACAAATGTG 400

(2) INFORMATION FOR SEQ ID NO: 1151:

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(A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1151:

10 CACCGTAGTT GCTACCGAAT ACCACCATGT CGCCAGGTTG TGCTAAGAAG TCCGGTGTAT 60
 TTTGGTATAC AGTTAGCTAA TCCGTCGAAG TTGTTAGCGA CGGnATATCT TTTGACCTAA 120
 ACCTTTTAGA GTAATCCAAA CAAACTTTTC CAACCA 156

15 (2) INFORMATION FOR SEQ ID NO: 1152:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1152:

25 TCAATATATT TATTTTCTAA TGTTAGCATT AGACTGTCAA TTAAGTTGCT AAGTTGTTCT 60
 TTTTtagTAA TTAAATAACG CATATAATCA TCTAAATTTT TCATTTTTC ATCTAGCATT 120
 30 AAAAGGTAGT GCTTGATATT ATTTCTACTG TTGCTCCAAA AACTGnTCAA ATATACGTCA 180
 CATAGTCATA CTACACCTTT ATATAGTTTA AATACCAATn GCATGACCTC GTG 233

(2) INFORMATION FOR SEQ ID NO: 1153:

35

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1153:

45 TATATTAnCT ATCGTTTtagT GAATCGTTTT TTAAAGTAA AGAGAATTTTC ATATATTACT 60
 GGTACAACCTA CAAGTGTTAA TAAAGTTGAT GAAATTmAAC CACCAATAAC TGTAGCAGCT 120
 AATCCTTTTCG AAATAAGAAT CGnGCTATCT TGACCAAATA ACAnAGGAAC TAATGCACCA 180
 50 ATTGTTGCAA TCGCCGTCAT TAATATCGGT CTAATTCTAG TACCGCCTGC TTCGATTAAT 240
 GCTTCTTTCA TCTCCATGCC CTGTTGCTCA TTATTAATAA CACGGTCTAT TAACACAATG 300
 GCATTGTGTA CTACGATnCC AATTCAACAT TAGCATACC 339

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1154:

10 GTCACCCGAG GAGATATnCA ACTATTACCA TCAAGATGnG AAAAATGGTg CCTTGGGCAA 60
 TTGGTTTTTTT CATTTTAATC TTAATTATTA TATTGTCTT TTTACTAAGA AACTTCAATT 120
 15 CACCTGAAGC GCAAACATAA ATATTAGTGA ATGCGATTGA GAATAATGAT AAACAAAAAG 180
 TAGCAACATT ATTAAGTACT AAAGATAATA AAGTAGATTC TGAAGAAGCA AAAGTATACA 240
 TTAACATATAT CAAAGATGAA GTTGGGCTTA AGCAATTTGT CAGCGACCTT AAAAATACGG 300
 20 TACATAAAAT GAATAAGAGT AAGACCAGCG TAGCTTCTTA TATTCAAACC AGATCTGGTC 360
 AAAATATATT ACGTGTAAGT AAAAATGGCA CACGTTATAT CTTTTTCGAT AATATGAGCT 420
 TTACTGCACC TACCAAGCAA CCAATTGTTA AACCGAAAGA AAAACAAAAA TATGAGTTTA 480
 25 AATCTGGTGG TAAGAAAAAG ATGGTTATAG CTGAAGCAAA TAAAGTGACG CCAATAGGTA 540
 ATTTTATACC GGGGACATAT AGAATTCCAG CTATGAAATC AACTGAGAAC GGTGATTTTG 600
 CAGGCCATTT AAAATTTGAT TTTAGACAAA GTAATTCTGA AACGGTAGAT GTTACTGAAG 660
 30 ATTTTGAAGA aGCAAATATA TCTGTAACCT TAAAAGGCGA TACAAAATTA AATGaTAGTT 720
 CTAAAAAGT AACTATAAAT GaCCATGAAA TGGCATTTTC AAGTTCCAAA ACGTATGGTC 780
 35 CATATCCACA AAATAAAGAT ATTACCATTT CCAGCTT 817

(2) INFORMATION FOR SEQ ID NO: 1155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1155:

45 AnAGAAAATC TACTCTTTTA TTTCACCGGT CCTTTCnTAT CTCTCATTTG GCATACTCCT 60
 50 TTTTCCATAT TTTCCACTTT CAnTACAGTG AATTTACATG TAATTTTACA AATACAATAG 120
 GAGTGCACAA TGGAATATAA CACTTATCTT TATAAAATTA TTTTATATAT TGaCGCACTT 180
 AAAACAATCT ACAAATAAAA TTATTATTTT TAGTTTTCAA TGAATAATTC ATTCTTATCT 240

ATTTAAAAAT ACATTTAACT GC

322

(2) INFORMATION FOR SEQ ID NO: 1156:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 777 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1156:

15 GTTTCCAAnG GAAnGnGAAA AGCGTCAACC AATGTAActA TTTAAAGTCA AAGTGTtTGA 60
 CCAAATtTGA CTTAATATGT AAAATAATGA GTAACAGTTA TTACAAGGAG GAAATATAGA 120
 TGAATtTAAT TCCTACAGTT ATTGAAACAA CAAACCGCGG TGAACGTGCA TATGATATAT 180
 20 ACTCACGTTT ATTAAAAGAC CGTATTATTA TGTTAGGTTC ACAAATTGAT GACAACGTAG 240
 CAAATtCAAT CGTATCACAG TTATTATTCT TACAAGCGCA AGACTCAGAG AAAGATATTT 300
 ATTTATACAT TAATTCACCA GGTGGAAGTG TAACAGCTGG TTTGCGATT TATGATACAA 360
 25 TTCAACACAT TAAACCTGAT GTTCAAACAA TTTGTATCGG TATGGCTGCA TCAATGGGAT 420
 CATTCTTATT AGCAGCTGGT GCAAAAGGTA AACGTtTCGC GTTACCAAAT GCAGAAGTAA 480
 TGATTCACCA ACCATTAGGT GGTGCTCAAG GACAAGCAAC TGAATCGAA ATTGCTGCAA 540
 30 ATCACATTTT AAAAACACGT GAAAAATTAA ACCGCATTTT ATCAGAGCGT ACTGGTCAAA 600
 GTATTGAAAA AATACAAAAA gACACaGATC GTGaTaaCTT CTTAActGCA GAAGAAGCTA 660
 AAGAATATGG CTTAATTGAT GAAGTGATGG TACCTGAAAC AAAATAATTC AAAGTAAAGA 720
 35 GTAGACTAAG CnGTCTGCnC TTTTGTATG AGTAAACCAA GGTGTCAATA ATTTGTn 777

(2) INFORMATION FOR SEQ ID NO: 1157:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1157:

50 TAATGTTGGT AAATGGGTTA AGGCTCAAGG TCGTATTGAA GAAGATACAT TTATTAGAGA 60
 TTTAGTTATG ATGATGTCTG ATATTGAAGA GATTAAAAAA GCGACAAAAA AAGATnAGGC 120
 TGAAGAAAGC GTGTAGAATT CCACTTGCAAT ACTGC 155

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1158:

10 GACTGGTAAA ATTTACTTGC AAGTAAAGCT AAAAGGTCAA ATAGATAAAG AACAACTTGT 60
 TTTTCAAAAT GACAAAAATG AAGAATTTCC TTTTGTATA AAAGATGAAA AGGATGACAC 120
 AATAGTAAGA ATTTTAATTG AACAGCATAT GGATAAAATC AATATGCATG TTAAAACGTT 180
 15 GGCTGAAAAG AAAAATCTAG ATAACAAAGA AATGGTGTAT TCTATTCATT TTAAAGAGAA 240
 AAAAGTACAA CATGATGATG CAAAAGAAGT GCCTTCAAAA CATCAAAATC AAGAAAATAA 300
 TCAAGATCAG CTTAAAAAAG ATATTGATGA CAAAaAAGAT AGTCAAAAAT CAGATACTAA 360
 20 GGGAAAGACG TACTAGCCTT TTTACTGGAA AAAGGGTTTA 400

(2) INFORMATION FOR SEQ ID NO: 1159:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 347 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1159:

35 GTTGGTACAG TGTTGAGTGG CTTTGAATAT CGAACACAAA AAGAAAAGTA TGACAATTTA 60
 TATAAATTTT TCAAAGATAA TGAAGAGAAA TACCAATATA CAGGCTTTAC AAAAGAAGCA 120
 ATAACAAGA CGCAAAATGT CGsATATAAA AATGAATATT TTTATATCAC TTA CTCTCGTCA 180
 40 AGAAGCTTAA AAGAATATCG TAAGTATTAC GAACCATTsa TTCATAAAAA TGATAAAGAA 240
 TTTAAAGAGG ATGGACCAGC CAGAAAGAGT GATTACGCGC TATCAGTCAG TACACATGTT 300
 AGTCCAGGAA TTTCTAGCAT CnGTGTGTGA ATGAnGGGTA CTTTATn 347

45 (2) INFORMATION FOR SEQ ID NO: 1160:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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ATAGTTATTA ATTAGTAGAA TGAGGATATT TAAATATAAA GGATAGTGTT GAACTTATGG 60
 ACATGAATTT CGATTATACA TGAACGGTGT TGTAGAACAA GCAAGGAATG AAATTGAATC 120
 5 TCGGGGATAT GAGCAATTAA CTA CTACTGCAGA AGATGTTGnA AAGTCCAAGA TGGnCACCTA 180
 GTTATGATCA TCTGTATGTG GTG 203

10 (2) INFORMATION FOR SEQ ID NO: 1161:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1161:

AATTTTCcNt TTCCATTGAC ATAACAATAT TTAATGGGGC CCAGTTACAG GAAATATCAG 60
 TTTAATTTTCG TCTTCAATAC CATAGTCATA ATATTGAGTT TCTTGTGTTG GAAAATTTCC 120
 25 TACATAGTTA CTCATTTTAA TTTGTnCAAT GTTTGAATTC GGAGGCACTC TGTTAGCATA 180
 TCTTTAAACA TTAAATATGG ATA 203

(2) INFORMATION FOR SEQ ID NO: 1162:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 220 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1162:

GCCATTTTGT TGATAAAGGT ATACTAAAGG TTATCGTTTT GAAATTTTGA GTAAC TAGGA 60
 40 TATGTTTCGT GTTATAGGAC CGGAATTTGT GGTATACGGT AAAATTTTAA TGCTATTGGA 120
 ATTTTAAAA ATGGAAAAAC ATGGACATTh AAATTGGAAT TTCATAATAT GTCCTAATTG 180
 45 GACTTAACTT GTTGGGAGTT CATTTTACTA TTnTATGGT 220

(2) INFORMATION FOR SEQ ID NO: 1163:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 409 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

TTCACGTGCT TTGCCATCTT TTAAGAAAAA CACAGAAGGC TTTTGCAATT GATTGTAATT 60
 GGATGCCATA GAGTAATGAT ATGCACCAGT TGATAATATA GCAAGATAGT CTCCACGTTT 120
 5 GACTGGATGA AGGTAATTTA GCGTCTTTAA TAATGATATC ACCAGACTCA CATAATTTTC 180
 CAGCTATAGT TACACTGtCA TCTGCTTCTT CATTTCTATT AACAGCAAT GCTTGATACT 240
 TTGCGTCATA AAGTGCAGTT CTGATATGAT CACTCATACC GCCATCGATT GAAACATATT 300
 10 TATTArTCTC TGGAATTTCT TTAATGGtTC CAACTTCATA TAAAGTAACG CCAGCtTCAC 360
 CTACAATTGA TCGTCCCGGT TCAATACCTA TTTCTGGTGC ATCTATACC 409

15 (2) INFORMATION FOR SEQ ID NO: 1164:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1164:

25 CTAAATAATT GTTAAATTT TTCTTTACTA TTTAGACTCT TTCGTTTGCC ATGACTTTGT 60
 TGACTTGCAA TGATATGAAC TTAATTTTTG CGAAAAAGG AATCTAGATT CATATATTCG 120
 30 GTAAATCTAC CTCTTCATC TTTTGAAGT TGTAATTCTA GCAATTCACG TTGTATCAAA 180
 TTTTGAATAA CCATTGTAAT ATCACGTGGT TGCATAGTTG AGCCCTTCTG AAGCAATTCA 240
 ATTGAAGGCG TTTATTTGAG TTTCAAGCA TAAATCAATT TAAGCAAAAG ACTAAATCTG 300
 35 CTCATCTAAA CCTAAGTCAC GTAAGGTCTA ATAATCnCTC GTATCACTAC GGTCTGCTTT 360
 AATGATATTA nCCAGTnCGT GCCCCTTTAA ATTAACCAaA 400

40 (2) INFORMATION FOR SEQ ID NO: 1165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 327 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1165:

50 TCGTGATTAT TATTAACATT TTTTAGTAAT TGATAAAAAT CTTTCTCGC TTCTGTAGGG 60
 CTAGTGATAA TCATATAAAC CCTCCTTTGT TTTCTGTTAC GCTAATTATA GCGTACGCAC 120
 TTGAGTACGT CATATTACCA ACGAGTTCAT CGTATnCTTA ATACCTATAT GCTATCGTTC 180

55

GGACACACTA CCGTnCCCTA CCGCTTAACC ATTTTCGGGC TTAAATATTT TnAAAATTTT 300
 GTGAGGATCC GCTTAAAAAA CCCATA 327

5 (2) INFORMATION FOR SEQ ID NO: 1166:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1166:

TTAGGATTTC AAAAATATGT CAGGTTTCT AACATAAAGC TTAAACATT GATATAACTG 60
 CGATTTTCGAC TTCTAAAACG aCATrAAACA ATCTACAGCT AAAATATTTT TTCAATTTT 120
 20 AAAAATAATC nGATAAATCT CCGCAAAA 148

(2) INFORMATION FOR SEQ ID NO: 1167:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1167:

nAAGGTTATC GCTCGTAAAG ATGTTGTTGA AGAAGTATTT GACGACAGAG ATGAAGTGGA 60
 35 TTTAAGTACA GCGCTTGTTA AAACCTGCA TATGAAATTG GTGTATTACG AGAAGAGTAC 120
 ACTAAAGTTT TGGTCGTGTA GGTCTCAGCA GCGAACAGCA GTATGCACGT CTnCGTGTGC 180
 TGACGTGAAT TTTATTTGAG GATTATAGAC AAGAGAGACA ACTTACTGGA TTTTGCCCTG 240
 40 TTG 243

(2) INFORMATION FOR SEQ ID NO: 1168:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1168:

TTATATACTA CTATAAAGTA ATCCAATCT CAAGAAGGTA AATGGGCAAT CAAAAGCTAA 60

55

CTACGATATG ACGCACAAAT GTTTAGGGTA GGTGTTGACA TGTGTACAAA AACCAGCAGA 180
 AAATGGTTGT ATTCTTAGGG AAGCATTTCAT CCTGTTTGTT TATGGATTCA TGTTACGTTA 240
 5 CGCAATATGT TTTTATGTAG CACAGCGAAG TTACAAGTTT ATACGCTATA TATCCnTTGA 300
 TnATAAGCAG ATGAAAnCGG C 321

(2) INFORMATION FOR SEQ ID NO: 1169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 191 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1169:

20 TCTACATATA AAATTACTCT AAAAATATGT ATAGTCATAA ATTGTTGGTT GATTTAATTA 60
 AAAGTATGGA AATTAAGGGG CTCTTATGTA TATAAAAAA TGAATTATGA TAAATGTAA 120
 GAnAATATTT AGGGTCGATT GGAGAGATAC CAGTGGTACC AATTAGAAGA CGACAGTTTA 180
 25 ATGTTACCAT A 191

(2) INFORMATION FOR SEQ ID NO: 1170:

- (i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1170:

AATGTGGCAA GGATGTGTGA TATGACTACA CATTTAATAT CATCCTACAT AATAATTTTG 60
 40 CGCGCCAAAT TATCACACAT ACCACACCTA CGATAACAAC CAGCAAATAA GGAGATAGCT 120
 ACACGTATTT ATCGTCCAAC GCACTACTAT ATGTTGTTGn ATGGGCACAA GTTACAAGTG 180
 CTGCGCGATA nCAAAAGGTA TACCCCTAAA ACGTCCCAA AnAATCGGTT GCCCTCTAAA 240
 45 TTGTTTGTGT GCCATGATTA GTAAGCTCCT ATGTTAGAAA CAAATTTTTA ATATGTATAT 300
 TAG 303

(2) INFORMATION FOR SEQ ID NO: 1171:

- (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 299 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1171:

5 AAAAAAGGTGA GAAGACAATA ACGnACGCCA AACTAAAAA ATCCATTAAC TGGAGAAATT 60
 ATTAGTAAAG GTGAATCGAA AGAAGAwATC ACAAAGATC CAGTTAATGA ATTAACAGAA 120
 10 TTCGGTGGCG AGAAAATACC GCAAGtCATA AAGATATCTT TGATCCAAAC TTACCAACAG 180
 ATCAAACGGA AAAAGTACCA GGTAACCAG GAATCAAGAA TCCAGACACA GGAAAAGTGA 240
 TCGAaGAGCC AGTGGATGAT GTGATTAAAC ACGGACCAA AACGGGTACA CCAGAAACA 299

(2) INFORMATION FOR SEQ ID NO: 1172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 821 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1172:

25 CCATAGCACC ATACCCATAA CCAACCCGGA TCCACTAACA AATAAGTAAT AATTnACACG 60
 TAAAGAAGTA AATAGTTTGT TTAGTTTTTT ATCAACATTA TCAATGTTTT CCTCGACAGA 120
 30 CACTGGAATT TTAACGATAG CTGTACCATT TGTAATTGAG TAGTTCGTTA TTTCACCCAT 180
 ACTACTATTT GGTAaaATTG TTAATTCTCC TGAAATTGTA TTGATTCTGT TTGAACGAAG 240
 TCCAATTGAT TTAAGTCTC CCTCTGCTAC AGTTGTACCA CCGTTATTTA TCTTAACATA 300
 35 ATCACCTACA TCAAATTGGC TTTCAAATAT AATAAAGAAT CCTGTAAtTA CGTCTTTAAC 360
 TATAGTTTGA GCACCAAAAC CTACTGCTAA GCCTACGACA CCAGCACTGG CAATTACCCC 420
 TTCAACACTA ATGCCAAATT TACTTAAAT CGTCGTAATA ACTATAAACC AAACGATATA 480
 40 CTTCACTACA TTTTGAACAA GAGATATTAA AGTTTTAGAG CGCTTTTTGT TACTCTTTTT 540
 ACTTTTATTT TGAATCTTAA ATCCCTGTTC AATCATTTTA TTCAGTATTT TAATAACTAT 600
 GAGGGCTACG ATAATATAAA TAACAATCAT AGCGATTTTA GTTGCAATGT TTTCATATGT 660
 45 TTCTATTTTT GTTAATGGCT CAAATAGAGA TGAAATAATA TTCATGACTT GATTCATGAT 720
 AAGCGTACT CCCTTCTATA TGATATATCA ATATTGtATT CATATTTtga TATACTTCCC 780
 50 AACCTACGAA AGTCTCAATA TATCTAGAAT CAAATGGTCA C 821

(2) INFORMATION FOR SEQ ID NO: 1173:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 318 base pairs
 55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1173:

	CCCGAAATTA AAATAATAAT GTATGAATTT TTAAATATGA TTTAAACGTT TTCAGTTTTT	60
10	ATGAAAACGC ATGCATTTTA CAAATAAAAA TGGTACGATG GCACTGGTTA AAACGTTTTA	120
	CTAAAAACAA ATCATGAGGT GTATAACATG GCTGTCTCTT GATCAGATCT TGATCCCCTG	180
	CGCCATCAGA TCCTTGGCGG CAAGAAAGCC ATCCAGTTTA CTTTGCAGGG CTTCCCAACC	240
15	TTCCCAGAGG nCGCCCCAGC TGGnCAATTC CGGTTTCGCTT GCTGTCCATA AAACCGCCCA	300
	GTCTAGCTAT CGCCATGT	318

(2) INFORMATION FOR SEQ ID NO: 1174:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1174:

30	GTTTTAAAGC GGTATAAAG GTAAATATGC AATATTATAA ATATCTTCTT CAGAACTAAC	60
	CGAATCTCTT AAATCATCT GTTTAGATAG CGTTTCAAAT TGATAAGTTT TAATTTTAAC	120
	CGTTACAGTT TTAGCTGACT GCTGTAATTT ATTTGACGTG CAGCTGTTTT CCTGACAATn	180
35	CCATACTGTC TTAAAnCTCT GCATCA	206

(2) INFORMATION FOR SEQ ID NO: 1175:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 653 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1175:

	TCTGCATCAT GATATTTTAC ATCATCACTT ATAAGAACGT CACCTACATT TAAACTTTCA	60
50	TCTAAAGCTC CAGCAGAACC TGTATTAATA ATGACGTCCG GTTTAAACTT ATTAATTAAT	120
	AATGTCGTAG AAATTGCAGC ATTAACTTTT CCAATGCCAC TTTGGGTAAT CACTACTTCT	180
	CTATCTTTTA AAATGCCAGT ATAAAATTTA ACATGTGCAA CTGaAATTTC GCTTAATTGT	240

55

TTTTGATTCA CCTCTTTTAA AAAATCCTAG CATTTGTTAT TTTATCACAT TTTAATCACT 360
 ACAACGACAA GTATCATGAT TTTCATTACT GTATAAACT TTTGCTTTAT TTTTATAAAA 420
 5 AGCTCTTTCA ATAAGTTGGT ATCATAAATA ATTATTTTGG AACTCATAAC AGTGAATTCG 480
 ATGCTTCTAA TTTGTCTATT TTCAAAAAC TAATCATATC AATTACATCA ACCAATCGTG 540
 TCAAGAACT TTATTAAATA ACAGGAAAAT GATATGTTTA AAATAATAAT GATGAAATAA 600
 10 GAGGATTTTA CAATGGCTGA AAATAATCAA AATAGTCTCG TAACAAAGAT AGC 653

(2) INFORMATION FOR SEQ ID NO: 1176:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 410 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1176:

ACATGGCCGT TnGnATCAAG ATCGTCAACG ATTGATTGGT ACAATTGAAG TGCCTATGAC 60
 25 ATTGGCAACC GTTGGCGGTG GTACAAAAGT ATTACCAATT TGCTAAAGCT TCATTAGAGC 120
 TACTAAATGT AGAGTCAGCA CAAGAATTAG GTCATGTAGT TGCTGCCGTT GGTTTAGCGC 180
 30 AAACTTTGTC AGCATGTGCG GCGCTTGTGT CAGAAGGTAT TCAACAAGGT CATATGAGTT 240
 TACAATATAA ATCATTAGCT ATCGTTGTAG GGGCAAAAGG TGATGAAATT GCTAAAGTAG 300
 tGAAGCTTgA AAAAGAACC CCGTGCAAAT ACACAAGCAG CGGAACATAT TTTACAAGAA 360
 35 ATTAGACAcA ATAGTAAAGG CGATAGCGAT TaaAGAAAGT TAAGTCAGTC 410

(2) INFORMATION FOR SEQ ID NO: 1177:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 146 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1177:

CATCAAGATA ACTACGGTTA TAATCCAAAC GACCCAACAT CATATAACTA TACTTACACT 60
 50 ATTGATGGCA CAAGGTAAC ACCATTACAC ATGGGAAAGG TAACTnGCAT CCAAGTCAAT 120
 TAAACCAAGA TAATGGCTAC TACAGC 146

(2) INFORMATION FOR SEQ ID NO: 1178:

55

(A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1178:

10 TGTTCCTGGT GGAACCTTGG TTTCTTAATG TCATTCCAAA TTGCTGTATA TTCATTCAAT 60
 GGTATTGAAC TTATAGGTGT ACTGCTGGTG AACGAAAGAT CTGAAAAAAC CTTACCGAAG 120
 CAATTAATAA TGTACTATCC GTATTTATAT CTATATCGTG GTnATATAAT ATGTCATCAA 180
 15 CTGGATnTAC GTCAATAGAC CTTCGTAACC TTAATATCGC GACAT 225

(2) INFORMATION FOR SEQ ID NO: 1179:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1179:

TGTACGCATA TGGTATCACT TGATGACCAA TTCACTTTGT CGAGAATAAC GTTATTTAAA 60
 30 GACATTGATT TAAAGAATTG GTATTnCGTT AATTGTATTA GACTTTTCAC AGAAGTAGCG 120
 ACAACAATGA TTTTCATCGTA ACACGTGCGC ATATnAAGCA TGGGAAAAGA CATGGnCTAT 180
 TGACCTGGCC TTTTGTGCAC TCGTACGATT GGTCAAACGT GGCTATATTG AAAGTTTGAA 240
 35 ACAAGATGCG ACGGACACAC ATGCACGGGT GGGGATAGAT CTTGAGTCTT ATTGAGACGC 300
 TGTGACTGTG GCTGACATC 319

(2) INFORMATION FOR SEQ ID NO: 1180:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 654 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1180:

50 TTTTATCTTG GTTTTGAAC AGATATGTGT AGTCAGGTAT AACATAATCA ATCCCTAATA 60
 AGTTATCATC AGGGAATTTG ATACCTGCAT CGATAATGAC AATTTCTGTCT TTATACTCAA 120
 CTGCATAAGT ATTTTTACCG ATTTACCTA GACCTCCAAG TGCATATACA CCTACTTCAT 180

55

TTCGTAATCT AAATGTGCGC CCTCTAATTT AGTGATAAAT TCGATATTAA AATTACGATC 300
 TTTCAAGTAA CGACGTACTT GTTCTTCTGT TTGAGCTTCA ACATAAAGTG ATTGTGTATT 360
 5 TTCACGCACA ATTACCTCGT CTCTGTTATG TTGATAaAAA ACTTTAAATA CTGCCATGTT 420
 AAAAAATCCT CCTAAGAATG TTTGTyTAAT TTATTGTTAA CCCTAGtAAA ATCGTATTGG 480
 AGTATATATC GATAAATTCA TTCCAATCAT CTCTATAATG TAACTTAATA ACGATTGGT 540
 10 TAATAACTAG GTTCATCATG TCGTTCATTT TAAAAAATTA GTGAAATAAC ACTAAAATTT 600
 CAGTTAAATC TTATTTTACA TGATGAATGA TAATAAATAA AGCAGTTTAT CTCA 654

(2) INFORMATION FOR SEQ ID NO: 1181:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 231 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1181:

25 CGGGTATATT ATAGACAACG TTTAAGGACT TCTTTTAAAC TAACTTGTTA AATGTTGCTG 60
 TATTTTGTGA TTCAACACTG TAATATAGTT CTTCTGACGC TGATGCATTG CTCATTGTAA 120
 TAGATATTAA AAGACTCAAT ATTATTAAAC TAATAATAGC GCGCTTTATG ATTTTCATAT 180
 30 TCTAATCTCA AATGAATTC AGAACTTTAT ATGTTTCAGG TGCGACAACA T 231

(2) INFORMATION FOR SEQ ID NO: 1182:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 245 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1182:

TAAGTTTATT AAGCTCTTGT CCGTTAGCAA TCACGCTACC GCTAGAAATT TGGTCAATTG 60
 45 AACTTAGTAC ATTTAATAAG GTTGTCTTAC CTGATCCAGA AGGCCCCATA ATCGCACGAA 120
 TTCGCCTTTT TGTATGTCAA GTAATATCTT AGGCTGAATG GTGCTTTACG AGTTTGAACA 180
 GTGCCGAAAA CGCAAGCCCC TTGATATCTT AAATGTGGAG ACTACAACnC ATCAGTGnCA 240
 50 CGGGA 245

(2) INFORMATION FOR SEQ ID NO: 1183:

55

(A) LENGTH: 490 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1183:

10 AGGTAAAGAT GATGGTGTAG AAGTTTATGT GCATTGCGAA GATCATGGCA TTGTATTTAA 60
 TGCAAGTCTA CCTTTGTACA AAGATGCCAT CCATCAAAAA GGATCAATGC GTAGTAATGA 120
 CAACGGTGAT GATATGAGTA TGATGGTGGG TACAGTGCTG AGTGGCTTTG AATATCGAGC 180
 15 GCAAAAAGAA AAGTATGATA ATTTATATAA ATTTTAAAAA GAAAATGAAA AGCAATATCA 240
 ATATACAGGT TTTACTAAAG AAGCAATTAA CAAGACGCAA AACGTCGGGT ATCAAAATGA 300
 ATATTTTAT ATTACATATT TATCAAGAAA TTTAAAAGAA TATAGAAAAT ATTACGAACC 360
 20 ATTGATACAT AArCAATGAT AAAGAGTTtA AAGAAGGTAT GCAACGAGCT AGAAnAGAGC 420
 TAAACTATnC TGCTAATACA AATACTGTAG CAACGTTGTT TAGTACGAAT GATGAAAGGA 480
 ATAGAAAAGA 490

25

(2) INFORMATION FOR SEQ ID NO: 1184:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1184:

CTCGCATTTT AATAAATCAT ACTCTTCTTT TCTTGCATAC GAATTAGAAT AACTCGCGAG 60
 ACCTATAAGT CTCTTTCCTC ACTAGATAGT TTATACTTTT GGTCnGTTGA AGTCAATAAT 120
 40 TTTATCTAAA GCTATAAAAA ATCTTTTGAT AGC 153

40

(2) INFORMATION FOR SEQ ID NO: 1185:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1185:

TCATTTATAT ACTGTATCAC GCTATCTTTA GTATGTGTGC ATnATCATTG GTTAGTGCCT 60

55

AATGAACGTT ATATTTTAAT TCATGATTTA CTAAGACCAA CAAT

164

(2) INFORMATION FOR SEQ ID NO: 1186:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 143 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1186:

15

CACAAGTGAC GTCATATTAT AAAAGTCACT CGGTTTGC GA TACGTTCTGT CTAAGAAATA 60

GCGACGTGCA ATTTTCATATT TTnTATAAAC ATCCGTTGAA AAAGGACATA AAACCATGCG 120

TTGAACCAGG GTCTATACTT TCT 143

20

(2) INFORMATION FOR SEQ ID NO: 1187:

25

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1187:

30

CGTACAAGTT AAAACGTTTA TACGATTACG AAAAACCACC GAAGAGTGAG AAAGATCCAA 60

TGGTTGTATA TGCAGTAAGT GCAGGATACA AATGGTTCTT TGCTTATCCA GATGAACATA 120

TAGAGACTGT TAATACATTA nCAATCCCTA AAGATGTCTG TTTATTAGCT CAGCATGAnC 180

35

ATACAGTTCG GTCACATAGT GTCAATTCA 209

(2) INFORMATION FOR SEQ ID NO: 1188:

40

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1188:

TTGGAATCGC TGTCGACGGA TAGCAACCTG GATTGTAAAA ATAATGTTGG CTTTAAAAAT 60

50

ACCGTGGCAA TATTAAATGA ATAATCGCTG CTGAATATAC ACCCAATGCA CATTGAACATA 120

ACATAAnCCC ATTTGACTCA TCTACGCCCA CTATTGGCTT TATAGTCACT GAACTAAGCT 180

55

TAT

243

(2) INFORMATION FOR SEQ ID NO: 1189:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 527 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1189:

15 CACCAGGCAT TACCATACCA GCACTCATAC CACCAATCAC KCTCGATAAC ATCAATACCG 60
 AAAAATTGTG GCCAACTGCA AACATAAATT CTGACACTGA AAACAAAATT AATCCTATAC 120
 ATATAATTAA TTTCTTCCTT AATTTGTCAG CTAGCGTACC ACCAAACGGC GATATAATCA 180
 20 TTTGAGATAA CGCAAAAGCA GCAACTAGTA ATCCTAAATC ACTACCAGTT AATCCCAAAT 240
 CTTTTAAATA AACAGGCAAG ACTGGTATTA CTAAACCGaT ACCTAAAAAA ATCAAGAAAA 300
 TATTAAATA TAAGACAAAA ATCTGTTTAT TCATATGCTC ACCTCTTTTT TCTCCATGTC 360
 25 ATGCTTAAAG CTGTTATTCT TCTTTCCAC GACAGATTGC AATTCATGCT AAATATTCGT 420
 AAAAAGTTTC TATATTGTAT TACAACATTG CTACATTGTA CAATATTTTt TCTTTGTAAT 480
 TATCACTATn TTCCATTAA TTGTATAATT AATGACATAT TnnAATA 527

30

(2) INFORMATION FOR SEQ ID NO: 1190:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 889 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1190:

AAAACGTGGC AGTAATTCAG TGTATGTTCA ATATGATGAT ATTATGTTTT TTGAATCATC 60
 AACAAAATCT CACAGACTCA TTGCCCATTT AGATAACCGT CAAATTGAAT TTTATGGTAA 120
 45 TTTAAAAGAA CTGAGTCAAT TAGATGATCG TTTCTTTAGA TGTCATAATA GCTTTGTCGT 180
 CAATCGCCAT AATATTGAAT CTATAGATTG GAAAGAGCGA ATTGTCTATT TTAAAAATAA 240
 AGAACACTGC TATGCATCGG TGaGAAACGT TAAAAAATA TAATAAGATA ATAAAGTCAG 300
 50 TTAACGGCGT ATTCAATTGT AAATCTTGTT GGATTTTAAC AAGATAACTA GCAAATGCAC 360
 TGTATAGCTG GCTTTTTTAAAT TTTATTAACA AAATTAAATA TGACGCGTGA ATTAAAAAAT 420

55

CTCTACAATC CTATGGCGCA ATTTTAAACA AAATATACTA AATtTGAAAT TGACAGTTTC 540
 CATAAATAAA ATGCTATAAT TTCCTACTCC GTGAATCTTA TTTTGTTTTA AAAACAGTG 600
 5 TAGCACAAGm TTCAACTTGT TTCCTACACT GTTTTATAAA TGAATTATTT AAAATGCTTG 660
 TTCAACCTCT TGTAATGTTG GCAAACCTATT AATAGCACCA TACTTCGTTG TCACTATTGC 720
 10 AGCAACGCGA TTGCTAAACG CTAAAATTTT CTCACCTTCA TTTTCAAATA ACTGAGTTAA 780
 ATTTAACACA TCGGTTGCTA AAATCCTGCT AATAACTGCA CCAATAAATG CATCCCCTGC 840
 CCCAGTTGTA TCAACAGGTT TTACCTTATA GCCACTATGA TAATGATTA 889

15 (2) INFORMATION FOR SEQ ID NO: 1191:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1191:

25 AGTTAAAGGC GTTGAATTAA TGGCCTTCCC ACACATGACA TATAACAAG CGTGCGCCTA 60
 TGGTCTGATA ACCAGATACA CGTTTGAATG GATTAATTGC GTTCTCAATT AGGCGTGATA 120
 TGGCTTTAAA GATTnAGTC TGTTGAAATG ATGGTGAATT AAAGCATTGC GCTAAAGGTG 180
 30 CACTGACAAT ATCTCGTAAA GATATGGTGC TTTAACAGAT TTGTAACATC TATGGTCTAA 240
 nGATACGGGG TTAA 254

35 (2) INFORMATION FOR SEQ ID NO: 1192:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 189 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1192:

45 GGCTCATAAG TTACACCTAA TGCATCTTCA TCTGGAAGCT GTGGTTTATC ATCTTCTAAA 60
 TCAGCAGTTG GCGTTTTTTC ATATAATTCC TTTGGCGCAC CAAGATACGC TAATAATTGA 120
 GCTGTGTATn CTAGGCATCC ATACCGTATT CGTTAAACCA GTATATTCA GCTGAATGAT 180
 50 CTGTCCTAC 189

(2) INFORMATION FOR SEQ ID NO: 1193:

55

(A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1193:

10 TTGATATTGA TCGATGACCG GTGATGTGAA ACTGAACTG ACCAATGAAT GAAAAAATGG 60
 GCAATGTTTT TGACAACAAT GGTCATTTAC CAAATAAAAA TATTGnCACCT ATTAATACCT 120
 GnCAAACGTG TTTGTTCTTA AACCTAAAAT GATAAATCCT ATTGAGATTA TGGACTTGGT 180
 15 AAGCTGCAAT CTTTTTAATA TCTTTATAAG CAATG 215

(2) INFORMATION FOR SEQ ID NO: 1194:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1194:

AGAATTTGcn ACTGGTTTAC CAACGCATCT ATGTTCCGGTC GCTATACCGC ATACAGATGT 60
 30 CGAACATATT AACCATAGAA CGTAGGTGTG GTGTTCTAGA AAAAGAAGTG CCGTTATTGA 120
 AATGGGACAC TTGATCAACA GCCGAGTGAA ATCGTTTT 158

(2) INFORMATION FOR SEQ ID NO: 1195:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1195:

45 ACTGATTGCC GTGTCTGTGG TTGATCATTG ACTAATTGTT GGCCATCATT GGnTTCTTGG 60
 TCTAATAGTC CTCTTGCTCC TCGTCGTAA CATTGATGCC AATCATGCAC CACAGCCTTT 120
 CGGTTTCATCA TAACATTTCT GCCAATGTCT CTACATGACA CGGGCTCATA TTTCTTTCTG 180

50

(2) INFORMATION FOR SEQ ID NO: 1196:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 274 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1196:

5 GTTAAAGCGA ATTATTCACA ATATAAAAAA TCATCTGATC AAGTCGTATT AGAATTAGGT 60
 ACAAATGGCG ACTTTACTGT CAAACAGCTC GACGATTTAC TTAATCAATT TGGaAAAGCC 120
 AAGATTTATT TAGTTAATAC ACGTGTTCa AGAaTTmTG AGGgCAAATG TAAATCGATT 180
 10 ATTaGCTGAC GCGGgCGAAA CGGAAGTCCC AATGGTCACA TTAATTGGAT TGGGTATTAG 240
 GCGCTTCACA AGGGACCTTG GTGGAATATT TTTG 274

(2) INFORMATION FOR SEQ ID NO: 1197:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1197:

25 ACGTAACCTA TATTCATCTC TGTTCCCAAT AATAATAACA ATACATAACT GATATTAGCT 60
 GTCTTTTCATC TCTAATTAAT ATGCGTCATG AGCTAATATC GGTTATTTTT TTGTGTCAAA 120
 nAATTTTTTAT TTTATCTCTC CATCGCATTa ATTG 154

(2) INFORMATION FOR SEQ ID NO: 1198:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 249 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1198:

40 AATCCTCACC CGTAATAAAC TCGTTTTGAA TGCGTTGTTC GAACTCACGG TATATTAAAG 60
 CAATATCCTC TAACTTATTT TTAGTTCGAG TTTGCATATT TTTATCAGCA ATAAAGTGTT 120
 45 CTAAATGTTT AGGCGTTACT GCATATTTTT TAAATCTTG AATTTGTTCT GTTAATTTTT 180
 CACTAAACCC ATAATATTTT GCTTGTGATT GATAAAGTTT TAAATACTTT TGTTGTTChT 240
 GAACAATGn 249

(2) INFORMATION FOR SEQ ID NO: 1199:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1199:

TTGGTAAAAA TCGACATCAA ATACTAAATC TGATCCATCT GAATCCCATG TTTAAAACCG 60
AACTTGTGCA TTAATTGTAA AGTTCAAACCT CTTTCATCTTC ATAGATCGCG ATGCGTCTTT 120
TAATTCTTTA GGTGATACTT TGTAGATCTA TAACAAAATT AnCTA 165

(2) INFORMATION FOR SEQ ID NO: 1200:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1200:

TTATTAGCGA TTAAAAATAT GTCCTTTTTT AATAAAGGAG ATATATGTTT AATTGGATGT 60
CAACATCGGA GTCATTGGCG AAAAATAGGG CTGCGGTCGA TGGAGTTCAA AACTATTTTA 120
ATGCATTACA TGTTGTGAGT nAAGAGCAGG CGTACTTTTC TTTTCAAGGA TGTGACATAT 180
CACAGAGCGT ACAATAGAAA CTCAGATACC ATTACATGGA nAGTCCGCGT CCAATG 236

(2) INFORMATION FOR SEQ ID NO: 1201:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1201:

TAATGCTAAA CAGTATTATG GAGATAATGG CTTAGTTCAA ATTTCTGATG nAAGTCAACA 60
CTTCTAAAAT TTGTAAATGA AGCATTAGAC AATAACGAAC AATCAGTTGA AGATTACAAA 120
AATGGTAAAG GCAAAGCTAT GGGCTT 146

(2) INFORMATION FOR SEQ ID NO: 1202:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1202:

ATTGATGATA GTATTGATGG TAATACCATA AACATACAGC ATTATCACAA GTAAAAGTAA 60
 5 GCCTAAATGT CCATAAAATC TACTTGTGTC AATATATGTC GGTATTATCG TAACGGGAAG 120
 TCATTTTCGTA CTTGATTAAA CTTTGTGTGTA ATTGCTTTAG TACCTTCTAA ATACCTGGTT 180
 GATGAGACCA CATACTGATA CCACCATAAC CATAAACAAA AGGTACACCA GAATTGGGCA 240
 10 TACTTCTTAT TCCATCCAAA CCTCCGTAAC CTAATTGCTA CGGGTAATAT TCCAGCACAC 300
 TAATAGTATT GATGTAATTA ACTGAACGGC CGCTnGATAA TAAGTCTTAC AGTCTTAAAC 360
 GTCCATGCGC ATCnTnACCC ATTCA 385
 15

(2) INFORMATION FOR SEQ ID NO: 1203:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 580 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1203:

ACATTGAACG AGTACAGAAA ACTTATTGnA AATAAAGGCT GTTAAAGATA AAGAAGAAGA 60
 TACTTACAGA GGTAAGTATT TTGCGGAAGA AAGAAAAAAC GAAAAATTGG AAAAAGAAAA 120
 30 TATAAACTA AAAAACAAAA TTTATGAATT ACAAACGAA GAAGATAACG AGGAGGACGA 180
 AGAAGACAAG GAGGACGAGA ACGATGTATT ACAAATTGG TGAGATAAAA AACAAAATTA 240
 35 TAAGCTTTAA CGGGTTTGAA TTTAAAGTGT CTGTGATGAA GAGACATGAC GGTATCAGTA 300
 TACAAATCAA GGATATGAAT AATGTTCCAC TTAAATCGTT TCATGTCATA GATTTAAGCG 360
 AACTATATAT TGCACCGGAT GCAATGCGTG AyGTTATAAA CGAATGGATT GAAAATAACA 420
 40 CAGATGAACA GGACAACTA ATTAACCTAG TCATGAAATG GTAGGAGGTA TGAnAAGTGA 480
 ATGATTTACA AGAGAGAGAA TTAGAAACAT TCGAACAAGA CGACCGATTG AAAGTAACTG 540
 ATCTAGACAG TGCTAACTGG GTTTTTTnAG AAACnGGAT 580
 45

(2) INFORMATION FOR SEQ ID NO: 1204:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
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ATCGTATGGT TGAGGCGAAT TTAAGTGAAG AATTAGACAA CGAATCTTGA TGAAAAGAnA 60
 ATGATTGGCT AAAATAGCAG CTAATCAAAT CAACGATAAT GAATGCTTAT TTATCGTGCT 120
 5 GGTTCACTTA CATTGGAGC 139

(2) INFORMATION FOR SEQ ID NO: 1205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1205:

AGGAGGATAT CAGaCTTACA rACTATTCTT TATCATACTG rAATTCAAAT AGACACCTTA 60
 20 ATTGaAGaAG GCGTTGACGC GCTACTTTTC rAAACGTATT ACGACCTnGG AAGnGTTAAC 120
 AAATGTCATT TCCACGGAAC GGGGAAAGGA AATACGGCGT TGCCAATCCA TTGCTCCAAT 180
 TGAACCGGTT GCAAACACAA ATTGACTTGG TTGAAGGGGC AGGCATGCA 229

(2) INFORMATION FOR SEQ ID NO: 1206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1206:

TCGACAAGTT TTTAACAGTT CGTTATTATA TGAATGTAAG TAAAAATTTT TTAGCTACAA 60
 CTTACATATT ATAAATGCAT AAATTAAACA AAAAGGGGCG AAAAAAGTTG ACTCATTAT 120
 40 CAGATTTAGA TATTGCGAAT CAATCAACAC TACAACCAAT TAAGGATATT GCTGCATCAG 180
 TAGGTATTTT AGAGGATGCA TTAGAACCCTT ATGGTCATTA CAAAGCTAAA ATCGACATTA 240
 ATTAAAATTa CGCCAAGAGa AAACAAAGGG AAgTTGTTTT aGTTAACTGc GATGaGCCCA 300
 45 ACACCAGCTG GTGaAGGtAA tCmACGGTTA CAGTTGGtTT AGCTGaTGcA TTCCmTGaGT 360
 TaATgAAAAC GTTATGGTTG ccTTaGGGGG CCTGCCTTT 399

(2) INFORMATION FOR SEQ ID NO: 1207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1207:

ATAACAATA CGATTGTAT GCTACTGTG TGAAGACAAC ATAAAACAAT ATGTAACTG 60
 5 ATATTGAGGA TATGGGCTTT CAAAATCCAn TTCAAAAAAG GTTATGTTGA AATATGACGC 120
 GGTGTTGAA AGAGACCC 138

(2) INFORMATION FOR SEQ ID NO: 1208:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 655 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1208:

AGTCGCCTAA CTTTTATTAT CAGTCCAATC AGTTTCATCA AGTATAAATG TTATTGCTTA 60
 TTTTGTATT CTGGCGTAT TTTTGTCT TCTGCATAGC GCTCTGGATT TTTCTATAA 120
 AAATCTGGT GATAGCTTC GGCTTTGTAA AATTGTGACG CTGGTA-TAT TTTGTTGCA 180
 25 ATTGCCTTAT CAGCATTAAT CGTATTTTIA AGCTGCTCGA TATAAGTCTC AGCGAGTTCT 240
 TTTTGATGAT CATTAGTGTA GAAAATAGCT GTTThATATT GAGGACCACG GTCTTGATAT 300
 TGACCACCTG TATCTAATGG GTCAATGACT GAGAAAAATA TTTCTAATAA CTTATTGTAT 360
 30 GAGAATAATG CAACATCATA TTGAATTTCA ACAGTTTCTA AATGACCACT CGTACCTGAT 420
 TTTACTTGTT CGTAAGTAGG ATTTTCAATA TGTCCGCCA TATATCCAGA AGTTACTTTT 480
 TCTATGCCGT CAAAGGTGTC AAATGGTTTC GTCATACACC AAAAGCAACC TCCGGCAAAA 540
 35 TAAGCTGTAT TAATATTCAT TTTTGACATC CTTTCCATTA GACCTTAGTA CGATTATTIA 600
 AGAAATCACT TGCTTTTTGA ATTGTTTTTA TATAACGTTA ATAnGnGATT ATnAT 655

(2) INFORMATION FOR SEQ ID NO: 1209:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1209:

CCGnCCCCAA TGGAAATTAC CTTTGGThCC CCATTTTAAT TGTAAATTA TTGGAGTGTT 60

AATCTCACTA TCTTCAAATA AGCTTGTGTA TAGTTTAACA GCTTCTTCAG CTTGGTTATT 180
 AAACATTAAA AATGTCGTGA TTTTGAAT ATC 213

5

(2) INFORMATION FOR SEQ ID NO: 1210:

10

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1210:

20

TTGATTGCAA CTTTGATAGT GAAAACATTT ACATGATGTT GTCAGTGGTG CACGGGCGTC 60
 GAGAACAAATC ATTGCGTTAT TGACGGTGCT GCCCTGCTGT CTCAGTTTGT TGATGCAAGC 120
 ACTACACGAA ACCCAATAGC nTCACCAGG 149

(2) INFORMATION FOR SEQ ID NO: 1211:

25

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 142 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1211:

35

AATGTTTCTC CTAATTTTAA ATGTTTAGGA ATATTAACTA GGATAATAAA TCCAGCGACA 60
 TCCCAAATGG GATTCATATA AGAATGTTGG ATGATAATnT TGGCCGTTAA TATACATATT 120
 TTCTATTATA AAATTGGGCA AA 142

(2) INFORMATION FOR SEQ ID NO: 1212:

40

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1212:

50

TTTAAATTTA GTCACCTCAC CTTTTAAAGC ATGTTTATAA AATGTTTGCA TCATCAATGC 60
 ACGTTCTGAA CCAGAGCCTT CAACACAAAG ATAAATTTGT ACAGCAATAC CGCCTCTAAC 120
 TCTTCGTTGC GATGATGGCA ATACCACTCA ATCCAACGCT CnG 163

55

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 765 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1213:

GTCACCTTTC ACGTCTTGAA GAAAAAGGCT ATATAAGAAG AGATCCAACG AAACCACGTG 60
 CTATAGAAAT TGTAAGTGAT CAAACAAATG ATAATATTAA TATGGAAGAA ACGATTTCATG 120
 TGCCAGTTAT TGGTAAAGTC ACAGCAGGTG TTCCTATTAC CGCAGTAGAA AATATTGAAG 180
 AATATTTTCC ATTACCTGAA CACTTAACAT CGACACACAA TAGCGACATA TTCATATTAA 240
 ACGTCGTAGG CGACAGTATG ATTGAGGCTG GTATATTAGA CGGAGACAAA GTAATTGTnC 300
 GCAGTCAAAC CATAGCAGAA AATGGAGACA TTATTGTTGC TATGACTGAG GAAGATGAAG 360
 CAACTGTCAA ACGCTTCTAT AAAGAAAAAA ATCGTTATCG ATTACAACCT GAAAATAGTA 420
 CAATGGAGCC AATTACCTA GACAATGTTG CTGTAATTGG GaAAGTAATT GGTtTGtACC 480
 GCGAAATGTA ATATTTTAAA CCGTTATATA TTATCGTAAT TGTTAAGCCC TCATTTTtAT 540
 AAATTTTGGG nCTCTTGAAA AAGTTACGTT TTCAAGAGGT TTTATTTATT CTAATCTAAA 600
 TTCAGTTCAA ACAGAAATTG CGAATTGTTA GATAATCTCA TTCTTTA-TA TAAATnTTGA 660
 ATTACAGATT TCTGCAAAAT GTTACACAAA TTAAACTCG CCCCCGTAAT AATTACAGG 720
 AGCGAGCCAT TATTATTTTT TTnTTCITT TTTATTAAGT ATATC 765

(2) INFORMATION FOR SEQ ID NO: 1214:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 495 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1214:

AGTTGCCATC AAAAATACAG AACCTAATnA TnACCTTTTA TGATTTTTTG TGAATTCAAA 60
 GTCACCTTCT TTTTnAAGCT TTAAATTTCT CCCCATTTTT TTAGCCCCCT ATAAGGATTG 120
 AATATCAATG CCTTCTTTCA TTAAATTTTC TCTAATTTTC GAAACAAATA ATAATGCATG 180
 TTCTCCATCA CCATGCACAC AAATTGTATC TGCTTGTAAC GTTACTTCCT TATTGTTTTT 240
 TGAAATAACT TTATyyCCt TCACCATCTT TAAACCTGC TTAAGTGCTT CGTCAGTATC 300

ATCAGCAAAC ACTTCAGAAG CTGTAATTAA TCCGACATTC TTGCTTCTG AAATTAGATA 420
 TGAATTTGCT AATCCTACTA ACACTAGTGA TGGATCAAAG TCATAAACAG CTTGTGCTAT 480
 5 AACGTTTGCh ATTnC 495

(2) INFORMATION FOR SEQ ID NO: 1215:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1215:

AnTGTCcAGG TACCCGTGGT CCAAATTCG ATGTACGTAG ACCATTGnCT CGTATTTGTC 60
 20 AGATTGTGTT AATGATTGTC TCTGTATTAG GAAGTTTATT CTCCATTTTA ACAATTAGAA 120
 AAATAGATCC GTTAAAGGCG ATTGGGTAGG AGGTGTGCAA ATGTTGAAAT TGAAATGTAC 180
 AAGTCATTAA GTGGATCTAC ATGAGCGTAA GGTcATTGGA ATAGGTTTGC TGTGACTCGC 240
 25 CGA . 243

(2) INFORMATION FOR SEQ ID NO: 1216:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1216:

GGGCTTCTTT CTAAATAAC TAAGTGAATT ATCTATATAT GAAGAGGTCT CCAATACTTT 60
 40 TTATATAATT CGTGATTACA TTCTATACTT TTAATTGTAT TTTCTGCGTA GGAAAGTGGT 120
 TTTATTAATT CGATTAGTTC GAACTACAnT CAAGAAAAGG TAAAATTTGT GCATGAGCAA 180
 GAGAAACATA CCTGAACCAA AGGCACCCGA ACAGTACCTA GGCCTAAGCG GCTAATTATA 240
 45 AATGCTCAAG CGCAnG 256

(2) INFORMATION FOR SEQ ID NO: 1217:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1217:

5 TTTATTTTTT CTCTAAACG AAACATTGCT TCCTTTTGTG ATTGTTTGT ATTCTTGTC 60
 AACACAACAC TTACGCGCTT CCATTTATCT GTGTATGGAT CTTTATACTT CTCGTAGTAT 120
 CTGTATTTAG TTTCGTTATT TTTGTTTTTA AATTTTCAA TCCACATGTT TATACCTCCT 180
 10 GAGAGAACGT ACGTTCTGTA AATTGTAAA AAATAATAAG GGTAGGTGGG CTACCCAAAA 240
 TTTAGTACTA GGTACTAAAT ATGTTATAAT AAAATAAAAA GTAGGTGATA AGATGACTCA 300
 AATTCTAGGG GCGCTTCTTC TTACAGGAGT TTTAGGTTAC ATACCATATA AATATCTAAC 360
 15 AATGATAGGT TTAGTTAGTG AAAAAACAA GATTATCAAT 400

(2) INFORMATION FOR SEQ ID NO: 1218:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1218:

CCAAGTGTC ATTTTAGATG ATTTTTTTGT TGACCTATCG CCTTAACTGA AGAACTGAT 60
 30 AAATCATCCA TTTCAAAAAT AGGTCTAGAA AAATCTGTTT CGAAGGCTT AAACGATTCA 120
 TATCACGAAT ATTTTAATC GTTATATCAT TTTCTGTAA TAATACATCT ACTTGCTTTA 180
 CGGGATCTAA CGAAGTTGTT TTAGATAATT CTTTCATCCA TTTATTTAAA CCTTCAGCTA 240
 35 ACGATTCTAT ATTTTCAATA TCCATCGTCA TACCTGCAGC CATATGATGG CCGCCAAATT 300
 TAGCGATTAA CTCTGATGT GCTGATAGTA TTTCAAACAT CGACACTTGA TCAATTGATC 360
 40 TGGCGGAGCT TTTGCATGAT TTTGCTCCCT ATCAATATTT 400

(2) INFORMATION FOR SEQ ID NO: 1219:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1219:

AAGATATTAG ACATAAAATC TAAAnACAGC AGTAAGATGA TTTATGATTA GAACTATCT 60
 TACTGCTGTT CACTTTTTAT AATACTTCTG AATGTCCTCA CTTATACTTC TAGTCACAGA 120
 55

GCATTCAATTT CTTGTcTAGC AACGTTCTAC TCTAGCGGAA nTAAtTAGCT ACCATCCTCG 240
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGcTCTCGC 300
 5 TTACTCAATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 360
 TTTTCACTTC GCCAAGCCAT TTTCTTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT 420
 10 AAAAAAAGAG ACCTCACGGT CTCAACTTGG CCTGGGCA 458

(2) INFORMATION FOR SEQ ID NO: 1220:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 494 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1220:

CAAAATTTAT TTCTTGTAAG GTACAATATA AGTTAAATGT TGTGTTAGG ATTGATTCTT 60
 25 TCATCTGAGC ATTTAATTGT AAGTCGCTAT ATTTAATTG TTCAGTATTT AmAAATAAAT 120
 TGAAAAATTC AACTGATAAT AAAGGTGTTT TAATCATACA AATACTTGAC GGTTCTGTAAG 180
 TAGTGTTTCAT TTGTAAGCAC CTCACATATT TGAATAGACA AATAGAGCCC TTTCAGGCTC 240
 30 TATTTGCTGT AATCTTAACA GCAGAAGCTA TTAAACTAC CAGTCTTAGC ACAACCAGGA 300
 GTACATAAAC TATGACTTGT AATACGTTTC TCACCTGCTG AATCATTTGA GTnATTGTTT 360
 GCTTTAACTT GCACGTCTAA ATCAAGAACT TTTCCATAG ATAAAACTC CTATTATTAG 420
 35 TTGAAGTTAA GGCCTACTTC AATTGTCATA TTATCCCTTT TCACACAACA AATCAATAAA 480
 TTATATAATT ATAT 494

40 (2) INFORMATION FOR SEQ ID NO: 1221:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1221:

50 ACTATTATTT TAATAGTGAC GACAGTTTTA ATTTTATTAA GTATTGCTTT AATTACCTTT 60
 ATGCAATACT ATTTACACA AGAnACCGAA AATGCCATAA GAGAAGATGC TAGACGTATA 120
 55 AGTTCACCTGG TCGAACAATC ACATAATA 148

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 401 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1222:

TCGCTTTTAC ATCAAATAAA TTATCTTTAT ACAATTTTCGT ATGAATTACT TCTTTATAAT	60
TATAAAAATG AGGAATTTTT TGATTGTTTA ATTCACCTGC TAATTGATTA GCTTTTTGTT	120
GGTCTTTAAT TGTAACGTCG TGTGGTGCAG TATATTTTAT TTCACCTGAT AAGGACGCTC	180
TACTTATAGC AGCAAAGCAA AGAACTGAAA CAGTAATCGC TGAAATGATT GCCATGACCG	240
TAAGTGAAAA AGCATTTTTTC TTAATACGAT ACATAATAGA TGATGAGAAC ATGACATCAT	300
TLACACTTAT AACACCTTkt CTAAACtTCT TCACCATTTT AAAA ACTAGA GARACAGAGC	360
TTTTAAAAAA TAAGnGTGCC CCAATCACAG TTGACAAaAA A	401

(2) INFORMATION FOR SEQ ID NO: 1223:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 176 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1223:

CTTGACCAAA TCCATTTTTT AACAAAAGTG GTCAAGTGAA ATCCCATCTT TCCAAATCAA	60
AAAAGAGCTA AAGCAAAATG CTCTAGCCCT TGaTATTACT GATTTC CATTTCCCAT CATtGTnTAG	120
CGTATTAATA TTGCTTCATG TACTGATCTC TTTCCCATTC AGAGACTTGA GTTCTG	176

(2) INFORMATION FOR SEQ ID NO: 1224:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 283 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1224:

AATACTTTTA CGATAATTAT AAAGGTTTCAT TCAAATCTTA GGGCAAAATG TATAATATTT	60
TTATGCAAAT TTAAAACaNT AACACTTATT TCAAGGTTCA ATATTTTGAG AATAAGGAGT	120

AATGCCAATC AAACCTCGCTC GAAATAGGGG GAAACGAGGC nATCATTTTT GACAATGAGT 240
 GTCAATAGGG AAGAATAACA ATTAGGAATG ACTCATAGGA GGA 283

(2) INFORMATION FOR SEQ ID NO: 1225:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 217 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1225:

AAAAGAAGAG AAGAAAGTTG AAGAACCTCA AGCACCTAAA GTTGATAACC AACAAGAGGT 60
 TAAACTACG GCTGGTAAAG CTGAAGAAAC AACACAACCA GTTGCACAAC CATTAGTAAA 120
 ATTCCACAGG CCATTACAGG AATTTAAGTC GGATACCACG TGAATnACGT CAGGATGTCh 180
 GCCGTTTACA TGACACGCTC TACATATTCA CCACTCG 217

(2) INFORMATION FOR SEQ ID NO: 1226:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 176 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1226:

TGGGTACTAT TTATTACGTA AAACTTTTCG TTAGCGATGC CGGCATTGCA AGAGCAAGGT 60
 TTACAAAAGC GGACTAGGTT TGCACCTTCT GCTGTTCCAT CGCATATGGA TTAGTAAGGT 120
 CTTTATGGGn ACTGTAAGTG ATCCGAGCAA TGTCGGATAA TCTAGGTCTT GGATAG 176

(2) INFORMATION FOR SEQ ID NO: 1227:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1227:

AATGAAAATA AAGAAGATGA TTTGTTGCA TATGGGTCTC CAGAACATAA TTATCAATTT 60
 GGTGGAAGTT TAATCAAAAG TAAAAATTTA AGCACGTTAT TAAAACCAGT ACATCAAACC 120

GCGGCCGTTT TAATTTTGTT TTCAAGTTAA TCATACTTAC ATATAAAAAT GAAAAGTTGA 240
 ATTTTATAGTA CAATTTCCAC TGTATTTATC TGTTAACCAC TTTATACCCG CAATATTTTCG 300
 5 TTGATCTTAT ATAAACACTT TTGGCTGCTT TTCCTTGACC TAGATTAAAA TTATAGATTT 360
 TCCTTGTAAG AGTGTGTTTG TAGTATCATA AATATGTAAA 400

10 (2) INFORMATION FOR SEQ ID NO: 1228:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1228:

20 ATCTAGCATG CTTTGGGAAA ACGATAAGAA TTTGGTGTTC GAATTTTCATA ACCAACACCA 60
 GCAGTTTCAA CAACTACGTG TGTAGGATAT AAATGTGTTC CTTGACCTTT GACATACGCG 120
 25 TACATTATAG GCACATCCTT ACATACTCAN 150

(2) INFORMATION FOR SEQ ID NO: 1229:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1229:

TCGGTACAGT GCATTTGGTG CGTCATGGTT TACAAGGnAA AAATAAGTGA TCACTATTTA 60
 TCAGTATGGG AAAAAGCAAC GACGTATCAA ATGTACCATG GCTTAGCATT ATTAATTATA 120
 40 GGTGTAATTA GTGGTACA 138

(2) INFORMATION FOR SEQ ID NO: 1230:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1230:

TTGGTATGTA CCTCCAATAG TAATTTCAAT AACTTTGTCT GTTGAACACT AAGAGCAATT 60
 55

CCTTGATTAT nCTAAGAAAA GTAAAAGCAC ACGGAGTATC CTATCAGAAA ACCAGTATAC 180
CA 182

(2) INFORMATION FOR SEQ ID NO: 1231:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 233 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1231:

TCTCTTTAAA TTGTACACAA TTCTGGATAA CTATCCCAT TTCTGTGGAT AAACACCTTG 60
ATGTCTTATT ACTTATCCTC GTTTTTATAT CCCATATTTA TCAACGGkTA TCGCTTTTTT 120
TCATAAAAAA aCACTACCGT ACCyCTTATT TAAGAAATAC AGTAGTATTA TTTTCAATAT 180
ATTTTAGCTA GChTTTCTAC GTCGTACAGT CGCGATTAAA CCTATACCTG CTA 233

(2) INFORMATION FOR SEQ ID NO: 1232:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 385 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1232:

GTTTTTGgTA AAAGTACTAA TATTaCCAA GTATTGAGTC ATATGTTAAA ACAAGATGCG 60
AATGATATTG GCTTTGCTAA ATTACTACAA AATGAGAATA ATCGTATGAG TTATAACGAG 120
TTAATGAGTG AATGGCAATC ACATCAACGT GCATTTTTAG AAGAGTTGAG GCATGTTGAA 180
ATGTTAAAAG AAGAATCTAT TAGAGCATAT GATGTTTATA AAAATTGTGA GTCTTTCTCT 240
AAGATTGAAC AGGTTATTAA TAGTGAAAAA ACAAGTATTG AAGAACAGGT ATATCATTTA 300
GATAATGAAA CGTTACGAGA CAATAAAGAA ATAGAAGTTT GGGATAATCG ATTTAATTAn 360
ATTGnTAGCC CAATGGnCCC TTAA 385

(2) INFORMATION FOR SEQ ID NO: 1233:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1233:

CTGAAAAGAT TCAACTAATC TGAGTCAGGT TACAATCTCA TGATAACCGC TCGCACCTCG 60
 5 GAGAAAGACG CTCAAACAGT ACAGAGCTCG ACCGCAGGAT ATTTTTTGTG AAAATGAACG 120
 TATGAGCTGT TCAGAnGGCA CTTTATTGCG CAATAAAACG GTAAAAATCC TGAAGTGAAG 180

(2) INFORMATION FOR SEQ ID NO: 1234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 453 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1234:

ACCATTTTAA TTTnCntTAT GACCTTGTAT GCCATTATCA aCAGTTATGA TTAATGTTAT 60
 20 GCyTTCATCA TGAGCATTTT TAAATGCTAG TTCGTTTGGT CCATATCTTC GGTAAGCGG 120
 TTAGGAATAT GCCATCCTAC TTGTGCACCT AAAAGTTGTA ATGTTATCAC TAAAATTGTA 180
 25 GTTGCGGTAA CACCGTCGGC ATCGTAATCA CCATAAACTA GGATTTTCTC ATCATTGCT 240
 ATCGCTCTTT TAATTCTTTC AATAGTCTTA GTCATATCGC TCAATTGnAG TGCATCATGA 300
 30 TTGATATCTG TATCTGAAAT GATGGATTCT ATTGCTTGTh CATCAATAAT CGATTTACTT 360
 nCTAATATTT TTTTACGAT TGGCGTTAAC TTAAATTTTG ATGTTAATTC ATCACTTATG 420
 TATTCAGCTG GTTTAGTTAA TTCCACTTA TAC 453

(2) INFORMATION FOR SEQ ID NO: 1235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1235:

CGTGATTAAG TTGGATACTA AAATTTGGGA TGTTAGAGAA TGTGATGAAG ATTTnCAGCA 60
 45 ATGTCCTGAA ATTAATGAAA TAAGAGACAT TGTTTTAAAG CGGTGGTTTG ATAGGTTTAC 120
 50 CAACTGAAGC AGTTTATGGA CTTGCAGCGA ATGCGGCAGA TGA 163

(2) INFORMATION FOR SEQ ID NO: 1236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1236:

GTTAACACAT CGCTTATAAC GTGTAAATAT AAACACTGTT TTATAAAAAC TTTTATACC 60
10 ATTACCGGCA CCGATAAATG TGTACTATGG AGCACAACAA TAACTGGAAT ACTTnGATTT 120
AATCCCGCTA TAACATTTCC TAAT 144

(2) INFORMATION FOR SEQ ID NO: 1237:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 204 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1237:

25 ATAGTTTAAG GTGATATTCA AACAATATTA GGTTTGATTT AACTATCAAG CATCTACTTT 60
GTCATGTTTA ATACCAGCAA ATAATAAAAT CCATGTCACG ATAATAAATG GCATGTTAAT 120
GCAGGGTAAG CCCAACCGGT CCAGCCATGG TGGTGGTACC CTAnTTGGCC nCCACCTACC 180
30 GGTTAATTAA CCACCCCCAA AAAA 204

(2) INFORMATION FOR SEQ ID NO: 1238:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 157 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1238:

CGGTCATTTT GGTTATThAA CAACTATACC TGAGGGGTGG TGGTAATTC GTATTGCCGA 60
45 TTCAGTTTIG TTAATATGCT GACCACCTGC ACCAGAAGCT CTGAATGTAT CAACTGTGAA 120
TAGCATCCGG ATTGGTTTCA ATCTGCTATG GCATCAT 157

(2) INFORMATION FOR SEQ ID NO: 1239:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1239:

5 TTAAGCATG TTCATAAATG TTTGCATCAT CATGCACGTT CTGGACCGAG CCTTCAnCAC 60
 AAGGTAATTT GTACAGCATA CCGGCTCTAA CTCTTCGTTG CGTATGCCTG CAATTTCTTA 120
 CCTCGATACT TAAGTCAATT TTCCGGGCAT AAGGGTGTTT ATTT 164

10 (2) INFORMATION FOR SEQ ID NO: 1240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1240:

TTGAAAACT GAAAACGGTG AAGTTTTACA AACAACTAAA ACAGATAAAG ATGGTAAATA 60
 TCAATTTACT GGATTAGAAA ATGGAACCTA TAAAGTTGAA TTGAAACACC ATCAGTTACA 120
 CACCACACAA GTAGTTCAGA ACTATAAGTT GATCAATGTC TCACACAGTG CATAATnGAA 180
 25 CAACATGCCG GTCTCAACAC TCACTAGGCA GAGGATCATA ACGGTCGTnG TAAGCTCGG 239

30 (2) INFORMATION FOR SEQ ID NO: 1241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1241:

40 TGATAAATAA TAGCGCCATC ATAAGTTGCA GGGTGTAAT CATAATTTCT ACCATGAGTC 60
 TTTGCCTTGA AAGACCGTGC ACCACTTTCT TTAAATCGG TAAACGATAA TGnCAAGTTT 120
 AAAATAATTT GGCGTGTTGG CATTGAGTA TC 152

45 (2) INFORMATION FOR SEQ ID NO: 1242:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1242:

ATCTTTACCT TTCACTGTTC ACTTATGTAC CATAATACTT CTGACAGTTA CTAATTAACA 120
GCAACTCTAA CTCATTTATA TTAACTA 148

5

(2) INFORMATION FOR SEQ ID NO: 1243:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1243:

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GGTACCAATC GATCGTTACA AACGTTTCGT TAAAGACGAT AAAAAAGTAC CAACAGGCAA 60
TGAATATCGT GAATTAGTAT TAAAAGCAAT TCACATGATT ATGCTTGGTT TCTTGATATA 120
ATATATTGTT GCTTACTTTA TTAACACATA TGCAATCATG CCGTTACAAT TAGACTTACA 180
TGGCTTTGTC AATTTGTGGT TATATATGTA CGCATACAGC TTATATTAT TCTTTGACTT 240
TGCAGGTAT AGTTTATTTG CGATAGCATT TAGTTATTTA TTCGGTATTA AAACACCACC 300
AAACTTCGAT AAACCTTTCA AAGCGAAAAA TATTAAAGAT TTCTGGAATA GATGGCATAT 360
GACATTATCA TTCTGGTTCA GAGATTGTAT TTACATGAGA TCTTTATTCT ACATGTCTCG 420
TAAAAAATTA TTGAAGAGTC AATTTGCAAT GTCCAACGTG GCATTCTTAA TCAACTTCTT 480
CATAATGGGG ATTTGGGCAT GGAACGAAG TGTAATACCA TTGGTTTAAAG GGGTTAAACC 540
ATGGCCAGCC TTGGTTAAAG GGTAnGGnCC AATAAGGACG GTGGGCGG 588

(2) INFORMATION FOR SEQ ID NO: 1244:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 376 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1244:

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ATTGCTGGAG AAAGGCAAGG CTTTGCAGGC GGATTGAACT CGACATTCAC TAGTATGGGT 60
AATTTCATAG GTCCTTTAAT CGCAGGTGCG TTATTTGATG TACACATTGA AGCACCAATT 120
TATATGGCTA TAGGTGTTTC ATTAGCAGGT GTTGTATTG TTTTAATTGA AAAGCAACAT 180
AGAGCAAAAT TGAAAGAACA AAATATGTAG CATAAGTATT TTGGTGTATA TTGATATAAA 240
GTAAAGCGTA ATATTATGAA TGATTAGCAT CGTTTTTCTT ATGAATTTTA TTAAGAAAAT 300

GTTATATGTh ACAAAA

376

(2) INFORMATION FOR SEQ ID NO: 1245:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 288 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1245:

15	CAATTTGTTT TAAAGCAAAT TCTTTACATT TCTCACGGAA TTCAGCTGTT GACATTTTCT	60
	TTCGGTCAAC ACCTTTTTTC GTTAATGGCT TGTTCAATTG GGTAACCAT GTGGTTATCC	120
	CCCAACCTGG GTACCGTATG GGGTGGCCAT TAGGAAACCC CTTGGCAATA GGTTTTTTAA	180
20	TAAACCGGTA nCAAATTAAA AGGTCCTTTT TTAATAAATT TTTGGTTTCC AAAGGGGCCA	240
	ATGGnTCCCC CAATTAATGG TTAAAGGTTT TAACCCCAAT TTTCCGGC	288

(2) INFORMATION FOR SEQ ID NO: 1246:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1246:

35	CATCATCAAT AGAACGGTAT TCGCAACGTC GTAGAAATCC CTAAACGAC GAGAACAAAG	60
	CAAGTCGACA TCAGTAAAC ATTAAAGATA TTATGGCTGA AGCAGAGAAC TTAATAACTT	120
	TTTATAAATC TATACnTCC AAAATGTAAA ACTACCAAAA T	161

(2) INFORMATION FOR SEQ ID NO: 1247:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 421 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1247:

50	TCACTACGTT GTTTAATTGT GGTAATTGCA GTTTTACAGG CTTGTCTAGT GAAGATTTAA	60
	AACTTAATTC AAGTGTTTTA GTCATGAATA TGTCTCCTG ATTAAATTGA TAAAGATTTG	120

TTAATTGGT CGTTTGATGC ATCAGGGTTA ATGTTAGCGA ATCGACGCTT AAATTCTGTT 240
 TGTTCGCCGT TAGCGTCTAC TTTAGTAAAT GATAATACAA TAGTGATGTG GTTTATTTtA 300
 5 CTCATATTTT AAAACCTCCT TTCACACTAT ATATCGAAAC AAAATAATAA AATGGCTAAT 360
 TTTATTTTCT ATGTTTAAAA TCTATAAAAn AGGCAATAGA TATGTGTAAC TAAAATATAn 420
 10 G 421

(2) INFORMATION FOR SEQ ID NO: 1248:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 409 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1248:

ATAAGCTGCT GTTGATAATC CAAGTGCTAA AGTTAAATAT AATATAGTGC CAAAAATTTT 60
 ATTCTTCTAT AAAAACACCT CTTCATATTT AATCCATATC TCTTTTTCGT TATTTATACA 120
 25 GAATTTTCTG AAAATAGTCA AGGTTAATTT ATTTGCTGCA AATTTCAACC ACTTTATGTT 180
 AAATGGACAT CAAAGTATAA TTGTATTATT ATTAAATTGT GCAGTGTATA AATAGACGAT 240
 30 ATGCAGGAAC ATGTCGCCTA TTGAGCCCGT TAAAAAGACG GTGACTAAAT GAGATTTTCT 300
 TTAACCATCA TTCGTTGTCA AAGTTTGGAA ATgATGGTTG TTTTTATTG TTTAAATTAA 360
 TCATTGCGAC TTCTATATCA ATGAAAGTTA TCTTAATATA TGAACCTCA 409

(2) INFORMATION FOR SEQ ID NO: 1249:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 217 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1249:

CTTCAATTA CGAACAAATC ATTACTAGTT TATTTAATGA TAATGACTGn AATTTAGCAA 60
 AAAACGTAAC ATGATCATTT AGCTTGAATT GGTAAGACTG TTTATCCAAC ATTTCCAGAC 120
 50 CAAATCACAC CGGTAAACG TCAAAATATA TTGTnTCTAT GCCCGTTTTT ACCAGTTATC 180
 TCATTGCAGG TATATTGATG AATTCACAAG TTGGTAT 217

(2) INFORMATION FOR SEQ ID NO: 1250:

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(A) LENGTH: 176 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1250:

10 CAGAACGTGC GGATCGTTTT TATGCAACCT AAACCAGGTA CGGATTTAGC GTGGTTAAGT 60
 GGCAGTGCAC TAAGTATATT CATTGATCCT GCATTTACAC GATGAAAGCA TTTATTGCAT 120
 GAGTGGGTAG ATGCATTTTG CTGGAATGAT TCACAAATGC ATTAGAGnAC ATTTAC 176

15

(2) INFORMATION FOR SEQ ID NO: 1251:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1251:

25

TTTCAACTTT CTAAATTATA ATATATCTTT TTAAAATAAG CTAGAATTTT TATATAATAA 60
 ATGTTAATAA CGAAAAGGGA TGATGCATAG TGATCGCAAG CACGCCAGAG GCCGATTTGA 120
 30 TATTGCGAGT TAGTTTATAT GGT TTGGGAT GATATGGATA GAATTGGTAA ACATCTCCTA 180
 AAGCATGGTA TAGTGCAATT nAAAAnCTGT GT 212

(2) INFORMATION FOR SEQ ID NO: 1252:

35

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1252:

45 CAGTAAGTCA ATTGAAATGG CTAATTTATT AAATCTATAA AAGCATAGAG CACTGTTGTG 60
 AGTTCATAAT CAAAGATTTA TAAATGThTC AGACTGCCAA TATAACATTT AGGACCTAGA 120
 ACATTGATTA T 131

50

(2) INFORMATION FOR SEQ ID NO: 1253:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 462 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1253:

5 TTAGTAGTCA TCGGTATTGG TGGTCTTAC TTAGGTGCAC GTGCAGCAAT CGAmATGTTA 60
 ACGTCATCAT TTAGAAACAG cAATGAATAC CCTGAmATTG TATTTGTTGG TAATCACTTA 120
 TCATCAACAT ATACGAAAGA GTTAGTTGAT TATTTAGCAG ACAAAGATTT CTCTGTAAAC 180
 10 GTTATTTCTA AATCTGGTAC AACTACAGAA CCAGCAGTTG CATTTAGATT GTTCAAACAA 240
 TTAGTTGAAG AAAGATACGG TAAAGAAGAA GCACAAAAAC GTATATTTGC AACAAACGGAT 300
 AAAGAAAAAG GnGCTTTAAA ACAGTTGGCT ACAAACGAAG GTTATGAAAC GTTTATCGTA 360
 15 CCTGATGATG TAGGTGGAAG ATATTCTGTT TTAACAGCAG TAGGATTATT ACCAATTGCA 420
 ACAGCTGGAA TTAACATCGA AGCTATGATG ATTGGTGCTG CA 462

(2) INFORMATION FOR SEQ ID NO: 1254:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1254:

30 ACTCATAAGT GAATGGTTGA TTACCACTAG TTAAACTTC ATATACTATA GTTCTTTTTT 60
 TTATTTTGCA ATTAGTTATT TTCAATTATAA ACTTCCTTTC AAACACTGCT GAAATAGACG 120
 TCTTTTTC AAATAAGCATGA TTAATACTTC AATTCTTTAA TCCACATATA TTAAAAAGTG 180
 35 AGGTAGTAGG TAATAAATAT AAGACTTAAA GTTAAGATTG CTTTTTTCAT GTTTCATAAT 240
 TAAACCTCT GTAAATTTAA GGTTAGTATT ATGAAATAAT GGATTGGTTT ATTCTTTAGT 300
 ACTAACTTCG TAGTAAATTA TATAGTTCGC TAAATTGTAT TTATCTACTA TATTTTGGGA 360
 40 ATAAACAATT TCCTTTTCTT TCTTCAGTAA ATTATAAAAA 400

(2) INFORMATION FOR SEQ ID NO: 1255:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1255:

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nAATCTATGT ATGGGGGCAT CCAAAGATT CATAGACTAC TTATTTGTTG ATGAAGCCGG 120
ACAAGCAATC CTCAAGC 137

(2) INFORMATION FOR SEQ ID NO: 1256:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 139 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1256:

TGAAATGTAG AAATTGAATT AGAAATGAAG ATTAAAAATC nACACGTATC GTTCAAGTGG 60
TGCAGGTGGT CAGCCGTAAA CACAACGTAC TCTGCGTACG TATTACCATT TCCACTGGTG 120
TCATTGCAAC ATCTTCTGA 139

(2) INFORMATION FOR SEQ ID NO: 1257:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 177 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1257:

TTACCAATTTA TTTTAACACC ATGTTTAGAC CAATTTGATC TGAATAAATT AATCGCTGTT 60
TGTACCTCCA AATTGTTACA ACGTACACCT TTAGTTTTTC TAAATTAATG TATATTCATC 120
ACATCTTCTT CAGTTAAGGG TCAAAGTATA ATTTGTCGAA ATTGTGAAGT CGTTGTA 177

(2) INFORMATION FOR SEQ ID NO: 1258:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 250 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1258:

AAGACCAACC GAAATGAATA TCGACATGGA TTAAGCCTAT ATTCAGATGT AAACGGCGAT 60
TATATTAAAA AGCCAATTAC AGAATGTAGT GGTTAATGAA ATATGCCCAA GAATGGGCTG 120
TATCACTTAG GTGTATCAAA CTGACCAAAA ATTGGAAGGA CTTTAGGCCA AAAACCATGC 180

TTAATTTTTC

250

(2) INFORMATION FOR SEQ ID NO: 1259:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1259:

15 ACATTTACGG GACATTTTCAT TACATCACCC TGCTTTATTT TGGATTATGG CCTAATTTAT 60
 ACTGATAAAT CTAGGAGGTG GAAAAAAGAA TGCCCTGCAA TTTAATTnCA TTTAACCAAA 120
 TAATGAAACA ATAAAAACA TTATATCGTT ACTTATTAAG TAATTTGGCA 170

20 (2) INFORMATION FOR SEQ ID NO: 1260:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1260:

TTTGTA CTCC GATACGTTGT ATTCAGGTG ATGACACTAG GAATTTGTAA TGATCAATTT 60
 CTCTAATTCT TTACAATTGA TAGAATTCTT CGATTTGTGG ATAGACATTC ATATCATTGT 120
 35 CTAATGATTT TTGGTGATTC ATAAATTGTG ACTAAAGCTT GGATGCTTTA GGATTGTAGC 180
 TGAGACACAT GTTGCGTGAC TnGGATTTA TCAATAATC TCAATCACGT GATCCnATCA 240
 CATTCA TCAG CTCACTAAAT CAAGATGATC GTCGTTTATG GGCGATTAAT GGCGTACCGC 300
 40 CAGTGTC CGC ACG 313

(2) INFORMATION FOR SEQ ID NO: 1261:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1261:

TAGCGATCAT TTAATCAAGG TTAGATTATT TAATGTCAGC ATTACGTTTG ACAATGAACT 60

55

GTTTGAGGTT ATCACAATGC CATTTAACAC TATGCGCACA TGGCTGAACT AATnAGCGAC 180
 GAGATGACTT CAAACCTTGA TTAGGT 206

5 (2) INFORMATION FOR SEQ ID NO: 1262:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1262:

AAGTGTGTAC ACGATAGCTA AACTCAAATA TCACAGAACA ACAAATGTCT TAGTACTTTG 60
 TGCCGGTGGT GGTACAAGTG GATTATTAGC CAATGCACTA ATAAAGCAGC TGAAGAATAT 120
 20 CATnTGCCAG TGAAAGCGGC ACTG 144

(2) INFORMATION FOR SEQ ID NO: 1263:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1263:

ATAACGACAC CTAATGCAAT TTGAATAAAG CAGTAGAATT TGTGGGAATC GATTATTGAT 60
 35 AACCGAACTA ATAATCACAG CAAAAATAAA ATTAAAAATG CTCTAATAGT GCCTACATnC 120
 TCCTCAAATT TT 132

(2) INFORMATION FOR SEQ ID NO: 1264:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1264:

50 TATGTCAATT TCGTAGAATT GGTTTTAnGC GCTATTTAGA ATAGCCATCA GAFAAAATCA 60
 TTATTTAAAC GTATAATAGG TCAAAATATA GAGAGTTACT ATACAAATTT CTAACTTTCA 120
 CTTAAAATAA AATATATATA ATTAAAGTGG AGGAGAAGG 159

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1265:

ATAGCTCAAG CAATCATTAT GTTTATAATG ATTGTATGGT TCTTTATAGA TGCTTTATTG 60
 ATTAATTAAT AAAAAGCTTA TTGCAAAATA TGTTTTTCGG TAACTGTAAT TTAGTGATT 120
 TATCATTAAAC AG 132

(2) INFORMATION FOR SEQ ID NO: 1266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1266:

CATGGATTTA TCTTAGCGAT TGGTCTAATT TTACCTTTAG GTGCACAAAA TGTATTTATT 60
 TTTAACCAAG GAGCTAATCA ACCAAAATAT AGATATGTAT TGCCTGCAAT AATTACAGCC 120
 GGGTTGTCAG ACAGCTTACT TATTATTATT GCAGTGGTAG GAGTWTCTAT CATTATTATG 180
 TCTTTACCTG TACTTCAWGC AWTATTTTAT ATAGTTGGTT TAATTTTCTT GATGTATATG 240
 GCTTGGACCA TTTGGCATGA TAAACCCTCA ACAGATGGAG AAACCAAAT TATGTCTCCA 300
 ATGAAACAAG TAAGTTTTGC TTTATCAGTT tCACTACTCA ATCCACATGC TATTTtAGAT 360
 ACAATTGGAr TAATTGGtAG TAGTGCTGCA TTATATAGTG GCnGC 405

(2) INFORMATION FOR SEQ ID NO: 1267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1267:

TCTTTATATT GCAGTACAAA ATTCGCGTGG AGGTTTAAAC CAAGTAGACC GCACAAGATT 60
 TAGCGTCTGA AGGTATTACT GTGTAATGCA TTCGCACCTG GnTATCGTTC AAACACCAAT 120

(2) INFORMATION FOR SEQ ID NO: 1268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1268:

TTTGCCCAAG TGACGTAAAG TACCCAATGT CCATTGTGAC TTGTATCGCC ATCAACAGTA 60
 ATCATATTAA ATGTATGGTC AGTCGAAGAT TTTAATAATT GATGAAGTGT ATTCGATTCA 120
 ATCGATGCAT CGTGTATATAA AAGCAAGCAT GTAGCCAATT GGGAAATCAAC CCGAnCTTGG 180
 CACACATGTA CGTTACACAT TAGAAnCAA GTGACCGACG GTAATCCTAC CCGCTCAACA 240
 CAAGCGC 247

(2) INFORMATION FOR SEQ ID NO: 1269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1269:

TCATTGTATA TGAGCAGATT GGCTAGGCGG TGGCTGGACT GACGGAATCG ACACCCGGCT 60
 GGGGTTGGGA AAAGTACAAG ACGCAACATG CTATGATTTT CCTATGTGGT TATCGTCCGA 120
 TTTAAAGTGA GCAGCGCACG GTCAGTCATC TCTCACAGnA CCTAAAAAGA ACAGTAAGCn 180
 CAACCTAAAG CAGTGGAAct TAAATCATC AAGGT 215

(2) INFORMATION FOR SEQ ID NO: 1270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1270:

ACAATAAAGA CTATTAAAG AGATATAGGT TAGATATTAC ACTTTTAGAG CAAGACGGTA 60
 TAAATGCAAG TAAATTCGTG TATTTATCAA TACAGCAGGT nGAGTGAAAG GCCCAGCAG 119

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1271:

CGTGGCACGT TAAGCGTTTA ACCATAGCAT TAAGATGATT GTCTAGCAGA GCGGATTTCG 60
 GGGCTCACTA CAGTGCATGA TGAACCTAAT GCTTCAAATG TAACATTAAA AATAAAAGCA 120
 ACGATGTCAC TTCTTACTTC TACATCTGCC ATnTTCGTGA TTTCGTATCT ATCCCGCATC 180
 TCATCTTGAA CGTACGAGCC TAATCGCCCh GCGCGATCCT GCC 223

(2) INFORMATION FOR SEQ ID NO: 1272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1272:

TAGTTACAAT ATCTGTCAAT TTCTGGAGAA CCACTAAAGC TATGCATAAT CCGCCTACC 60
 TCTTCAGCAT GTCCTCCAA TAAGATATCG GTACAGTCTT GAGnTGCTTC ACGGTTATGA 120

(2) INFORMATION FOR SEQ ID NO: 1273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1273:

TTGCGCGGCA GTAAAATTCA AACTATTGGC GTCATTTTGC CTAGCTTAAC AAATCCGnTT 60
 TTCTCAGCAC TGATGCAAAG TATTCATGAC CATAAACCAT CTGATGTTGA TTTATGCTGG 120
 TTAACA 126

(2) INFORMATION FOR SEQ ID NO: 1274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1274:

GATTCTGAAG GATCAATACn ACATGTACAA TTTTGGCGTA GGTGCAAAGG CATCAGGTTT 60
 5 GCTTGCTAAT CTACATCGAA GCGGCTACCT AAATTAATGA GAAATCACAC TCAGTTAATG 120
 CATGTACTAG C 131

(2) INFORMATION FOR SEQ ID NO: 1275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1275:

TGGAGTATTA CCTCAAGTGA ATACAACATA CCTGTTGGAA GATTTTTCAA AACTTTAATT 60
 GGACCAAGTG ATGCCATTGA TGAGTTAAAT CCTAATAGAT TCAGGTTACC TCGGATGATT 120
 GATACTAATT TGGCCTGGCG CACGCTTTAG TANTAGTGG 159

(2) INFORMATION FOR SEQ ID NO: 1276:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 577 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1276:

GAAGTAAATA ATATATAGAA TATAACAGGA AATAAAATAG ATAATATTAA TGTTGTTTTT 60
 TTACGCATTA TAACTTTAAA TTCGATTTTC AAGTAACTTA GTATCATAAT TAGATCCCCT 120
 40 TTGCTTTTTTA TTGnTGAAGT ATGAATCAAC AATTGAGACT tTTTGATTTT CAATATCATC 180
 CAAATTAATA TGAAGTTGTT GAAGATATAA AATCGTATCA TTTACATTG AAGTAATAAT 240
 TTTsATAGTG CCATTATGAT TTTyycTGAA TAACTAAATC ATCTTTATCT AGTTTTAACT 300
 45 TTCTTATATA TTCATCGGAT AACGTAATCT GAGATTGCTG ATTGGTTCTA ATATGTGACG 360
 TTGAATCATT AAGTATTATT TCTCCATTTT CAATGAGAAT AATTTTGTCT GACATACGTT 420
 CGACTTCTTC AATATAGTGC GATGTATAGA GTATCGTTCG ATTATCTTCT TTAAATTTT 480
 50 CAATAATTGA CCAAAAATAT TCTCTAATTT CTATATCCAT AGTCGATGTT GGTTTCATCTA 540

(2) INFORMATION FOR SEQ ID NO: 1277:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1277:

CTAAAnTAAG GTAATAGTTA CCAAGTACCA TATCTTGTGG ATGGTGTACT ACAGGTTTAC 60
 CATCTTTAGG TTCAAGATGT TTTGATGACT GCTAACATCA ACATTCTTGC TTCAGCTTGT 120
 GCCTCTTTTG A 131

(2) INFORMATION FOR SEQ ID NO: 1278:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1278:

GTTTGCATA TTTTAGGCAG ACAACCTAAC TTTACAGAAA CAGGTATCTT TTCTGTTATG 60
 TGGAGTGAAC ATTGCTCTTA TAAACATTCT AAACCGTTTT TAAAGAATTT CCTACGCAGG 120
 TGCCATGGTT TGGGCTGGAG TCAGGTGCGT TGTGTATAGC TGATnA 166

(2) INFORMATION FOR SEQ ID NO: 1279:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 418 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1279:

CATAATTATG AAAATGATAT GATTTTTATT AGACCATTTA AAAAAGCATA ATTTAAATCG 60
 AAGGCAGGAC ATTGAAATAT GAAATTTTCA ACTTTAAGTG AAGAAGAATT TACCAACTAC 120
 ACCAAAAAGC ACTTCAAACA TTATACGCAG TCTATAGAAT TATATAATTA TAGAAATAAA 180
 ATAAATCATG AAGCACATAT TGTGGGAGTG AAGAATGATA AAAATGAAGT TATAGCTGCA 240
 TGTTTATTAA CAGAGGCACG AATTTTTTAAA TTCTACAAAT ATTTCTACTC TCATAGAGGT 300

ATTCATTTAT AAAAATAGAG GAGTATTTAT TCTTGTGAT CCATATnTAA TAGAGAAT

418

(2) INFORMATION FOR SEQ ID NO: 1280:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 449 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1280:

15	GACATATCAT AAATTACATG GTGATAAAAT TnTCGGCTAC GATACTAACG GATTCCCGAT	60
	TACCTGGTTT TATCCATTAG GTGAAAAGAA AGTTGAACGT AAGGCACCAA AATTAGAAAA	120
	ATAATTAAAT AAAACAGCTT AATGATGTAA TGAAATTAGT GAGTTAATCA CTGACTTCTA	180
20	CGTCATTGAG CTGTTTTTTT GTGCTTTGTT ACAAAGCATT ATTGAATTTA TTTTACGTGT	240
	TCATATTTTG AAACATCAAA GCCGTCTTGT TTAGCTTTGT TGATAATGTC TTTGATTGAA	300
	TGTAGTCCTT TATCGGCGAA GTATGATCTT AAGTTGTCTT TTGTAGCTTG GTCAGCATTC	360
25	TTATCTAATA ACACATCAAT ATAACCTAAT TCATGTTCTA AGAAGTTTGC ATCATCATGT	420
	AGTACGAGTC CATTTTGAGA ATAACTTT	449

30

(2) INFORMATION FOR SEQ ID NO: 1281:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1281:

40	TATTTATATG TACTGATGAT GAAGTTTATT ATCTATCAAG TGGATCAAAT CCGAAATATA	60
	ATCAGTATAT GGGTGCATAT CATCTACAAT GGCATATGAT AAAATATGCA AAATCACATA	120
	ATATTAATAG GTATAATTTT TATGGAATAA CAGGCGTCTT TAGTAATGAG GCGGATGATT	180
45	TTGGTGTTC ACAAATTTAA AAGGGTTTTA ATGCACATGT TGAAGAATTA ATTGGTGATT	240
	TCATCCAACC AGTAAACCC ATTCCAATAT TAATnTGCCA AACCTnAAT	289

50

(2) INFORMATION FOR SEQ ID NO: 1282:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 402 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1282:

5 ATTCAGGTCG AGGTGGCCCG GCTCCATGCA CCGCGACGCA ACGGGGGAGG CAGACAAGGT 60
 ATAGGGCGGC GCCTACAATC CATGCCAACC CGTTCCATGT GCTCGCCGAG GCGGCATAAA 120
 TCGCCGTGAC GATCAGCGGT CCAATGATCG AAGTTAGGCT GGTAAGAGCC GCGAGCGATC 180
 10 CTTGAAGCTG TCCCTGATGG TCGTCATCTA CCTGCCTGGA CAGCATGGCC TGCAACGCGG 240
 GCATCCCGAT GCCGCCGGA GCGAGAAGAA CTAATTGATA CAACACTTTC TCAACCTGAT 300
 CTTCTTTACC TTCTACATAG CGCGTGAGCA GAACCATCTT GATGgCACAG CTAAATAATG 360
 15 CaAtgGGAAT GATGTATGAC ATTCGGGGTG CATAATTTCT CT 402

(2) INFORMATION FOR SEQ ID NO: 1283:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1283:

 TATTGACAAC CAGAGTACAA ACAGCAGCTA TATTATAGAC TTAGGTCTGA AGTGGTAGTG 60
 GCGGTGGACT ATTGTTGCGA CTGGACACCC GAGATATTGC TCAGCAhAGC ATCATATACA 120
 30 GGAAGTATTA AAAGAGACTT GncGAGTAAC AAATACTGAA GTAATAAGAT TAAAAGAGTG 180
 AGGTGTATAA TTATCCTCGT TCTTTTATAT TAGTATGATA GAGA 224

35 (2) INFORMATION FOR SEQ ID NO: 1284:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 146 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1284:

 CGTGGGAGAT TGTGCATATT GATTATGCAA GGAAGnACGC CATAAAAGTG GATGGCCAGA 60
 CATCATTAAT ATTATTGATA CCACATCAGA AGGTATTCAA AGTGAATCGG TGATAAGTGA 120
 50 ATCAATTAAG TCTGCCAAAG AAAAGA 146

55 (2) INFORMATION FOR SEQ ID NO: 1285:

- (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1285:

10 ATTTGCGGTG ACTGGACTTG GATCCGCAAC TTGGTAATTT AAGGAATTCT TGTCATTATA 60
 AGCCCTCCAT TTCATGATTT GATTTGCCAC TCGGTAACCA TTGGGGTTAC AGCTTCACTA 120
 GGGGAnATAC GAACCTC 137

15 (2) INFORMATION FOR SEQ ID NO: 1286:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 594 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1286:

25 GCTATTGATT ATGGTTAGCm TGTGTTTCwC TTTACTCATT GTTCCTTGGt TAAGCTCrAA 60
 AAAAGCACGT ACTTTAAAGA AACATGCAGC TAATGAACAG GCCCGATTTT TAAATCATTT 120
 TTATGATTAT AAAGCTGGTA TGGATGAACT ACGTCGATTT AATCAAATTA ATCATTATCG 180
 AGATAATTTG ATGGCTAAAT TAAATCATTT TGATAAATTA CAACTTAAAG AGCAACGCTT 240
 TTTAACGATT TATGATTTTA TATTAAATAT TATTGCTATG CTTTCGATTT TTGGTAGTTT 300
 35 AGTTCTAGGA TTAATTCAAA TTAATGCAGG CCAACTAAAT ATTATTTATA TGACGAGTAT 360
 AGTTTTAATG GTCTTAACTT TATTTGAACA AGCTGTACCA ATGACAAATG TCGCGTATTA 420
 TAAAGCGGAT ACTGACCAAG CATTGCACGA TATTAATGAA GTGATATCTG TACCTTCTAC 480
 40 TAATGGAAAA AAACGTCTTA ATGATAAGTA TGATGCAACG AACATTTATG AAGTTAAGGA 540
 TGCTAGTTTT AAGTATTGGA ATCAGCAAAC GTATGTnTTG TCGGATATTh ATTT 594

(2) INFORMATION FOR SEQ ID NO: 1287:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1287:

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TGAAGTAGTA ATAAACCCGG AACCTAAAA CTGGATGGAG GATGAAACCA AAAAGGAACC 120
 AGCCAAGCCA AATTGGGGAA ACCAGGACGG CCCAATGGAG GTCCAACCAA TCCAAACCCC 180
 ATTCCGCTAA TGGCTATGGG TCCCAATTAG GAATCCAATG GATGGATGGA TTn 233

(2) INFORMATION FOR SEQ ID NO: 1288:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1288:

AATCCCTGTA CGTTCGTAAA GCTAGCTGGn TAATAAAAAA GAGTCTGGAA AGTAGGCAAC 60
 AATCAATGAC AATGAGCAGA TCCAATCGCA GTATGCTTAC TCGTGTAAGA AACGCAAACA 120
 TGGTGCGTCA CG 132

(2) INFORMATION FOR SEQ ID NO: 1289:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1289:

TATCTGATAA TTCTGTACCC AGGCGTTTTA ATATGTTTAT CTGGTGTCAAT GATACATAAA 60
 CATTGTACCT TTAGGTCATA CGATGTCGCA AATAACTGCT CTTGCCGTTA CAACACCATT 120
 ACGGTTATAC ACTTnTAGCC AATCATTATC TGGG 154

(2) INFORMATION FOR SEQ ID NO: 1290:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1290:

AAAAGTGGCA CATGCGGCTG TAAAGTCCTC TGTTTCTGAT AAATCATAAC CTATATACAT 60
 GTCTACCTTC CAACTCATCT AAGAAATAAG TCATATTTTT TTGAATGTTG GATAATCAAT 120

(2) INFORMATION FOR SEQ ID NO: 1291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1291:

CTTAATGCTA	TATATTCTTT	GTTTTTGATA	CCATTTTCATC	GTCTTCTCTT	GATTTCTAAA	60
CAATTTAGAA	AATAAAAGAA	TATACGCTTC	AGACTTATTA	AAACCCGCTA	TATCATCTTG	120
ATATTGTATT	AACAATTGAG	TAAAGCTGTG	TATTAAGTCA	TCTTTCTTCG	ATGCAATGGT	180
AGTTAATGAT	TTTACACGAT	AAGCATATTT	ATCTGTAAAT	AACTTAGCAA	CTACCCCAACC	240
TAAATCATGT	CCTAGAATAT	GTGCCTCATG	AATATTTAAC	TTCTCCATTA	GAATTTTTAA	300
ATCCTCAACG	TGATCGTTTA	AATCGTATGA	TTCACTTTTA	GAAGACTTGC	CATGACCTCT	360

(2) INFORMATION FOR SEQ ID NO: 1292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1292:

TGTGTTAGTT	GTTTATGTTG	TTGATATATA	CTGCTCGTGC	ACATGGTACC	CAGACGATTC	60
AACGnTGAGT	ACACAAAATA	CAAAATCTAC	GGCACATGGT	ACCGTTTATA	AAAGATGTGG	120
AACCTTACTA	GCATTTGTTG	AGAACGCTAC	ACGTTTAAAT	CAAG		164

(2) INFORMATION FOR SEQ ID NO: 1293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1293:

TTAATTTTCT	ATATATTCT	TAGGTTATAT	TGGTATCTAT	GCCAGTAAGT	GACATGACGT	60
TAGATCATTG	AATCCAAGAT	CGAnACATTG	GGACATATTT	ATTAACGACA	TGGCTTCAAC	120

(2) INFORMATION FOR SEQ ID NO: 1294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1294:

GTCATGChTA ACAGGTGAAT ACCTAGTAAT TCAGATATTA TCATTTATAT ACCCTCTTAT 60
 ATTTTAGTGC ATTATCTCGA AATCGAGATA CTTAATGTAA ATTTTAGTG CAGCCTACAC 120
 TTCGTGATTG GGCAnTAGTT CTTAAACGCT GTGGTAAGAT GTTAATTCAT CCTTGGTTAA 180
 CACACAAACG CTTGGTTAAT GCTCAGCAGC TAG 213

(2) INFORMATION FOR SEQ ID NO: 1295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1295:

AAGAAGTTTG AAGTCTATGA AAACAATCAA AAATTGCCAG TGAGACTTGT ATCATATAGT 60
 CCTGTACCAG AAGACCATGC CTATATTCGA TTCCCAGTTT CAGATGGCAC ACAGATGAAA 120
 TGTTTTCTCGn CCAATGAGAG GGAGAACATA GTATCAATAG ATG 163

(2) INFORMATION FOR SEQ ID NO: 1296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1296:

TAGCTTTAAT ACATTCTGAT TTTTAAACGC TTCGAAATGT TTTAGTAAC TAATTTTGCC 60
 ATAATCCCAA AAACCTCCTTG ATTATTAAC TGCnTTTTGAT TGGCTACATT AAGGCTTTAT 120
 ACACATCAGC TCACCATGCC CATATCTACT AATGGTTATA TCCCTAGAGT CCCAGCGATA 180
 TAACATCAAC GCTTACnGGA GTTTCAG 207

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1297:

ATGGCATCGG TTGGTTATGA AAAGnCAAGC CATGGGGAGG CCATATTTGG GGTGGAATCA 60
 TACCTGGAAC CTTTGGTGCC TACCACCAAT TGGTAACGGT TTTACCATCG GATTTT TAGT 120
 GATACAGCGA TATGTTTTGT ACAGG 145

(2) INFORMATION FOR SEQ ID NO: 1298:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1298:

TCCAAAAGTT AAAGGTCAAT TGAAACAGAn AAAGCTTATT ATGTCTGGAA AAGTATTAAA 60
 AGTAATGGTA TCAAATGACA TTGAACGTAA TCATTTTGAT AAGGCATGTA ATGAAGTCTT 120
 TCAAGCGTTG AATTGTGGT 139

(2) INFORMATION FOR SEQ ID NO: 1299:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1299:

GATATTGGCA ACCTTCAGCC GATGACCTCA TGGCAAATGA TTGGGAAGTT ATAAACCCAA 60
 CTAGAGACCA GGAATTATTG AAGCAATTAT AGAAATGCTA TCAATGATAC TTTTAAATT 120
 GTTTTAAAC TCATTTTCAA AGTAAACAAC AGTCTTGTCT GAAATTGTTA CATGATAAAT 180
 AGTGTTACTA GCATACACGC CGTTTAGGAA CCCAGAGTTT TTAAGTTTAT TTAAATCGTA 240
 TTTTACATCT TCGAAATGTA GTTTTGA AAA ATACTTTGTA TGTATATCTT TAGCACTTCC 300
 AAAATTTATT GGCAGGTAA TTTAATCGAA CCTAACTTTA CACATTCTAA ATAATCTTTG 360

(2) INFORMATION FOR SEQ ID NO: 1300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 693 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1300:

CTACAGTGCA ATTAAACCAT GAAGTTGTTG ATTTTGAACA ATTATCAAAT GGTCAATGGG 60
 AAGTTACTGT TAAAAATCGC CTAAGTGGTG AGAAATTCAA ACAAGTAACT GACTACGTAT 120
 TCATCGGTGC TGGCGGTGGA GCAATTCAT TATTACAAA AACAGGTATC CCTGAAAGTA 180
 AACATTTGGG TGGATTCCCT ATCAGTGGTC AATTCTTAGC TTGTACAAAC CCAAGTTA 240
 TTGAACAACA CGATGCCAAA GTTTATGGTA AAGAGCCACC TGGTACACCA CCAATGACTG 300
 TACCTCATTT AGATACGCGT TACATTGATG GTCAAAGAAC ATTATTATTT GGACCATTTG 360
 CTAATGTTGG ACCTAAATTC TTGAAAAATG GTTCTAACTT AGATTTATTC AAGTCTGTTA 420
 AACATACAA CATTACAACT TTATTAGCAG CAGCAGTnAA AACTTACCT TTAATTAAAT 480
 ACTCATTTGA CCAAGTAATT ATGACAAAAG AAGTTGTAT GAACCACTTA CGTACTTTCT 540
 ATCCAGAAGC ACCTAATGAA GATTGGCAAT TATACACTGC TGGTAAACGT GTACAAGTTA 600
 TCAAAGATAC ACCTGAACAC GGTAAAGGAT TCATCCAATT CGGTACAGAA GTGGTTAACT 660
 CACAAGACCA CACTGnAATT GCATTATTAG GTG 693

(2) INFORMATION FOR SEQ ID NO: 1301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1301:

CATACTTGGG TAATGCTGCC CATGGnACGC TGGnACAAGG TAAAGTTGCA CGTTTAATTT 60
 GTGnATGTAT ATAAACAGA TGGGAACACC ATTTGAAGGG GATCCTCGTG CAAACTTAAA 120
 ACGTGTATTA AAAGAAATGG AAGATTTAGG cTTCACAGAC TTAAACCTAG GACCTGAACC 180
 AGAATTCTTC TTGTTTAAGT TGGATGAAAA AGGGGAACCA ACTTTAGAAC TTAATGATGA 240
 TGGTGGATAT TTCGATTAG CACCTACAGA TTTAGGTGAA AACTGTCGTC GTGATATTGT 300

TCAACATGAA AtTGACTTaa ATATGCAGAT GCTGTTACAG CATGTGATAA TATCCAAACA 420
 TTTAAATTGG TTGTTAAAAC AATCGCACGT AAACATAATT TACACGCAAC A 471

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(2) INFORMATION FOR SEQ ID NO: 1302:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1302:

20

CATGTGATTA AGAACGTTCA CTGATGAATT TTTGATGATC GTTCGGTTTT TGTTTGGAAT 60
 TTAATGATTA TTTATACAAA AACAGCCGTA TTTCAAGCCG TACATTTTAA ATTTAACTAA 120
 ATTTGCATCT AGTTAATAAT TGCATTTATC AAATTTGTCT TATTGATCCA ATCTAATTTG 180
 TACTCACAAA CTAGTTTAA ATTCTAACTT TATCTCTCAG TTCGTTATCA ATCATCAGAC 240
 ATAAACCAAT GAAGCAATCA GAAACACTC TAATTTTCTa TTAGAAATTT GntTTAATAT 300
 AAAAAACAG GCTTACTTCA TATAATTTAT GAAATAAACC CGTCAATTTT TGTTTAATAT 360
 GCTTGGTGAT CTnTTATTCT GCGTAATAAT GCTAAACCTG 400

30

(2) INFORMATION FOR SEQ ID NO: 1303:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 128 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1303:

40

AAAAGCTTAG TTGAACTTTC AACGTATCTT AGCTACTGAA GGTGCAGAAG TTTTAGAAGC 60
 AAAAGACTGG GGTAAACTnC GCCTAGCTTA TGAAATCAAT GGATTTCAAA GATGGGCTCT 120
 ACAACATC 128

45

(2) INFORMATION FOR SEQ ID NO: 1304:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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TCCTTCGGAT TCTAAATGGC ATTGGACAGT GTTTACAAGC TCGCATTCTT CCACTTTTTTG 60
 CAATTTCTTT TACAATTTCT AAAGCTTCAT CAAAGTTTCC TTCAATAGnA AACGATTCTT 120
 GCACCATACA TTACTGACTT G 141

(2) INFORMATION FOR SEQ ID NO: 1305:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1305:

GACTGGTAAA CACTAAGTGA ATTAGCTGGA CAATGAAAAA TATCCACAAT CATTAATTAA 60
 CGTACGCGTA ACAGATAATA TCGTTGAAG AAATGTTGAC GTTAAGAGTT ATGACTAANT 120
 AGAGTAGAAT GATGGTGAGG TCGATTTTAG TAGACTCTGG AC 162

(2) INFORMATION FOR SEQ ID NO: 1306:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1306:

TTCTTAGTTG CTCGAAGTAA TAATTTGCTT AATAATGATs TAGCTGTTAT TGTGTCATAT 60
 TCTAAAGGTG CCATAAATTT AAAAAGTATA GTAGTTGTTT TAAATTTAGT TGTGGTGAA 120
 ACTTTGATAT GTATATTTGG TTGAGATTGT CTACTCAAAT ATATAGCCTC CTCTATATCT 180
 TCTTACATCT ATATTTTCT AGTGATTTTA AATTGAACTA AGCTATTTT CATATAATTT 240
 AATGAATACA AAATAGGTTT ATCTGATTCA TTATAGTGCG TA 282

(2) INFORMATION FOR SEQ ID NO: 1307:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1307:

AAGGAAAAA CCCTTGGCCT TTGGAAAAA CCCAAAAGGA AAGGGGTTTA AAAAAAANA 120
 AAGTTTAACC CGGTTGGCCC CAATTCCTGC CCGGGGAACC CAAAAGGAnT TTAAAAAAG 180
 5 GAAACCCAAT TCCCGGCCGG AAAAGGGTTT TTAAGCCCAA CCGGATTTTA AGGAAAACCA 240
 TTTTAAGATT ACCTGGGAAA AAAAACCGTT TAGGAA 276

(2) INFORMATION FOR SEQ ID NO: 1308:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 692 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1308:

20 TGTATTTAAT GCTCGTACAC ACAATTACAA AACTGCAAGA GAAAAAGCAT TGAGTAATAA 60
 TCATATTCCA GAAAATGTAT ATGACAATCT AGTAAAACT GTACATAAAT ATTTACCATT 120
 GCTACATAGA TATACTGAAT TGCGCAAAGA ATTGCTAGGT TTAGATGACT TGAAAATGTA 180
 25 TGATTTATAT ACACCATTAA TTAAAGATAT TAAGTTTGAA ATGCCTTATG AAGAAGCTAA 240
 AGAGTGGATG TTAAAGCAT TAGAACCAAT GGGTGAAGAA TATTTAAATG TAGTTAAAGA 300
 AGGCTTAxAC AATCGTTGGG TCGATGTCTA TGAGaATAAA GGTAACGTT CAGGTGGCTA 360
 30 TTCATCAGGT GCACATTTAA CTAATCCATT TATTCTACTT AACTGGTCTA ATACTATTC 420
 AGACTTATAC ACATTAGTTC ATGAATTTGG GcATTCaGCA CATAGTTAcT TCaGTAGAAa 480
 35 ATTCCaACCg TCaAATTCTa GTGACTACaC TATTTTTGTC GcTGAAGTTG CaTCAACTTG 540
 TAACGAAGCA CTTTTAAGTG ATTATATGGA TAAACATCTT GATGATGAAA AACGCTTATT 600
 ATTATTAAAC CAAGAATTAG AnCGTTTCAG AGCTACATTA TTCCGACAAA CAATGTTTCGC 660
 40 AGAATTTGAG CATAAnATTc ATGCAATTGA AG 692

(2) INFORMATION FOR SEQ ID NO: 1309:

- (i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1309:

GGACTATTCG ATGATAGCTT TTTTGACTGG ATTTACTAAA ATGAAAGCAA GTACTATATA 60

atCGAGTAAT ATCTATATAT GACATTTTAA A

151

(2) INFORMATION FOR SEQ ID NO: 1310:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1310:

15 TGTGCATTG ATAATATTCA CTATGATTCG TGGTCATTCA CATCGTCTAC GCTCACCGGT 60

CTAAACGTAC CTAACCCAAC ATGTAATGAA CAAATGCGAT ATTAnCACCT TTATT 115

(2) INFORMATION FOR SEQ ID NO: 1311:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 164 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1311:

30 CACCCAACTG ACCTCAATGG TATAATGCAT TTGTGAATAC CGAATATCAT TGGAAATATCT 60

CCTATCATAG GAATATAATA TGTATATATC TTCGTAATCn TGTTTCATTTT TAAGAAAATC 120

AATAGAAGTG TATCGATTAA AACTACATTT GAACCATTAC TTTG 164

35 (2) INFORMATION FOR SEQ ID NO: 1312:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1312:

45

GAGGAAAATC GAAGTGAAAT TATTAAAATA TGGCGATGGT GGAATACGAA TAGATGGTGG 60

TTTAATAGGC GGCTTTTATTC GGGTGTATT GTATGTAAAG TGAAAAATTT AAnCCCATTT 120

50

CAAATTGGTG ATATCGTTGC G 141

(2) INFORMATION FOR SEQ ID NO: 1313:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1313:

	AATTGGTATT ATGCATAGTG CAATGGATGC TGGTATTAAA ntCCAGAGGA TTACAATTAT	60
10	TAGTTTCAAT AATCACGATT AGTTGAGATG GTTAGCCACA ACTTTCTAGT GTATCACCAT	120
	TATATGTATC GGT	133

(2) INFORMATION FOR SEQ ID NO: 1314:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 629 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1314:

25	TTGCAATTAG AATGCTGTTT CACCCCTTTA AACCATACTA TATATTTAAA TTTAGAGTCC	60
	CATTTACACC AGGTTTAATA CCGAAAAGAC GCGAAGAAAT TGCAACTAAA ATTGGCCAAG	120
	TGATTGAAGA GCATTGCTT ACAGAACTT TAATTAATGA AAAATTGAAA AGCGAGCAAT	180
30	CACAGCAAGC AATAGAATCT ATGATTCAAC AGCAGTTACA AAAGTTGACG AAAGATCAAT	240
	TGTCAATAAAA ACAAATTACT TCTCAAATCG tATTGATTTA GAACAAGTAT TACaAACTAA	300
	TGGAAATCAA TATATTGAAT CACAATTgAA TAATTATTAT aCAAAGCaTC AAAACCAAAC	360
35	AATAGCATCT TTATTGCCAA ATCAACTTGT AACATTTTTTA AATCAGCATG TAGATAACGC	420
	AACAGACTTA TTATGTGATC GTGCAAGGAA TTATTTATCA TCTGCAAAAG GCACACAAGA	480
	TATTAATGAT ATGTTGGATA CTTTTTTCAA TGAGAAAGGT AAGTTAATTG GTATGTTGCA	540
40	AATGTTTATG ACAAAGAGA GTATTGCAGA TCGCATTCAA CAAGAACTTA TACGTTTAAC	600
	ATCTCATCCT AAAGCAAGAA CAATTGTGA	629

45

(2) INFORMATION FOR SEQ ID NO: 1315:

50

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1315:

55

ATACAGGTAC GTTCGTTATC AATGGTGCAG AACGTGTAAT CGTATCTCAA TTAGTTCGTT 120
 CACCATCCGT TTATTTCAAT GAAAAAATCG ACAAAAATGG TCGTGAAAAC TATGATGCAA 180
 5 CAATTATTCC AAACCGTGGT GCATGGTTAG AATATGAAAC AGATGCTAAA GATGTTGTAT 240
 ACGTACGTAT TGATAGAACA CGTAAACTAC CATTAAACAGT ATTGTTACGT GCATTAGGGT 300
 TCTCAAGCGA CCCAAGAAAT TgTgACCTT TAAGGGGACC AATGGAATAT nTACCGTAAT 360
 10 ACCTTTAGGA GGAAAGACCG GCACCTGAAA CCACTGGAA 399

(2) INFORMATION FOR SEQ ID NO: 1316:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 778 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1316:

ATAAACATTT TAAnATGTAA TThAGAAATT TTTTAGTAC AAAATCTTC TTAATAATGA 60
 25 TTAAGGAGGT CAGTAATGAT TGAAATTAAA ACATTAACGA ATAATGATTT TAATGAGTAT 120
 AAGAGACTTG TTTGACAGT CAATGAAGAA TTCACTCAAG ATTCACATTA TAGTCAAACA 180
 ATGACTGACA CCTTAATACA TGACATTTTA AATCAAGGTT CACCGAAATG TATTGTATTT 240
 30 GGCTGTTATG AAAACGAAAC ACTTATCGCA ACAGCTGCCT TAGAACAAAT TCGATACGTT 300
 GGAAAAGAAC ATAAATCATT AATTAAATAC AACTTTGTTA CTAATAACGA TAAATCGATT 360
 AATAGCGAGC TCATTAATTT CATTATTAAT TATGCACGGC AGAACAATTA CGAATCTTTA 420
 35 CTTACATCAA TTGTGTCAAA CAACATAGnn GCTAAAGTTT TCTATAGTGC ACTAGGATTC 480
 GACATTCTTG GTTTTGAGAA AAATGCAATT AAAATCGGAA ATACCTATTT CGATGAACAT 540
 40 TGGCTTTTTT ATGATTTGAT TAATAAGTAA TACAGTTTTA TATATTCTAC rTTTCTCATA 600
 AATTCAAATC ATATAGGTTC TATTTTTCAT ACAACTACTC TACTATTGAG TAGTTGTTTT 660
 TTATTTGATA TGATAACAAT AAGTTTTTTT CAGAATATTC TATGTTTTAG GGGTGTCAAA 720
 45 ACTTAATGGG TAACCGCAAT TATTCATGGA nTTATCnTAA GCGATTGGGT CCTAAnTT 778

(2) INFORMATION FOR SEQ ID NO: 1317:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 465 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1317:

5 TGCACAAGGT GGTGCAGCAA TTGCAGCGTT CTTTATTATT AAACAAAATA AGAAGTTAAA 60
 AGGTGTGGCA TCTGCCGCAG TATTTTCAGC ATTACTTGGT ATTACAGAAC CGGCTATGTT 120
 TGGTGTTACT TAAAACTAAG ATATCCATTT ATTGGCGCTA TCGTTGGATC AGGTATTGGT 180
 10 TCAGCATATA TTGCTTCTT CAAGGTTAAA GCAATCGCAT TAGGAACTGC TGGATTGCCA 240
 GgATTtATTT CAATCAATCC AGTACATGCA GgATGGTTAC ACTaCTTTGT TGGTATGACA 300
 ATATCATTcA TCATTGcTAT AACAGTTACT TTAAtTTTAT CtAAaAGAAa AGCAAATAAA 360
 15 GAAGTTGTAG AATAAAAAA GAGGTATGAC AGTAATCAAA GTATCAGTCA TTGCAAATGC 420
 AATAGGATGA AACTTTAAGC TGTACATCCT TtnAATTAG TTATA 465

(2) INFORMATION FOR SEQ ID NO: 1318:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1318:

30 GACTTAATAT AACTGATCTT TTGCTATTAT TGAAACATAT TTATAAAGAA AATAGCATTG 60
 CATAATACCC AAGCAATAAA TACTATAATA TTTTGGAGT AACTAATCAA ACATCTAAGA 120
 CATGATTGAT AnCACCACAG AAAAATAAGA 150

(2) INFORMATION FOR SEQ ID NO: 1319:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1319:

45 CCACCTTTTA ACGTACGTAT CCATGAATCA TATGATTAAT TTAATATCAT TATTACTTAT 60
 TTCTTATCTT TATTnTCTTT TTTTCTTCTG AAAAGTAGTA ATGAACCTAT TGATGCTAAT 120
 AATCCCCAAA T 131

(2) INFORMATION FOR SEQ ID NO: 1320:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1320:

TAGTGTCCAA ATGAAAGTGT GGCTACCTAT AGCTGGTCCA TGAAGCTTTA TTTTAACTG 60
 10 GTTTGTACAA TATTTAAATA TCAAAATCTT CTCGCGnTTT GGACAGTTT TTTGGTATTA 120
 ACCATTAATA AACGGAAAGA 140

(2) INFORMATION FOR SEQ ID NO: 1321:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1321:

CTTATTATAT AATTCTAATC CTAGTACATT ATACATTTTA TCAAATAGTC AACTGGATAA 60
 25 CTTTGAAAGT GAATGATnCT TTTAAATAA AGAAGATAAT ATAAAGTGCT TGATAATGGA 120
 TTTGTAGTTG ATGATTTAAA 140

30 (2) INFORMATION FOR SEQ ID NO: 1322:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1322:

TCGTTGCAAC ACAGGCACTA TTTTACCTTT ATATGTTGTA ATAGTTTGAT TGCTGCCATT 60
 TAAACAACCA CCTTCTTAC TCCACAAATT TACCATGAAT AGCGCGCGCG CCATAGCGGG 120
 45 ATACTAAAGT GTTCTGCACC TTGCCTGTCT CCTTCAAnTT TCGATTACTG TAGAGCACAA 180
 GTACG 185

(2) INFORMATION FOR SEQ ID NO: 1323:

50

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1323:

5 ACCTGCAATT TTCGTTATTC AAAACAATAA CTATGCAATT TCAACACCAC GGAGCAAGCA 60
 AACTGCTGCT GAAACATTAG CTCAAAAAGC AATTGCTGTA GGTATTCCTG GGTATCCCAA 120
 GTTGGTGGTA TGGTGCGGTA nTTGGTTT 148

10 (2) INFORMATION FOR SEQ ID NO: 1324:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1324:

20 GAAAGCATTG ATGGACAAAG ATGAACCACC AAATGAATGG CGATTAGATT CCAATTGATA 60
 TGGCTCACGG AAAATTTATG CTACAATTGC GTCCAGTAAA CAGTGGCACT AATAGTCCAC 120
 25 TTAnGCTCCC TAGTGGATGA A 141

(2) INFORMATION FOR SEQ ID NO: 1325:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1325:

TTATACTATC GTGAAGGGTT TATTACTCAA TTAATGCCTA AAAAGGATAA AAGTTATTTA 60
 GTTATTGATA ATTTTAATCG TATAGATACA GACATTTTCC AAACGTATAT TAATGTGTTA 120
 40 GAAGGCTATG AAGTAACATT ACCACGTTAT AATAAAGACG GTAATATGAT TAAATGGTCA 180
 CGACAAAAAG ATTCTTTCTA TTAT 204

45 (2) INFORMATION FOR SEQ ID NO: 1326:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 147 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1326:

55

TTTGTTAAAA GTCTTCATTT CGGATGAAGC TTTATCTATT GAACGCTCCA AATTATTTAA 120

AGCAGCTTTT TCTTTATTAA CAGCTGT 147

5

(2) INFORMATION FOR SEQ ID NO: 1327:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 530 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1327:

CATTnAATGA AGAAACTGAA CCCnGAACTA TACGACGCAG AAGGCAATTT AATTAATAAT 60

AGTAAACAT CCAGCTTAAT CCATTGATGT GTTATAAAAG TGAAAAGCTC CAATCAAAGT 120

20

TGACGCTCAA ATAGTTTAAC TTTGATCGGA GCTTTTTTAT AATGTATACC GAAAGGTTCA 180

AATATTATAT AATGGTAGAA TTGAAAGAGA ATATAAAAAA GTGAGGATAT AAAATGAAAG 240

25

TTAATCCTAA TAATATAGAA TTAATCATTG GTGCAGTAAA AGAAGAACAA TATCCAGAAA 300

CAGAATTGTC TGAAGTGCAC TGAGCGGTCG ATCTAATGTA GGTAAGTCTA CATTTATCca 360

ATAGTATGAT TGGCAGAAAA AATATGGCAC GTACATCACA GCAACCCGGC AAAACGCAAA 420

30

CGTTAAATTT TTATAATATA GATGAACAAC TTATTTTTGT GGATGTTCCA GGGTATGGAT 480

ATGCTAAAGT AAGTAAACA CAACGTGAAA AATTGGGAA AATGATTGAG 530

(2) INFORMATION FOR SEQ ID NO: 1328:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1328:

AAGAAAGTTT GATCTAGGCC AACCTTTCTA ACAACGATAC GACAGTTTAA TAATGTCTCA 60

45

TATCTTGACT TCCCATGATG ATATGGTCGT TAATCACATC AATGACTTAA ATCTGGATna 120

ATAGATGCGA ATGGATCTTG AAAAATCATT GTA 153

50

(2) INFORMATION FOR SEQ ID NO: 1329:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 115 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1329:

5 TGTAGTTCGT TTGTGCTCTA ATTAAACGGT CGAAACCATG GATTAGACCT GCGATTACAA 60
CTGCAATGAT ACCTGAAGCA TGAAGTTCTT CTGnTAAAAA GTATACGACA AAAGG 115

(2) INFORMATION FOR SEQ ID NO: 1330:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1330:

20 AACAAAGTTAT CTACATCTGC TGATAGGCAT ACTATTACTA ATAAATAATG CATCTTTTTG 60
CCAGATGTTT TCTTAATCAA TTGCACCAAC GAATGGCACT CTCATCTGTA Gn 112

(2) INFORMATION FOR SEQ ID NO: 1331:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1331:

30 TTCATTGCAG ACAnTTGGTG AACCATGTGG ACGAACTAGT CCTAGATTAA GATAAGAGAT 60
35 TAGTGAnCAT TGCCACCACT GCAATTAAAC ATTCTTGGA AAATTAACCTT AAGTTAGAAT 120
CTTAATGCAT ACAGATACGG CGAAGATGAT GCCAAAGAAC GTCACGACTT TATGATGATG 180
ACTGAACCCA GTTTTTACGG AAG 203

(2) INFORMATION FOR SEQ ID NO: 1332:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 269 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1332:

50 ATGATGTACT AATATCTAAT AAGCTTGCTA AGTCTTGAGA CCTCATTTTA ATCACCTTTT 60

55

GACTATCTAT TTCTGTTAGT ACGTTTGACA TATTAATCAC TCCaCyTTAA CGCAaTAWAw 180
 TTTAwTAGCG TTGGCTATTG TTGTTTAACG CGATGGnATT TACAACCTGT AACGTAAGAG 240
 5 AATGAAAAAT AAGCTGnATA TGTTGTTTG 269

(2) INFORMATION FOR SEQ ID NO: 1333:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 142 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1333:

TAGCTTTTGC CCAATATGGT GAATCATGCG CCGTTCTGTA ATAATCTTCA CTTGGCATTTC 60
 20 TTGGAATTG AACACATCC TGTTCATTTT TATAGAnTGC TTAAATGGTA CAGCTGAAAA 120
 ATCAAAGTAA TGTCCTTTTC TG 142

(2) INFORMATION FOR SEQ ID NO: 1334:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1334:

35 ACTGATGCCC AATATGCATC TTGnCAATTG CAGGTGTGCA TGAATAACA CATGACAAAT 60
 CTGCCTGACT TTTTGCTGAC CCATAAATAA TTGGnCTAAC TTTTTCATC TTGATCTTGC 120
 ATCCTTGCCT TCCTATTTAA AATGCTACAA ATAAATTGCG CGGCGAGTGA ATTTTAATGT 180
 40 TTTACAACGC TGTTCAATAC CTGGGAATAA G 211

(2) INFORMATION FOR SEQ ID NO: 1335:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1335:

CTTGAATCTC TTGTGCCTCT GTGATGTATC ATCAAATTAT TTGCACTGCT TCTTCTTTTA 60

55

TCCGCTCGC

129

(2) INFORMATION FOR SEQ ID NO: 1336:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 633 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1336:

15	CATGATGGCn TCTTACCAA GGCGATTTTA AGAGCAATGA TACCAAGATA TTTTAAATAC	60
	TGATCAAAGT TCAGGTGGTA GCACAATTAC ACAACAACCT GTTAAAAATC AAGTTCTTAC	120
	CAACGAAAAA ACATATAGTA GAAAAGCAAA TGAATnCGCC TAGCAATTAG ATTAGAACAC	180
20	CTACTCTCAA AAGATGAAAT TATATATACA TATTTAAATA TAGTTCctTC GGTAGAGATT	240
	ATAATGGCGC TAATATTTCC GGAATTGCAT CCGCTTCATA TAGTCTATTT GGTATTCCAC	300
	CAAAAGATTT ATCAATTGCA CAATCTGCAT ACCTTATCGG TTTGTTGCAA AGCCCATATG	360
25	GCTATACACC CTACGAAAAA GATGGAACGT TAAATCGGA TAAAGATTTG AAATATAGTA	420
	TTCAAAGACA ACATTATGTA TTAAAGCGTA TGTTAATCGA AGATCAAATC ACTGaAAAAG	480
	AATACAACGA CGCATTAAAA TATGATATTA AATCACATTT GTTAAATCGA AAAAAGCGTT	540
30	AATTGATGCT CACTTTTAA AGTAACCACA ACAATGAATC CAAATATTAA AAACAGCAGT	600
	AAGATTATTT TCAATTAGAA AATTCTCAC TGC	633

(2) INFORMATION FOR SEQ ID NO: 1337:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 317 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1337:

45	ATCAATATTT AGCAGTTATC ATTATGCTTG AACGGTGGT AAAGGCGGAG AAGTCATCCA	60
	CTTTTTCCTA TACTACAAGG ACCTTTACTT TAAACAACG AATTTACAAA ATAAAAGGCA	120
	TAATTTCTTT TCTGTCACAT CGCTCATTCT AACTACTAGA CTTTAAAAT CGTTCCTGTA	180
50	ATTTAACTC AATCAACTnT CAATTAATGA TGCATAATAT GATTATAAGT ATAGTAGTTA	240
	ACTTCAAATA TCTTAGAAAT GTCCTGTACT ATATCTCTTT TATTCTCAA AGTCATAGGT	300

(2) INFORMATION FOR SEQ ID NO: 1338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1338:

TACGGCATAT ACCTCGTTCA TCAATGTTTCG TAAACATTAT TTAAAACATC TCTTACATCT 60
 TCGGTTGGAA GTTCTTCATA GTCGAATTTT ATTGTnTTAT CAAAGTTTTT CATTTGCGAC 120
 ACTCC 125

(2) INFORMATION FOR SEQ ID NO: 1339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1339:

GAGCTTCGTT CCATTGTTAT CAAACGATTG CCATTCTGAA ATGCTGTAAA TAGCATGCTT 60
 CAAATCATCT TGTGCCTGCA GCAGTTTCTT TGnAATATGC TTCATATCAT T 111

(2) INFORMATION FOR SEQ ID NO: 1340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1340:

TCACACGTTT AGTTTTCTAT GAATACCAAT ATTTTAACAC CATGTTTAGC CAATTTGTCT 60
 GCTAAATTAA TCGTGTGTTGT CCTCCAAATT GACACGCACC TTTAGTTTTT CTAAATAATG 120
 ATATCATCAC ATCTCTCAGT TAAAGGTCAA AnATATTG 158

(2) INFORMATION FOR SEQ ID NO: 1341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1341:

5 GCTTCAGGTC AATTAAAACG TTCAAGAGCT TTCACATCTC ACTTATTCGC AAACAAGAGC 60
 ACTAAACAAA AACGTCAATT ACGTAAAGCT AGATTAGTGT CTAAGAGCGA TATGAAACGT 120
 GTAAAACAAT TATTAGCATA CAAAAAATAA GAACAAATAC AGAAATCGGT AGGAATTACC 180
 10 TAAGGAGGAA TTTTATATGC CACGAGTTAA AGGTGGAACA GTAACAAGAG CGCGTCGTAA 240
 AAAAACGATT AAATTAGCTA AAGGTTACTT CGGTTCAAAA CATACATTAT ACAAAGTAGC 300
 TAAGCAACAA GTAATGAAAT CAGGTCAATA TGCTTTCCGT GACCGTCGTC AACGTAAACG 360
 15 TGACTTCCGT AAATTATGGA TTACACGTAT CAACGCAGCA 400

(2) INFORMATION FOR SEQ ID NO: 1342:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1342:

25 GTTGAACAAG GGCAACAAAA ATTTGAGGCG AAACAGATTT TTGAATGGTT ATATCAAAAA 60
 30 AGAGTAGATT CGATTGATGA AATGACGAAC TTATCGAAAAG ACTTACGACA GCTTTTAAAA 120
 GATAACTTTA CTGTTACAAC TTTAACAACCT GTAGTAAAAC AAGAAAGTAA AGACGGTACA 180
 ATTAAATTCT TATTTGAATT ACAAGATGGC TATACAATTG AAAGTGTTTT AATGAGACAT 240
 35 GATTATGGAA ATTCAGTATG TGTAACGACA CAAGTAGGTT GTCGCATCGG ATGTACGTTT 300
 TGTGCTTCTA CACTTGGCGG CTTAAAAAGA AACCTTGAAG CTGGCGAAAT TGTTCACAA 360
 GTTTTAACAG TTCAAAAAGC CCTTGATGCT ACAGAAGAGC 400

(2) INFORMATION FOR SEQ ID NO: 1343:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1343:

50 GAAAATTTCA TCAGGTGTTG GCgTGGAACG TACATTCCCA TTACACACAC CAAAATTGA 60

55

TTTACGTGGT AAAGCTGCTA GAATCCAAGA AATTCGTAA TCAGCATTTA AACAAAGCTA 180
 TGTATGAGTC AAATTGCGACT CAAACAATAA AGCCATCTAG GTCACCTTTA TGGAGTGATA 240
 5 TAGATGGCTT TTTTGCTGT TTAGTTAATG TAAAGTTGAT AATGTAATTG TTTATTCCTT 300
 CTCTATTCAT AACGTGTTTG CTCAAAATGG TTATATAAAC AAAAATCTAC TAAGTGCCAT 360
 TGAAAAGGAC TTAGTAGATT TATTAAATAT ATGCGTAA 399

10 (2) INFORMATION FOR SEQ ID NO: 1344:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 134 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1344:

AACTTACAAC ACCAGGTAAT AACAGCAATA AAGGCACCAG TTAGTGCGGT AATGCCAnTA 60
 TCTAGGCCTT TAGGTTGCCA TAGTACGAGA TGTAGAGGTA CTAGAGGAAT GAGTGTGCT 120
 25 AAAGTTGTCTG TCGT 134

(2) INFORMATION FOR SEQ ID NO: 1345:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1345:

TCATAATAAA CAAGTTCACA TGAATCACAA CATCTGAAGA CAATGTTCAA AATGAGGCTG 60
 40 GCACAATAGA TGATCGCAAG TCGnATCATC ACACAGTACT GAAGCAAGA 109

(2) INFORMATION FOR SEQ ID NO: 1346:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1346:

CCATATCTGG nACGACCGAC ACCTTTACCA CCAACGATTG GTGCCATTTG TTTGCATAAG 60

(2) INFORMATION FOR SEQ ID NO: 1347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1347:

CAATTGAAAG GTGAATTTTA TAGGTCCATG ACAAATAAG GCTTGTTAAA GCTTATTAAC 60
 ACAGTTTCAT CAAATAGTTA AATTAGTTTT TGTTTTGCAA TAAATTGGGT ATAGATTACA 120
 AnTG 124

(2) INFORMATION FOR SEQ ID NO: 1348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1348:

CATCAGTGGC CTGATCACCC CAACATTTGA CATCAATGCA TACCAGTTGA TTTGAACAAT 60
 GATTGCATG AGCTATCATC AAGTTTGTCT TTAAGCTACT AAACCCACGA ACCATGTTAA 120
 CCCCCTGGTC ACCATCACCA ATTGCTCGAT CTAATTCAGT TAATTCAGAT TCATGTTTTT 180
 TAAACGTTTC TTCTAAATTT AATAAACGTG CTTTCATATC ATcAtTTCAT TGTGCaCtaT 240
 AAaTGtATAT TaTTCATATT CACTTCThAT TTAAAGTATG ACTTGTTGTT GGTGCTAAAA 300
 ATGChTCCAA ATATTCTGGT TTAThAGGCA CGATAGT 337

(2) INFORMATION FOR SEQ ID NO: 1349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1349:

CAGCACGTAA ATACAACAAA GCGATCCCCA GCTTGTGGCA CATCATTAAT ACCTGTAATT 60
 TCAACAGGCG TTGATGGACC AGCCGTTTTG ATTCTTTGAC CTAAGTCATT ACATGCCGAA 120

(2) INFORMATION FOR SEQ ID NO: 1350:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1350:

CAATTTTACT TTGAATTTCT TTTTATCTT TTCTAGTTTT ATCGTCCCAC TCTTCAATCC 60
 ATTTTTTAGC TTTATCTTCA TTATTAGTCA ACTTGCCTAT TTCTTTTAAT ATTCTTTATG 120
 ATTGTATTTA TTGTATGTAT ATGGGATTGT TGGCGCTATT TTTTGGTATT TTTTATATT 180
 TTTATCCATA GcATCTACAA CAATTAAATC TGGTTTTGcT TTAGCAACTC TTTCAACATC 240
 ATTTTCTCCA ATATAATCAA CCCCTTTTAA ATAAGGTTTT AAAATTGAAG AATCTTTAGT 300
 TATATCTGAA ACAGCAATTG GTTTGATTCC TAACTTTATA AAATCACCAA CATAAAATCC 360
 AGTTAATACA GCAACTCTTT TAAGGTTCTC nGGGACTTT 399

(2) INFORMATION FOR SEQ ID NO: 1351:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1351:

TAAAACTTAG GCGGTTTTGC ATGATTATAG CGCTCAACAC GTTTGAAATT ATAGGTCATC 60
 TCTGGTATTC TTGTACGATT CTMTTCCAA TCTAAATCAA AGTTTCAAT TTCTTCTTTT 120
 GAGTTTAGAC TTAATCGATC ACGTTCATGT TCTTTAAAAG ATGGAATAAC TTGTTTAAGT 180
 GACCCTTCCA TTCTTAATTG ACCATGTGAA AACCAAGCTA TGTAAGTTACT CACTGTGAA 240
 ATTTTATCAA TATCATCACC AATTGACACA ATCGTTAAAT TATTTTCAAT ATAATCATTT 300
 GTTAATTCOA TCGCACGTTT CATAAATTGT GGTGTTAAAT AGTCAATAAC ATGATTTAAA 360
 ATAATAATAT TTGATTTTGA TGAGCGTGCA ATACTTAATA 400

(2) INFORMATION FOR SEQ ID NO: 1352:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1352:

5 AAGGGAACAA AAGCTGGAGC TCCACCGCGG TGcGgCcGCT CTAGAACTAG TGGATCCCCC 60
GGGCTGCAGG AATTCGGCAC GAGCATATCT AGTATTTT TAG GACGGAGGnA GTACATT 117

(2) INFORMATION FOR SEQ ID NO: 1353:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1353:

20 AGTTCAGGAG AGTTATAAAT ATTAGGGTGG TACATGCCCC AAATCATTGG AATTGTTAAA 60
GTAGATTTTA CAGTTTAGAG ATAACAGACA TGTCTATATG AAGGGCTGTC TACCCTCGTA 120
AGGTTATATC CTACAGnTGA ACGTATCAAG CTT 153

(2) INFORMATION FOR SEQ ID NO: 1354:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 159 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1354:

35 TGTTGTAACA GCTCTCTATG TTTACGTTGG AAGTATGGTT TATTTTTCAT CTTACATTT 60
AGTTCCTTAT TTAAAGTGA TAGAGCAATT GCACTCGTAG GTCAAGAAGC GGGATGCCAA 120
CACAAAGTTC ACAAGAnAAT ACACTTTTGA AAATATTGG 159

(2) INFORMATION FOR SEQ ID NO: 1355:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1355:

50 CGnCTTCCTT CAACCATTGT AGAAGTTGTC TCATATACTT ACTACGGCTT GCTAATACTC 60

55

(2) INFORMATION FOR SEQ ID NO: 1356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1356:

GGATTCATTG GTGCTTATTT ATTTACATTC AATAATGAGA nCTTTACACA ACCAATTGGT 60
 CAAATTATAG ATGTCAACAT GTTCTTCGA CACCTACAAA AGATGCACAA 110

(2) INFORMATION FOR SEQ ID NO: 1357:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1357:

TAATGGTGGG GTATATTTAT ATTAGTACCG AATTTTAGGn GCCTCACTAT CATTTATCAA 60
 ATTATTTAAA GTGGGATCCT ATCGCAATCA ATTGGCAGGG GCAGAATAAT GGCATTAGTC 120
 GTTGAAGATA TCG 133

(2) INFORMATION FOR SEQ ID NO: 1358:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1358:

GTGTCGGTAA GTCCACTTTC TTAAATCATT ATCGTCCAGA ACTTAATCTT GAGACAAATG 60
 ATATATCAAA ATCATTAAAT CGAGGAAAGC ATACTACAAG ACATGTCGAA CTATTCGAAC 120
 GTCAAAACGG TTATATTGCA GACACACCTG GATTCAAGTGC TTTAGATTTT GATCATATAG 180
 ATAAAGATGA AATAAAAGAT TATTTTCTTG AATTAAATCG ATATGGTGAA CATGTAAGTT 240
 TAGGAATTGT AATCATATCA AAGAACCTAA TTGTAATGTT AAGCATCAAT TAGAGATAGG 300
 GAATATTGCG CAATTTAGAT ACGACCATTA TTTACAATA TTTAATGAAA TTTCCAAATA 360

(2) INFORMATION FOR SEQ ID NO: 1359:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1359:

CTGTTTTAGT CTTATTGATT GCCTGACCAT TAACTAAGTA ATTTGTGTTT GAAGCGGTTA 60
 ATTGAGCAAT GATTGGAATG TCGTATTTCT TTCTCGTTTCG TGAAATGACA TTTGTAACT 120
 CTTCTAGGTC GTAATACGTT TCGAAAAGTA GCGCGTCAAC GCCTTCTTCA ATTAAGGTGT 180
 CTATTTGAAT TCAGTATGAT AAAGAATAGT TTGTAAGCTG ATATCCCCCT GTTTGGATAC 240
 CTCTAAACCC CACCAACTGG GGCCCAATAT ATACGTAAAC TnTAATTGGC nGGCTTTTTT 300
 GCGATGCGAC GGGGGGCTGG AGGATGCTTA ACCTTAACCT CCAGACCGAA CCGTTTAACC 360
 TTTCCAAAAT TGCACCATAG GAATGGGTGG AT 392

(2) INFORMATION FOR SEQ ID NO: 1360:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1360:

CCATGGTTAT TTTCTTCACA TTTCATGTAT ATATATTTGT TTATTATCTG TCTCTACTAG 60
 ACTGTAACTT CCAACATATC TGTTTTATAA ACCAGAGAGC AGTCATTCAA TAAATAAACA 120
 GATCTGAGGG CCAACTGGCA TGTTGTCAAC TTATGATATT 160

(2) INFORMATION FOR SEQ ID NO: 1361:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1361:

GTATCCTAAA GATTCAAGTA ATCGGAGCGT TGTATTGCAT GAAGGTACAT TCGGGAATGC 60

ATATTTATTC ACGATnTTAT TTAGCGAC

148

(2) INFORMATION FOR SEQ ID NO: 1362:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 147 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1362:

15

AAAATTACTA TGAAGATTGC ATTAGGATGC GACCATATTG TTACAGATAC AAAAATGCGT 60

GTATCTGAAT TTTTAAATC AAAAGGACAT GAAGTCATTG ACTGACACTT CACTCATnAG 120

TGGCGACAGT GTACGTATCA GACTTAG 147

20

(2) INFORMATION FOR SEQ ID NO: 1363:

25

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1363:

CTGGCAAAGA AGACAACAAC AAGCTGGTAA AGAAGCAACA ACAAGCCTGG TAAAGAGACA 60

ACAACAAnCT GGCAAGAAG ACGGCAACAA GCTGGTAAAG AAGCAACA 108

35

(2) INFORMATION FOR SEQ ID NO: 1364:

40

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1364:

GACAATGTTG CTGTAATGGG GAAGGnAATG GGTGGTACC GCGAATTGAA TAATTTAAAA 60

CCGTAATATA TAATCGTAAT TGTTAAGCCC TCATTTTAT AAATTTTGA CCTCTTGAAA 120

AAGTTACGTT TTCAAGAGGT TTTATTTATC CTA 153

50

(2) INFORMATION FOR SEQ ID NO: 1365:

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 184 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1365:

TAAGAGAATT ATATGCATTC CAAACGAAAC nAACAGAAAA ACGGACCAAA CTAAGTGTCA 60
CAAGTACAAT CGCTGTACTA CTGCAAAACA CGCAAAACGA ACACTTACGT ACACACAAAA 120
AGACCACCAT TCACGTCGGG ATTATTAAAA AGGTAGTCTC GTACATTTAT TAAACTACTT 180
ACGT 184

15

(2) INFORMATION FOR SEQ ID NO: 1366:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 452 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1366:

25

ACATTAGATG GGTCAATCAT GTTATACACG GTGATTTAGG GGAGTCAATC AAATATAAAA 60
GGCCGGTAAT TGATGTTATT GAGGAAAGAA TTCCAAATAC AATATTACTC GGTGCTATGT 120
CATTAATTAT TACTTATATT ATCTCATTIG CTTTAGGAAT AACGTCAGGT AGATATTCTT 180
ACAGTTTGAC GGATTATACT GTGCAAAATAT TTAATTATTT GATGTTAGCC ATTCCATCTT 240
TTATTGCGGG AGTATTTGCA ATTTnTATTT TTTCTTTTGA ATTACAATGG TTCCCGTTTC 300
AAGGTTCTGT TGATATTAAC CTAAAGAAG GTACTTTTGA ATATtATATG AGTAAAATAT 360
ATCACACATT TTTACCTGCA TTCACTTTAG GTTTATTATC TACTGCTGGT TATAwTCAAT 420
ATTTACGTAA TGaTATTATT GAAAATTCTA AA 452

40

(2) INFORMATION FOR SEQ ID NO: 1367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1367:

50

TTGTGAGTAA TTGGACAATA TAAGTGTGG TCTTGGATGG CATATCCTTG GTACGACCTG 60
GGCAACTTGC TTCATAGCGC AGTTAGGAAC TGATCAATCA TTGGCGTTTT GATACCTAGC 120

55

(2) INFORMATION FOR SEQ ID NO: 1368:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1368:

TGGTGCAAAT TAAAACGGTT GCATATGCAC GTACGACGTA TTGCTAAATA CAATCAATTA 60
 TTACGTATCG AAGATGAATT ATTTGAAACG CTAAATATGA CGGTATCAAA TCATTCTATn 120
 ACTTAG 126

(2) INFORMATION FOR SEQ ID NO: 1369:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1369:

TGnAAAGTTC ATCAGGGAGC CATTTTTACA ACACAGGGCA CATACGGGTT GTGTTTAGGT 60
 GCAATTGCCC CAAGCGGACA AAGCATTATT TAAAGTTTCA AGTTCITCAA CGATTTATTA 120
 GTGCACAGGA TCCTGTTAAG AGGTATTTTG AAGACTTCCG 160

(2) INFORMATION FOR SEQ ID NO: 1370:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1370:

AGTAATTCTG CAAATGCCGC AGATAGCnGT ACTTTGAATT ATGAGGTTTA CAAATACAAT 60
 ACCAATGACA CGTCAATTGC TAATGACTAT TTTAATAAAC CGGCAAAGTA CATTAAGAAA 120
 AATGGTAAAT TGTATGTTCA AATAACTGTC AACCACAGTC ATTGGATTAC TGAATGAGT 180
 ATCGAAGGAC ATAAAGAAAA TATTATTAGT AAAAACACTG CCAAAGATGA ACGCACTTCT 240
 GAATTTGAAG TAAGTAAGTT GAACGGTAAA ATAGATGGAA AAATTGACGT TTATATCGAT 300

AATGGACCA_n CTGATGTAGC AGGTGCTAAT GCACCAGGTA

400

(2) INFORMATION FOR SEQ ID NO: 1371:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1371:

15

CATCAAGAAC ATGTGAGACC ACAATTTGAA TCACTTGAAA AAATAAATAA AGACATTGTT 60

GGATGGATAA AATTATCAGG AACATCATT AATTATCCAG TACTACAAGG TAAGACAAAT 120

CACGATTATT TAAATTTAGA TTTTGAGCGA GAACATCGAC GTAAAGGTAG TATTTT_yATG 180

20

GATTTTAGAA ATGAATTGAA GAATTT_nAAT CATAATACTA TTTTATACGG GCACCATGTC 240

GGTGATAATA CGATGTTTGA TGTGTTAGAA GATTATTTAA AGCAATCGTT TTATGAAAAA 300

CACAAGATAA TTGA_nTTTGG CAATAAATAT GGTAATCTCC ATTGC 345

25

(2) INFORMATION FOR SEQ ID NO: 1372:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1372:

35

TTGAAAAGCA GTTTGGATTT ATGCTCAAAC CATGGACGAC GGTTAGGTTT ATGAATGTTA 60

TTCCAAATAG GTTCATCTAT AAAA_nCTAGT GGAAAGTGA AAAA_nAGT GGACCTTCGA 120

40

TAATACGATG TATTTATCGT TAGAAGCAGT AATA 154

(2) INFORMATION FOR SEQ ID NO: 1373:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1373:

GAGCCTAATT ATTCAAGCCA AATCGCATAT GAAATTGATA AAGAAGTTCA ACGAATCGTT 60

55

CTATACnAGA ACTATC

136

(2) INFORMATION FOR SEQ ID NO: 1374:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 358 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1374:

15	ATCTTTAACA ATTAAAACCA TACTATCTTG AATCATCATC AAATTTAACG CATGTGCGTC	60
	AAGTTGTTTC ACTTTAAAGA CTTCAATTATT AAGACCGACC TTAGACTGCT TTTTAAAAAT	120
	AGGTACATTC GTAATCATAC CTATACTTTG ATTGTCTAAG TGTAAATTGT TTTGGTGATA	180
20	TCGATTATAA TCTTGTGCAG TAAAAGCTGT AATCACTACT GATTGTCTTG AAAATATCGC	240
	GCCTTCATTA CCAATGAAGT CTATTGGaAT aTCATCACTA GCCTGTTTTA ACTTGTAATA	300
	AGCACGATTC TnTTCTAAAG AAGCTCTAAA TAATGTCGTT TCATATACTT TGAAGTCT	358

25

(2) INFORMATION FOR SEQ ID NO: 1375:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1375:

35	ATATTGTGTG CTAAATTTGC TTAAGTATGT TTTTGTGTTG nAAGTAAGCA TATGTTATTG	60
	TCTTTTAAAT TGTGTGAAAA GTGCTGTTTT CATAGAATTA ATATCAGACA TCTTTATTAG	120
40	TA	122

40

(2) INFORMATION FOR SEQ ID NO: 1376:

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 467 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1376:

50	CATTTTCTTC GGTTCCTGTC TTTTATGCG TAGATTTATT TTCTTGTTCT TGGTTATTAC	60
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55

CGATAATTAC GATGGTAATA AGAAGTTTTT TCAAATATAA CGCCTCCATG TTAATGAAAA 180
 GTAGTTGATA CGTGAAGCTA AATAATTnAT TTCAATATTG CCATAATCAT TTTAAAAAAT 240
 5 AAATATTAGA AAAGTAGGCG ATATTAATAT TTTcATTGTt TTTTGTGTAC TTCAATTAGT 300
 ATAACAAAAC TGTTATGTAT TTATAAATAT AATCATTAGT ATTTTTATGG CTGAAAAAGT 360
 TATAATAAAA GTGTAAGGAA TAAAATATTT GTATGGAAAA GAGAGATAAT TATGAATAAA 420
 10 ACCAGTAAAG TTTGTGTAGC AGCAACATTA GCATTGGGCA CACTGAT 467

(2) INFORMATION FOR SEQ ID NO: 1377:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1377:

AGGTGTTAGA ATTTATTTTA AGTGTtATAC GTGTCTTCCA GAAATTGTAA TGGCATTATA 60
 25 TTTATnAAAAG TGTTGGCAGG TTATTTTCAG GTGTATTAGT TTAGGTATCA TTCGTAGTAT 120
 GCTTGGGA 128

(2) INFORMATION FOR SEQ ID NO: 1378:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1378:

GGACGCTAGA GGATCCCGGT CTGGAAAATA TCGTCCAGAA CTTAGAAATA TGAAAATATT 60
 CCCAAGACCA ATCGATAATA TATTGCCAAT ATGGCGTGCT GTTGGTGCTC CACCTGCAAG 120
 TGCTATTAAA GCGGGAAAAC AAGGTGTGCC AATGATGATT ACAACCCTTG GTGGCCCAGC 180
 45 AATGAACTTT AAAGGTTCTA TAKATGCTTA TCGTCAaKCG GCAACTGAaG CAGGTTTCGA 240
 TGCTTCGCCT AAGTCTTTAC CAGTAAGTAC AGCGAGTCTG TTTTATACAG CTGAAACAAC 300
 TCAGGATGCT ATGAGAGAAT TTTATCCACA TTTGAATACA GGGATGTCAT TTATTCGTGG 360
 50 TnGTTGGTTA TCCGAAACAG CAATnGCTAA TTCGTCAGTT 400

(2) INFORMATION FOR SEQ ID NO: 1379:

55

(A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1379:

10 AACTACAACA ATTTAACGAC CAACCTTAAA AaAATACGCT CTTATGCATT GGATTAGTCC 60
 TGATTATACA ATTAACTGA ACAAATACCC ATCATTTAAA AGACTTAG 108

(2) INFORMATION FOR SEQ ID NO: 1380:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1380:

25 AAGTGGGGGG AATCAGTATG TTACATTTAC ATATATTAAG TATTAGCGAT TATTTTATTT 60
 ATCGCTACAT ACTTAACCAT TTCAAAAATT CAAGGCGGnT CACCATTTTC CAACCCGT 118

(2) INFORMATION FOR SEQ ID NO: 1381:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1381:

TCATGAAAAC ATTTATTTTA AAATTTGATA TTTGTTCAAT AATATTCGAA ATTAACTTnT 60
 40 GTGTATAGAT TTTCTTTATA TCCTGAGAGA CATGTACTAT AATGTTTGTG AATA 114

(2) INFORMATION FOR SEQ ID NO: 1382:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1382:

CGGTATTGAT CATATAAATA GTGTTTAGAT GCTATAGTCG GnTGA CTTAA GTAATTTAAA 60

55

GTTTTCTTCT GCCTTGCTTA AAGATATATG ACAGGGTGCT GGCAT

165

(2) INFORMATION FOR SEQ ID NO: 1383:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1383:

15

TTTGGTGTGA TGGAGTATAT TTAGGTGTGG AAATCAAGAG GGAATTCCAT TTTCAAACAT

60

CCAATTAGAG TCGnAATAAG AACTCGCTAT CGGTCCAATT AACTGATTCA G

111

(2) INFORMATION FOR SEQ ID NO: 1384:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1384:

30

CATTTAAATA ACGTTGTGAC CATGTGCTTT ATGCTATGTG CTAGAAAATC CATGTTTTTA

60

TCTAATTCT TAATAAATTG ACATTAAGTT GGATTCTTGT CnCTTCACG TTTCGACATT

120

GGATGACTGA ACGCATGAAA TCAG

144

(2) INFORMATION FOR SEQ ID NO: 1385:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1385:

45

TCGTTGTGCA GCAACTGCAT TACGCTGTCT CATTAAATGTA AGCGCAATGG CCATTTGGTT

60

TTTCnATAGT GGAATACTTG TCAAAATTGA ACATTGTATC TTC

103

(2) INFORMATION FOR SEQ ID NO: 1386:

50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 533 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1386:

5 CCAGnACAAA TACAACGTTA TATTCAACAA TTAGAAGACT TAGnATAGAT ATAAATTGAG 60
 GGAGGACATC GATATGGCAT TTGAAGGGTT ATCAGAAACC TTGCAAGCGA CGATGCAAAA 120
 AATGCGTGGT AAGGGTAAAC TTAAGTGAAGC TGATATAAAG ATAATGATGC GTGAAGTAAG 180
 10 ATTAGCGTTA CTTGAGGCTG nACGTAACT TTAAAGTGGT AAAAGAATTT ATTAACACAG 240
 TATCAGAACG CGCATTAGGT TCCGATGTAA TGCAATCATT AACACCAGGG CAACAAGTTA 300
 TTAAATAGT TCAAGATGAA TTAACGCAGT TGATGGGTGG AGAAAATACG TCGATTAAAnA 360
 15 TGTCAAATAA ACCACCTACT GTTGTATGA TGGTTGGTTT ACAAGGTGCT GGTAACAA 420
 CAACTGCAGG TAAATTAGCA TTATTGATGC GTAAAAATA CAACAAnAAA CCTATGTnAG 480
 TTGCAGCAGA TATTTATCGT CCAGCAGCGA TAAATCAATT ACAAACAGTA GGG 533

(2) INFORMATION FOR SEQ ID NO: 1387:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1387:

30 TTATTTACAA GCCATTAATA TATTTTAGGT TTGTTCTGCA TCGATTCATT GGTGCTATTT 60
 TATTTACATT CAATAATGAG ACTTTTACAn CAAACCAATT GGTCAAATAT AG 112

(2) INFORMATION FOR SEQ ID NO: 1388:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1388:

45 ACACCTACAG TTAATAGTAT CAGTGCACAC TAAAGTCCTA ATACTTTCAA CCATGACTAA 60
 TGATGTATCn TCTTGCCCAA CGAACGCGTT TGCCCAAATT GAATTAGACT GGACGGAC 118

(2) INFORMATION FOR SEQ ID NO: 1389:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 147 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1389:

CGACGACACA ACTTTATAAT AAAATCTTAG ACAATAACGA AGGGTATTAA CAGAACTTGG 60
10 TGCTGTTAAT GCAAGTACTG GAAAATATAC TGGTCGTCGC TAAAGCAAAT TTTTGCTCTG 120
ACCTnCAATG GTACTTGTG GGAATA 147

(2) INFORMATION FOR SEQ ID NO: 1390:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 161 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1390:

TTTTTGATCA TGATTTTTGG GCATGGATCA ATCACTTGCT TGGCCAATGG TCTTTCAACA 60
25 ATTTGGATAT CTGACCTTAT TCGCTTTATC TAGCACTTTT GnCAATTGT TGGCATTGGA 120
AAACATGTGT TTAGATTTTT GTATGCCTCT CGCAGGCTTT T 161

30 (2) INFORMATION FOR SEQ ID NO: 1391:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1391:

40

GCCGCACGCG CGCGATTCTC GGCCTAATAA GAAAACAAAT AATTCCAATT CATATATGnA 60
CATTTTTGCC TCCTTATTC TTGAAAATGT GGAATTGGAA TT 102

45 (2) INFORMATION FOR SEQ ID NO: 1392:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 412 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1392:

55

AAAATGCTAT TAACAACGTA TTAAATAATC AAGATTACCA TGGTATTAAA GATAAACCAT 120
 TCGCATTATT CGTAACTGGA TTTTTCGACA ATGTAACAGA TAATACTGTT GGTATTAACT 180
 5 TTAAGACAAA AGACGGTTCA ATAGCAGTAT TTATGCGTCC AGATATTGGA GAAACATTTA 240
 GCGAGTTTAG AACATTCTTA GCCGTCTTGT TAATGTTGTT ATTATTTATC TCGATTTTCAT 300
 TAGTTATCGC ATCAnCCTAT TCAATCATTC GTCCAGTAAA AAAGTTAAAG CTAGCGACCG 360
 10 AACGCTTAAT TGATGGTGAT TTTGAAACAC CTATCAAACA AACnCGCAAA GA 412

(2) INFORMATION FOR SEQ ID NO: 1393:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 186 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1393:

AGCAAnTGGA TTGCAATGAG TTTCTTATAT TTACAAGGTG GTAGATTGAT TGATGTTTTA 60
 25 ACTGCGATAT TAGCAGTAGT CTAGATACCT AGTCACTGAG ATTTTAGATC GAGTTACACG 120
 CACATTATCC GATCTGTCTA TATGGATATC CGTATGACTA CCTATCCCAC GGACTGCACA 180
 TACTGG 186

30

(2) INFORMATION FOR SEQ ID NO: 1394:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1394:

TCTTTAAAAG AATCAGGAGC TTGGAAGAAG TATATCAGGA TCATTAAGTC AACAAATTAC 60
 GCGATATGAA AATTTGAATA ACAATTTGnA AAAGCATGCT TCCGATAATC AGCAAGCC 118

45

(2) INFORMATION FOR SEQ ID NO: 1395:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

GGTTACCTCG GATGGATGAT TACTATTTTG GGCTGGGCGC CGGCTTTnGT TATTAGTGGT 60
 GGCAATAGTG GCAAAGTGTC ACAAAAAAAT CCAATAGCTG GAAACCCGGG TATATTTGGG 120
 5 TATTAACGCC GGTGGCCGGG ATTTGGCCAA TCGCATTAAAT TTAATGGCCA TTGGG 175

(2) INFORMATION FOR SEQ ID NO: 1396:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1396:

AGAAACTTAG ACGATTAGTA TCATATATTA GAACACnGCA CCGAACTTGA AATCATGGCT 60
 20 GATATCGCAC CTTGAAGAAG CAAAAATGCC GCACGACTTG GCTTTGATAT ATTGGCACGA 120
 CTTACATGGC AT 132

(2) INFORMATION FOR SEQ ID NO: 1397:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1397:

AGAGGTCCGG CTATCTATCA AATAAAGTGG TCATTTAAAG CGTACACTTC GGGTGCGTTG 60
 35 ATTTCTTACT TTAGGTGTAG GACAATTGTA TCGCATCTAT CTTTACnCTA CCTGCATTGT 120
 T 121

(2) INFORMATION FOR SEQ ID NO: 1398:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1398:

CGTTCGTATA ATCTCACTTG CATChTGAAT TGAACAACAT CCTGTCATTT TAAGACTGCT 60
 50 AAAnGTACAG CTGAAAACCA AGTAAGTCCG TTTCGTCTGG CTGTGAAATG GATCAAGGAG 120

AAACACCTCA TCCAAAGTTC AG

202

(2) INFORMATION FOR SEQ ID NO: 1399:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1399:

15 CGTTGGATCA CTGATGCATT CATAAATGGG TGAACnTAAT GTAATGTTAA ATCTATCACA 60
 GCGCGATAAC AGCAAGAATA TAGTGAACAC CATAAATTGA GCATATCAAT GCCATATTCA 120
 TGGATACACA TAGTTCACCT GGTGGTCGGT GAAAGCCTGT AGATG 165

20 (2) INFORMATION FOR SEQ ID NO: 1400:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1400:

30 ACACCTTTGT TTTTGCAAAG CTGTACCACA AAGTACTGGG TAGAATTCTA CGTTATATGA 60
 GnCTTGGCGT ATAGCTTCTT TTAATTCATA AACTGTAAAT TTCTTCG 107

35 (2) INFORMATION FOR SEQ ID NO: 1401:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1401:

45 TTTTGTCTAG nAACATCTGC TTCTAATAAT GATCGATCAG CAGCCATTGT GCTTAATCTT 60
 TCATCCCACA TCACAATCTC AATAGAAGGA TAAGCTTCTA ATAATT 106

(2) INFORMATION FOR SEQ ID NO: 1402:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1402:

CAATGTTAAA CCTACACCGT TAACAGCACA CATGATACTA AATTGTTGGG GTGTCATATT 60
 5 ATACAATGTT GAGTAAATAA TGGCGATGCA GATGAATAAC TA 102

(2) INFORMATION FOR SEQ ID NO: 1403:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1403:

TTTATTATTT GTGCTACAAC TACTTAAAAA AATCAGTAGA TATAGCATTAA AACATATTTT 60
 20 CATCCCCyTG AATTTTAAAA ACTTTTTCAT AAGCAACACC TCTAAAAATA AATaCAATAT 120
 ATTATAGCAA ATAGAAATTA TTATTTTGTT AAATTATGTT GTnCATGTT 169

(2) INFORMATION FOR SEQ ID NO: 1404:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1404:

TTAGTTGATA AGTAAATCCG AGTGACATTG GGATTCACCC CAACCGACTC TATTCCAGTC 60
 35 TGAAATACGT GAACCCATAA nATCCTATGT CCAGATTTAT ATTTCT 106

(2) INFORMATION FOR SEQ ID NO: 1405:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1405:

TATTTTTCGA GCAGAGATGT TCGCGACAAG GTTTACGCCA AATTGTCACCT GCTACTGCCA 60
 50 TGTGTATTGC ATGCAAGTGC AGGnAATATA TTGAACATTT AAACGATCAG TTTAATTCGA 120

CTTTAATAAG CAATTTGTAC TGACTGTCGA CATTGCGTCA TGGTCTGTTT TTGTTTAACT 240
 ATACTATnGG TGC GAAGTAG GCCTATGTTT AGAGGTCTAA CATGCCGTAG GTCTAATGGA 300
 5 TCAGGAACC 309

(2) INFORMATION FOR SEQ ID NO: 1406:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1406:

GTGGACCTGC AGTTAATTCA ACGATTTCAA GATGGGCGCC AAGAACGAAA CGTGGCCGAT 60
 20 ACTTAGGATT CTGGAATCAT CACATAATCG TGTGCATGAG GTGTTTCACT TTGGGGTCTA 120
 ATGATTCTTC ATGGAAnGTA TAGG 144

(2) INFORMATION FOR SEQ ID NO: 1407:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1407:

ACCTTTGCGT CCAGAATTAG CTACATGGTA AAGCTTCGTG TTACTATTTT AGGGATATCT 60
 35 TCAACnCGTT TCACTTGTAT AATTGTTTTT TGTAATTGGT GAAGTCATAG TATAG 115

(2) INFORMATION FOR SEQ ID NO: 1408:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1408:

ATTGGTATTG GCGCTGTAGT ATAGCTTCAT TATCTGATGC CATTAGTATA CGCACACTnT 60
 50 TTATTTATGG GCGTGGTATT CATCCTTATC GGGATCAATT ATTGGGTTAC ATTTT 115

(2) INFORMATION FOR SEQ ID NO: 1409:

(A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1409:

10 AACCAGATGa AAAGCAAATA TACATATATA ACTCTACATG GGGTCGTGGT TTGGATATTG 60
 TTCATGATGC ATTCGGTATG CCAATGACAA AGCAATATAA AGATAAATTh CAAGAAGATA 120
 AAA 123

15

(2) INFORMATION FOR SEQ ID NO: 1410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1410:

25

CTnTTTATAT TGAGGATTTT GTATCATATA TGGATAATCA TTAAAGGTGT ATGCTCTTGT 60
 TATCAGATCG CTACGGGTAA AATCGCTTCT ATAGGGCATT TACATGCCGG CTTCTGCCGG 120

30

(2) INFORMATION FOR SEQ ID NO: 1411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 455 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1411:

40

TTCGTATTG CGTTTAGAGA ACATGCGCAC AAAGGACAAA TTCCAGGTGT TAAAAAATCA 60
 AGTTGGTAAA ATCAAATTTT GTACTTTAGC CCATTTACAA TATCAATAAA ACAATGTACA 120
 GTATATACGA ATGCTATAAA CTGAATGTTT TCTCATATTA ATAAGGAAAC ATTCGGTTTT 180
 45 TAATTTGCAT TAAAAAATAA TTAGTTTTTA AAGGGGCTAT TTAAAGTGAA AATATTTGAT 240
 TACGAAGATA TTCAATTAAT ACCTAATAAA TGCATAGTTG AAAGTAGGTC TGAATGTGAT 300
 ACAAATATCC AATTTGGTCC GAAAAAATTC AAGCTACCTG TAGTTCCTGC GnATATGCAA 360
 50 ACAGTTATGA ATGAGAAATT AGCGAAATGG TTIGCTGAAA ATGATTACTT TTATAATCAT 420
 GCATCGTTTT GATGAAGAAG CAAGAATACC TnTTA 455

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1412:

ACAATGTCAA ATCACAATAG CTGTTGTAGG CATTGTGATTA CAATGAACTA AAGGCAAAAT 60
 TGGAGCAGTT ATCCATGAAT GATTAATAAC AACAnAAAGT ATGGGGTCAA GTTTAGGG 118

(2) INFORMATION FOR SEQ ID NO: 1413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1413:

TGTTGACGAT ATAGGAATTA GCAAGAAATA GGCTAAGATA GTTTCGCACA ACTTGGGGCC 60
 CAnCCACTTG CTTGTTTGTGA GAATTAGGGG TCCATTTCTC GTGTTGGGGC CCGAACTAAT 120
 AGTATGAATA TATATATCTA ATATTAAAC GGCAATATTT ATATGGTATA CATTTTTATA 180
 TTTAGTnTTT GSTATAGACAT GCTAATTAGC ACTTTCTAAA AAGGGTTGAA ATGATATACT 240
 GATGA 245

(2) INFORMATION FOR SEQ ID NO: 1414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1414:

TTTTTGTTAT TCAAAATTTA GAGTGTGTTA TATGATAACG GTTTTTTCAT AGCGACTTGA 60
 TCATTTTTCG AAATGATGAA AGATATGCAA GTTCAATCAA TCGGAACAAA AATACTATAT 120
 TATGGTAAGA AnTTCCCGAA GACTAGCGCA CTCACACACA AGTGCATCCT CGCGAACAAT 180
 GCGCACTTTT CACAAGCACA CAAACACAAG GCACAAGTGC ACGCAnTATT AGACAATGGT 240
 CTACCTACCA GA 252

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1415:

ATCTGCTGGA AGAGAAAAAA GACGCTCTTA AAAGTGGCTT TAGAAGGTCA AGATATAGAA 60
 GATATTAAAT CTAAAAAGA AGGAAGTTGA AAAAGTGATT CCAGGAATTT TC 112

(2) INFORMATION FOR SEQ ID NO: 1416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1416:

CTCAATTACA TTCAAGAAAA TGGGTGGAAT TACACAACGT TGGACTGAGA AGTATAGTTA 60
 ATAGCGCAAA TGCTATAAGC CTATATATAA AATGGGCACA ATTATTTTCAT GTACCAACAA 120
 GAAC 124

(2) INFORMATION FOR SEQ ID NO: 1417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1417:

TTCAAGAGCA CATACTGTAA CTCGTACGAG AATTTTTTCA AAATGACGCG TCAATCTCAA 60
 TATCATCATA TGGTATTCCG AGTAATACCC CTCGCTACCT TTTTATAGGTA GCGTCAATAT 120
 T 121

(2) INFORMATION FOR SEQ ID NO: 1418:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1418:

CTACGCCATC AAGAGGGTGT TAGTGCTATT AACTATTGCG GCGAGAGCAA TTAGTCGAAT 60
 5 GCAAATTAGG ACAAGTTGAT GAGTAACTAC nGCCAATATC GGTAAGTTTC ATGGCGGTTC 120
 AGC 123

(2) INFORMATION FOR SEQ ID NO: 1419:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1419:

20 CTTATAATCC TTACnGCAAT TTCACCTTGT ACGGAATTAA ACAACGGAGG CATTTACTTA 60
 CCCCCTTTAC TTAATACGTA CCAAACTTG GTCGTATTCA ACCATTGGG 109

(2) INFORMATION FOR SEQ ID NO: 1420:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1420:

35 GCTGTnGTGC TGCCAAGATG CTGATTGAAA AGTATATATG ATTGCATCAG TAGAAGAGCG 60
 AGCAGAAAGA AGATATAAAG ATAATCAGTT AAGAGGTGTC GAATCAAATT TTGAAGATT 120
 A 121

(2) INFORMATION FOR SEQ ID NO: 1421:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1421:

50 TGTTTTTACA GTCACATACA CTAGGCATCC TAGCATTATC TAAATTTAAT ACCATCGCAA 60
 CTTGCGCTTT AATCTTCAAG GCCAATTAAA CCTCCTTCAT CTTTCTAACT GCTTAnATAT 120

(2) INFORMATION FOR SEQ ID NO: 1422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1422:

GCCAAATCATT GTCAATGTTT AGGCATCAnA TTTATCGAAT GATTTTCATT TGCCATGATC 60
 AGTCAAGGCG GGGATTTTATT CAAAAATTAT GACGCCTAGT AAAAAATTTT 110

(2) INFORMATION FOR SEQ ID NO: 1423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1423:

ATTACCTTGC ATGAATTTCC ATCTGTCAAA TGTGCGCCTT CACGAATTTG TTCGATAAAG 60
 ATACGTTGGT CACCGTGAAT AATTTACCA GCTGCATTTn TCCATGGACC A 111

(2) INFORMATION FOR SEQ ID NO: 1424:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1424:

TGTTGTGTGA TTGCGTATTC TCAGGTGAAT TCTTACATAT ATAGTACTTT TTGTTTCCGC 60
 TTGATTTGAC CTTCATATC TTTCACATTC TTCGAAAATT GATCAAAGCh CTATTGAAAA 120
 ACCGTATCAT ATACAnACCT CTAATTTTTT TGACTAACAA AAAGAATTCT TTGACGTATC 180
 AACTATATCA TCATGACTTC 200

(2) INFORMATION FOR SEQ ID NO: 1425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1425:

5 TTTCTATAAT TTTAGACTAT TTCTACCATG TTGCTGAACA ATTTACTTAG ATAAAAATTA 60
 TnAAATTTTG GTCAATTAAC AAAGTTAGTT TGTtAAAACG TATACTTTAA TTATTCGG 119

(2) INFORMATION FOR SEQ ID NO: 1426:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1426:

20 AAAATGGCGT TGCATTTTAC TCTAATAACG CTCAAGGCGA CGGCAAAGAT AACTTAAAGG 60
 CACCTATTAT CGAACATAGT ACTCCTAnCG GACCTGGAAT TTAAATCAGA GCGGCC 116

(2) INFORMATION FOR SEQ ID NO: 1427:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1427:

30 TTTTATTTAC GTATAAGTGG GCGTTAGGTG TCACAGCGGT TGTCGATCAA AATATCATCA 60
 35 TCAATCTTGT ATATGGGTTT GCGGATTCTT ATTTTATGAT TTTACAGAAC TATCCTAGGC 120
 TTATTCTTTA TTAAAAGATG CAACnAGTTA TATAAAAAGA CGAATCTATC AACGCGAGCT 180
 40 GCTCACAAGG CATCTCnTAT AGCGTCCACA TC 212

(2) INFORMATION FOR SEQ ID NO: 1428:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1428:

50 GAAAAATTGG TTCTGAATAT AATGGTGCCG TATACTTTAC GCCTCAAATC AAAGATTTTA 60

55

ATTTTAATGA AAAACATCGG TCGAATATAA CATAAAAAAA CGTCTATATC AAAAGCATCA 180
 TGAATAAACA GAGGAGCACA AAAATGAnTA AAAATATAAT CATCAAAGT ATTGCGGCAT 240
 5 TGACGnTTTT AACATCAATA ACTGG 265

(2) INFORMATION FOR SEQ ID NO: 1429:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1429:

CGTACGAAGG ATTTGCAAAC TTCTTCATTC AACAAGCTAA AGAAGAACGT TTCCATGGAC 60
 20 AAAAGATTTA TAACTATATT AACGACAGAG GTGCACATGC AGAATTCAGA GCAGTTTCAG 120
 CACCAAAAAT TGACTTTTCA AGCAT 145

(2) INFORMATION FOR SEQ ID NO: 1430:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1430:

35 ACACCGCTAA GCGTATTAAG ACAGGATCTG AAAATGGACA CATCGCAATC GAATTATTGC 60
 AATGCCAAGT CATATCGGGG GTGAACCGCA ATTTCAGGnA TTAAGTGGAT AGGTA 115

(2) INFORMATION FOR SEQ ID NO: 1431:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1431:

50 nATGTATTnG TGAAAAGGTC CTGAGTGGAC AAAAGACCTA AATATTTAAT GGTCGATTAT 60
 CGCACGTCCA TAGTTGGTGA ACAGGAACTT ACACGTACAT CTAATCGCAG ACTATGCGTA 120
 AACTTTGGAA ACTGCTAGTC ATTGAAGCGT GGTATGTGTA TGCACGTAAA TATGCATTAG 180

55

(2) INFORMATION FOR SEQ ID NO: 1432:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1432:

GGAATGATTG ATAAATTGGA CTACTTAAAG ATTTCCGGTAT CGTGCATTT GGCTCAGTCC 60
 ATGTTTAAATC ACCTATGnTG ACATGGTATG ATATTAGTGA CTACCAGAGA TATGGATGAT 120
 TTGGAACGTG GAGGACTTGA TCGTT 145

(2) INFORMATION FOR SEQ ID NO: 1433:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1433:

TTTATTGCAT TTACATAATA ATATCCTTTT GTTGTTTTGG TATTTCTATT CATATACAAG 60
 ACCATACCTT TAACTTTCAG AGCTTCCCCC TTATTTTGAG TTGCCATTTC AGAACCAATA 120
 ATCCATGTAC CTTTATCATT TTTATCAAAT TCGTCATCAC GATAACCTn 169

(2) INFORMATION FOR SEQ ID NO: 1434:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1434:

GATCTATAGT TCTGTAATCT GACGTGCTTT GCCATGTGCA CCACTCGTCn TAAAAATCAC 60
 TTACACTTAA CCCTTTTCCA CCTTTATCGT ATCCACCTTC AA 102

(2) INFORMATION FOR SEQ ID NO: 1435:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1435:

5 TTCTTATTAT ACAAATAGAA GCCATGTGTG CTTATATCGC AGCATCATGA CTCCTTTTTC 60
 ATTTGAATAT ATAAATAATA CAGnCGCTTT CGAATAAATT TAGGCTAATT CTACCA 116

(2) INFORMATION FOR SEQ ID NO: 1436:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1436:

GGGGGTTTAT GTACTGGTGG ATCTGCAAAC TACTTGCGCT AAAGAATATA CAGATATGGT 60
 20 AAnGAAAAGT TTAGATTCAC ACGCCATCAC AATGGATTAG AAAAACCGAA TTTCTTCAGC 120
 AATTCTACAA TTTCTAGTAT ACGC 144

(2) INFORMATION FOR SEQ ID NO: 1437:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1437:

35 GTTGCTGGGn AACCTATGGT CGAACATGTA TTGGTAAAGT GTGAAAGGCT CTGGTGGCGA 60
 TCAAGTTGGT AACCATCGTA GTACATGGTG CTGTAAATGT A 101

(2) INFORMATION FOR SEQ ID NO: 1438:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1438:

50 AAAGATGGTG ACATTTTATA TAATCCGAAT GTGCCAAGTT ATTCAGCAAA GTATCAATTA 60
 AGTAATGATG ACTACAATGT GAAGCAACTT AGAAAGAGGT ATGATATACC AACTAnGAAA 120

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AATTTAGAGT TTACATTTAT AGAAAATAAA GAAGAAAACA TCTATTTTAC GGATAGTATT 240
 AATTTCAAAC CTAAGAATA GGGTTAATAG AAGTTTGAAA TGAAAATTTT nTAAAGTGTG 300
 5 CAAAATAATT TGTCGCTTTA G 321

(2) INFORMATION FOR SEQ ID NO: 1439:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 135 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1439:

CAGTTGTAAT GGGACCTGGG CCAATCGGAT TACTTGTAAG ACAAGTGTTA AAAAGTAAAG 60
 20 GCGCAACTGT TGTGGGTACT GGGTTGGGAC AATTGACCAA GTCAGATTAG ATTAAAGCCA 120
 GAAGGCCATT GCCAC 135

(2) INFORMATION FOR SEQ ID NO: 1440:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1440:

35 AAATTATTTT GAACACTTTA TGAAATTTTT ATTCAAACCT TCTATTAACC CTATTCAGTA 60
 GGTTCGAAAT TAATACTATC AGAAAAATAC ACATTTnCTT CTTTATTTCT 110

(2) INFORMATION FOR SEQ ID NO: 1441:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 436 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1441:

50 TCTCTTTTGG ATTCATTAAG ATTGChGCAT CGATACCAAC GTTmAACGGT GATTGTGTAA 60
 TGAATTTTGG CCACCAAGCT TTTTAAACAT TATTCITTTAA TTCAACACCT AAAGGACCAT 120
 AATCCCATGT GTTTGATAAA CCACCGTAAA TATCACTACC AGGGAACACA AAACCTCTGT 180

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5 GAAAACGCCC CATGGAAAAT AACAGCATAG TAAATATGCT TTA~~CT~~CCAT GGGACGAGTT 300
 AATATTTTAA ATTGTATATA ATACAAAAnA AGTnACGTAT TTAACCCGCG GTTCCACCCA 360
 AATTAGTGTA GTCACTCGCT TTTATTTTAA AATGATTCGT TGCGCCAATC TTATTGTTAA 420
 GCTTACACTA TCCTTA 436

10 (2) INFORMATION FOR SEQ ID NO: 1442:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1442:

20 ATTTT~~TT~~AGAA GCATACTGCG AACGTCATCA CATCGATTTA CATATCAAAA AGTTAGATT 60
 GTCGCATAGT CTCGACCGAA ATAACAGCAT TCAGAATGAA GCTCGAATTA AACGTTACGA 120
 ATGGTTTGAT GAAATGATGA ATGTATTAGA AGCGGATGTA TTGCTAACGG CGCATCATTT 180
 25 GGACGATCAA TTAGAAACTA TTATGTATCG TATTTT~~TT~~AnT GGGAAATCAA CACGTAATAA 240
 ACTAGGATTT GATGAGTTAT CGAAGCGAAA AGGTTATCAG ATTTATCGAC CACTTTTAGC 300
 TGTCTCTAAA AAAGAAATAr AACAAATCCA AGAGAGATAT CATATTCCAT ATTTTGAAGA 360
 TGAATChAAT AAAGATAACA AATATGTTAG AAATGATATT CGTAAnAGAA TTATTCCAGC 420
 TATTGATGAA AATAATCAAC TTAAAGTATC GCATTTATTA A 461

35 (2) INFORMATION FOR SEQ ID NO: 1443:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 143 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1443:

45 AAAGGTGATA AAAACAAAG GCATTGTAAA TTA~~CT~~TGAAA ACCAAGTGAG TTATTACACG 60
 ATTCTAATTG GGATAATGCG CGATATTTTA TTCCACACTT GTTACATTAT TGCTTTACGT 120
 50 GGGGGTTAGC GTGGAnTCAT CAC 143

(2) INFORMATION FOR SEQ ID NO: 1444:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs

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1743

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1444:

TGGTGTGGT TCATCAGTTG TAAACGCGAT TGTCACAAGA CTTAGAAGTA TATGTACACA 60

10

GAAATGAGAC TATATATCAT CAAGCATATA 90

(2) INFORMATION FOR SEQ ID NO: 1445:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 218 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1445:

ATTGAACAGT GACAACAAAT GACAACAATG AATGACCAAC TGAGTTGCAG AATTGACCGA 60

25

CCTGACTTGC TGTnAGATGT GCATTGCCTG TGACCACTTA ACTGCTGTTT GTACATTATG 120

ATTGTGCACG TGAAGTCTTT GCAAATGACT TTAAACATTA TGCTGCTAGA GCCATCTTTT 180

AAAGATGTTT GGACTAACGT nCATGATGTG AATATCTG 218

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(2) INFORMATION FOR SEQ ID NO: 1446:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1446:

TTTGACTTGA CATTATAGAA CACAAATTCA TTTGAACTA TGTTTTCAAA TTTATTTATT 60

GTTACTGGGA ATTTCACATT ATTAGATTTA TTTATTTTCT TTTGA 105

45

(2) INFORMATION FOR SEQ ID NO: 1447:

(i) SEQUENCE CHARACTERISTICS:

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(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1447:

AGACTGAAAA CTGCATATGC AGAGGCGATG AAACAAAATG CCAT

104

(2) INFORMATION FOR SEQ ID NO: 1448:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1448:

TTGAATTAAC TGAAGAAATA GCACTGCAAG CAGGATTGTT GATATGACAA CATTGAGTC 60

AGAATGGCAA CAACAACGTG ATTCGTGCAC TCCAAGCACG TGCA 104

(2) INFORMATION FOR SEQ ID NO: 1449:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1449:

TATTAATTTT TTTTAATATG GAATATTCAT TGCATCGCTT TCCTATTCTT CAAGCCCACT 60

TTTTATCTTC ATATACATTA ATTAACCACC kTCAAACATT GTCGTTAGAT TCGCCAAATT 120

GAATCTATTT TTAGCACAGC AAAAAACCGA ACTGCTGAAA TAATGCATCT CCAACAGTCC 180

GGTCTATTAA ACTATTTACT TATCTTTATT AAACAATTGA CATGATTTAT TAGAATAACC 240

CAATTGGCAT GACCATGCAT CAGTAACATC CATGTTTAAT GGCTGCTGGT TTTTtaggTA 300

AACCAGGCCA GAGTCATGGn TGGCACCTGn GCAACGCnAC GATAAAGCC 349

(2) INFORMATION FOR SEQ ID NO: 1450:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1450:

GATTTTATAT AAATATAGCT TTTCAACAAA ACAAATGATT GAATTTCTAG GAATTGAGTC 60

ATTAAAAAAA CACTTGAAAA ATTCAGGTGG GATTGCGCTA TTGCCGGAAT TTATTGTTGC 120

AGAAACAACA TTGaTAATTA ATCCTGAATC GAATAAGCAm GTACTTGAAT CTTTTGTAAA 240
 AGATGTTTTT TTATAATTAT TGGTGAAAAC GTGTAGTTAT GGTGAAACTC AAAGATAATA 300
 5 ATTTAAATGA GATGTTAATG AAAAAGTAAT TCAATATAnA ACAGGTGATT TAnATCTTAA 360
 TAAGGnTAAT TCCAGGTTGA ATTCCAATTG CGGGCATCAT 400

(2) INFORMATION FOR SEQ ID NO: 1451:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1451:

20 TCGGTTATAG TTGCTATTCT CAATTATGTT CGCGATAATT TTAAGTAAAA GTAAGCACAG 60
 ATATTGAATT TGATAGGAGT TAATTGATAT ATACATACGA ACTTTCATGG ATCACTTAAA 120
 TTnG 124

(2) INFORMATION FOR SEQ ID NO: 1452:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1452:

35 TGTATTAAAA ACCTTCCACC TTAAAAAGCA ACAATGCGGT GTCCTTTAAA TTCAAACATA 60
 ACCATATACG AATTACTCGA TAATTCTGTG TGTTTAATTG ACAGATGTCG TGTGAATTGA 120
 40 TnATTT 126

(2) INFORMATION FOR SEQ ID NO: 1453:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1453:

55 ACTTTGGCAA CATCTGGAAT ATCATATAAA TCAAGTAACT TACCTAACCG ATGATTAATA 60

CTAACAGTTG TTTCCATGCC TACACCTCAC GATATTATCA CTATTCATAT TAACATTATA 180
 TGTAAGAAAT TAAAATCTTT TGAAGCATTa AGATTACTTA TCATTnTAA ATTCAATTT 240
 5 AACTAACAG TAATTTATGT AGCTTTTGnA ATTCTCATAA 280

(2) INFORMATION FOR SEQ ID NO: 1454:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1454:

ATATTCTTTA AATTAACTG ATCACTTGAA TAATTAACAT TACTTAATTC TATGGCATTc 60
 20 ATGATGATTc CTCCTCATAA ATGAACGTTA AAATATCCTG CAGTTCCTCA AGTGACATTT 120
 CGATGGCTTG CGCTTCATTa ACCAATTCTT TAACCAAATT TTCAATGCTa AAAAATTGTT 180
 TCTCTTTTAA AATAGGAACT ATTCTTnGCT CCTTAACAAA GgCCCTTTT CCTCTAATTG 240
 25 TT 242

(2) INFORMATION FOR SEQ ID NO: 1455:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1455:

ATAAAATTGC AGACTTAGAT TACTCTTGTT CAGCATTTTT AATGTATATC GGTATAGATA 60
 40 TTGATGTGAC AGATCAAGTG AGACTTGCAT AntGGTATTT TATTCAGATG 110

(2) INFORMATION FOR SEQ ID NO: 1456:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 551 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1456:

ACCAAGTGGTT GCCTTTTTAA GTCCCGCGTG GGACAAAAAT TAACCTCTTT AACTTGCAA 60
 55

AAAGCGCTTG CAATATATTT TCGATTTGtT ATTCAACmAA ACGTTTTATT tTATTCGCTG 180
 TAGTCAAATG TATACCCTTA TACTGACTCG aTAATCATTT GCTTATnATT TGAGACTAGG 240
 5 ACATAAATca ATGCTCTAGA ATCCAAAAAG TCACATTAGT AGTAGTTAAC CGAACGAAAA 300
 TGCACCTTGTA ACAAGCTTTT TTCAATTAAA GTCAGGGGCC CCAACATAGA GAATTCGAA 360
 ATGAAATTCT ACAGGCAATG CGAGTTGGGG TGGGACGACG AAATAAATTT TGCAAAAATA 420
 10 TCATTTCTGT CCCACCTCAC TCAAAATAAA TTTCACTATC CGTAAAATAA ACAACTAACT 480
 ATTTAAGTAT CATCTCTCCC CTAATTAACA ATTATAAAAA TAAGAACCAA TATTCGAGAC 540
 15 AACCTAATTA A 551

(2) INFORMATION FOR SEQ ID NO: 1457:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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. (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1457:

ATCnGGGGCT GCATAAGCGA TATCAAGTGT GAGCATTGAA CGATTCAGGA CTGACCAGCA 60
 30 CGCCGTTTGC CTGCTTTGAA AGATCCACCG ACAAATCCGC CAACATCGT 109

(2) INFORMATION FOR SEQ ID NO: 1458:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1458:

ACCAGAGCCT CTTTGA CTTC CTAAGTCGAA TAGCATCGTT GATATAGTTA AAGATGACGC 60
 45 TAGATTTAGn AATCCAAACT CATAACACCT CCACCATTC ATCACATCTG GA 112

(2) INFORMATION FOR SEQ ID NO: 1459:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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CCCCAACCAA TTTTAAAAA AAGGGGGCCT TTGGGGGGGC CAACCAAGGG GGAACCCCTT 60
 AACCCCAATT TTGGCCAATT TTAAAGGGAA GGCCTTGGAA CCTTTTGGG AATGGGCCGG 120
 5 TTTTAAACCC TTGGTTTCCG GAAGGGGAAA ATTTTAAAA AAACCGGAAT TGGTTGGCCC 180
 CCTTTAAATT AAAAAGTTCC CTnAAAAAnA AATTCCCCCA AGGG 224

(2) INFORMATION FOR SEQ ID NO: 1460:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 135 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1460:

20 TTTCGACAAT CAATTGACG TCAGTGCCAC TCCATCTATA GTAAAGCGTT GATACTTTCA 60
 ATAATAACTG GATCACTGTC TAATTATAAA TGGATTCTTA CATCCCACCA TAATAAATn 120
 CATATGTTCA TCACC 135

(2) INFORMATION FOR SEQ ID NO: 1461:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1461:

35 TTATAGAACC TCGTACTCCT nTCGACACTT GAATTTAAAT CAGAGCCGCC AGTGGAGAAG 60
 CATGAATTGA CTGGTACCAC TCGCAGAAAG TAATGATTCT AAGCCACTTG ATTA 114

(2) INFORMATION FOR SEQ ID NO: 1462:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1462:

50 GTTGAATTGT TGGTGATGTG GTTACACGAA TTTCGAATAA TTGTTCTTTA CGTCAAAACG 60
 TATCGTTCCA AAGTAATCCC CnGGTAATAG TTACCAACAA GTTCA 105

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1463:

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TTGTATGACT CTCGGACTT TGGTAAAATT GTGAACGCTG GntGAATGAT TTTTGTTTGA 60
 CAATTGGCCT TATCATCATT AATCGTATTT TTAAGCTGCT CGGATATAAG TTCTCAGCGA 120
 GTTCTTTTTG ATGTATCATT AGTGTAGAAA ATAGCTGTTT GT 162

15

(2) INFORMATION FOR SEQ ID NO: 1464:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1464:

TAAATTGGAA AGTCACATTC AAnATGCGAA AATGTTTTAA AATGTCCTGT AGGTGCTTAA 60
 TAGTTTTGCA TTGCAAATT TTAAGTGAACC GGTTTAAACG AAT 103

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(2) INFORMATION FOR SEQ ID NO: 1465:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1465:

AAATTGTATA ACTACCAAGC TTATATGAAA TGGTAAACAA AATATTATCA CTTGTTTGAT 60
 AAGTAGCGTG GAAAATATTG TATCTTTCTA AATGTACACG TTAGAAnTCA TGCTTATGTA 120
 TTACACGCGG GGCAGTGGTA CCTAAGGGCC TAT 153

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(2) INFORMATION FOR SEQ ID NO: 1466:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1466:

TTTCAGTAAC ATATGAAAAC TTAATTAACG ATGTTTCAGTA GGTTCATACA TTTTACTTTA 60
 5 TGATGCTTAA TTGAATTACA nTTAAGATAT GACCAGCTAA AAAGAGTTAA TGTGATATTT 120
 AACC 124

(2) INFORMATION FOR SEQ ID NO: 1467:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1467:

AAGGAATTAA GTTTGCGACA CCAGCAAATA GTACTAATAA AGGAATATAT GGTAAGTCAA 60
 TAATTGAATA ACCGATATAT AAGAATATAC CTAAAATAAC ACTGACAGTT ACTTGACCTT 120
 GAATGTAAGA TTTTAATGTA AAGTTTAAAT CAGTTAATAA ATCTACGAAA AATACTTTAC 180
 25 GTTCACCTTT GAnAAATTTA GCAACAGCTG GGATAAATTT TTCATGGTCT TTTAACATAT 240
 AAATTAAGAA GAATGGAACC ATAATCAATA AGAAGATGGT TGAAATTAAT GATGTAATGT 300
 ACTGTAATGA ATTAGATAAn ATATTAGnAA CGCCATCACC CATTGATTTA ACCA 354

(2) INFORMATION FOR SEQ ID NO: 1468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1468:

TGCAAACTAG GAACAATAAT GTTAATATAA CTATGATGnA AGTTAAAAAA TAAAAAGGAA 60
 CACTCTATAA TATGAATTAG GGTTTACAGT TTTTGTAGTA TTTTACAGTA TCAAAGTTTA 120

(2) INFORMATION FOR SEQ ID NO: 1469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TCTAAATGCT GACTAAAACT AGCAACACGA GACTCATTAT TATTAGACAC GATTGTAATA 60
 GTGATTCCCTT TTTCATTAGC TTCCTTAAAC CATGCTTTAA CACGTTCTGT AGGTTCTTTA 120
 5 ACATCCCAAC CTACTAGCGT ATTATCTAAA TCTGTAATAA TACCTTTAAC GCCTTTGTCC 180
 ACTAACTTGT CTAAATCAAT TTGAAATATT GATTGAACAT ATGAATTCGG CATAAAAAAC 240
 TTGCGAACTA AACCCATTTA ACTCACCTTT ACCTTTTAT AATTGAGACA CTAATGCTTC 300
 10 AACAGTTTGA CTTGATGATA CAGCTGCTTT TTCTAAAAAT GCTTCGAAGC TCATTTCCGC 360
 TTCTCCATTT GCTAAGTCTG AAAGTGCACG AACTACAACA AATGGTACAT TAAATTGATA 420
 15 ACATGTTTGT GCAATTGCAG TTGCTTCCAT TTCAACCGCC ATCGCATTG GAAATG 476

(2) INFORMATION FOR SEQ ID NO: 1470:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1470:

CACCATACAT GGGTAAGGAT ACTACTCAA TCAACTTGAA ACCAATAATH CATGACCATA 60
 TGTGTGCCAA TGAATTCAAT TGGAAAGACA ATGATGAGAT ACTATTAAAA CGATTATATT 120
 30 TATTGTCAC TGTTCAAACG CACTCCTTTT CCAAAT 156

(2) INFORMATION FOR SEQ ID NO: 1471:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1471:

AACAAAAGTT TTGAAAAGCC GGGTGCCAGC GAAAACCTAA AAAGCACTTT ATCAGAAAAA 60
 45 GCTAAGAAAA AAGATTAATA TTCATTCAAT AAATATAAAT CCAATTTAAT TTGTTGTTTA 120
 AGGTCTACAA GTGTATGTTT AATATACAAT TCATCGTTTG ACGGTAAATC AGATACTTTG 180
 AAATCTTGTC GCTCAACCTC TAGTAAATCG AAATCGCTAC CAGCTGAATT ATAGGTTTTA 240
 50 AGTTCACCCT CTTCAATGAT TCTGTTTTCA AAGTCTTTAA TAACTATAAA TACTGGTTTA 300
 CCGTTGTTAT TAAACAACCT GTCTCTTTTG TCTAATAAGC TTATACAATC CAAATTCATA 360

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(2) INFORMATION FOR SEQ ID NO: 1472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1472:

CTAGGATTnC ATCTATTTGG GATGAAAATA AGCGTTTCCT GAATCCACAA GAATATCCAG 60
 TCGATTTAAG CCAGGCATGT TGGGGTAATA ACATAACGTT TTTTGA 106

(2) INFORMATION FOR SEQ ID NO: 1473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1473:

TATCTTACCT ACATTGTTAT CTGATGGCTG TAATCATTAA ATCTATAACA CCGAGTTCCT 60
 CCATTAATTA TCAGCTTCAT TCGACTGCCT TTTTATnTTT CGTACTATTA CGAATTT 117

(2) INFORMATION FOR SEQ ID NO: 1474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1474:

ATGCA¹ TCGAAnCAG CTGGGAGATA TAGGTAGTAT CCTAAAGAAG TTCAGTTAAT 60
 CGGAGCGA¹ GTn GCGATG AAGGTAACAT TGCGGAGTGC CAACAGGCCA AGTAAAACTT 120
 AACGGCAACC ATGCCTTATA TTAAATGCCC TTCCGGGAAA GGAC 164

(2) INFORMATION FOR SEQ ID NO: 1475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1475:

5 ACAGCAAGAC GTGACAAATC AGATACTATT AGTCATCAGC GTTAACATGT GGATAnGTGT 60
 GAGGTACGAA TAnCCGAAAG GAAATACGAC CTTTAACATT CGCGCACAAA ATGAGCTCAG 120
 GCGCCTGCCT TGCCCATTTT TTAAATTATT TCCCTGGAAA TGATTGCTG TGTGCTGTTC 180
 10 TGTCCACAAC AACACGATTA ATGCCATGAC 210

(2) INFORMATION FOR SEQ ID NO: 1476:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1476:

20 AGGGTGATTT CACGGTTCGT CTGCCCATTT AATTGCGCAT TTTGCACACC ATCTACCGTT 60
 TGCAATTTTG GTATTAATTG TTGCATGCAG TACTGTCCGT TGACTTTGnT GCAAGTGCAT 120
 25 GCTCTTTC 128

(2) INFORMATION FOR SEQ ID NO: 1477:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 641 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1477:

AAAATCTGGT AAAGTAACTA GAGTTTAATA AATATATTGC ACATAAAAAA TGTGACCTTA 60
 40 TGTGGAGGAC ACATTTACTT AAGAACTAAG AGCTCAACCT CTTAGTTCTT TTTTGTGTTAC 120
 CAAACAATAC ATAATGGTTC ATAGTGAAAT TCGAACTATC AATATAATTT GGTTAATACG 180
 TTTAATAATG GTTCTCTGTC AAATTGGACT TATGGGTTCA ATATCGATTT TGGCACATAA 240
 45 ATCAATGTAC TAGGACCTAC AATTTTCCTT TCAATAATAA ATCAGCCCAT AATCTTCATT 300
 AATTACAGCG TGATTCATCT ATTATTATGT TATAAATkCT ATCTATAAAC GTCAGTTTAT 360
 TAAATAACTC ATGCACTTTA TTAAAAATCC TCACAAATTT GAATATACTT AATTTAAATC 420
 50 TGTACTTCTA ATTTGCAAAA TCAACCCATC ATGTACAGTT ACTTTGCTT GCAAAGACTC 480
 AATTTCATTT GAAATAGTTA AAGTAGAACC TATATnAAGC ATTTGTCTAG CTAAATTATA 540

55

GATAACTCTT ATCTTTTTCa ACTGTAGGTG ACCTTTAGGG C

641

(2) INFORMATION FOR SEQ ID NO: 1478:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1478:

15

TTAACCGTGA TGCAGAGTAG TAAGTGGATn CATGCTCTGT TATGGATGAC AAGACAAAGC 60
 AGCGAATATT GCGTACTGCG ATTGATGAGC AGATGCATAT GATTGGATTG GTGCAGCTGT 120
 C 121

20

(2) INFORMATION FOR SEQ ID NO: 1479:

25

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 133 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1479:

ACCATTGCTT AGATAAATAC CTCGCAGTGA ACCGCATTAG TATAGCACTT CTAGCTGATC 60
 GCATCAGTAA AGTATGCTAT TAATGTCTCA GTTTTATCTG TAATGCATGT TTAAGTTAGT 120
 CATAGCATTA Ttn 133

35

(2) INFORMATION FOR SEQ ID NO: 1480:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1480:

TTTTGGGGnT TTtAAATTTT AAATTCCCGn TGGGGGAAAT TCCCTTAAAA ATTCCCAACC 60
 CTTTTAAGGG GTGGGGGTTT TTTTAGGGAA AAAGGGGCCG GGGGTTAATG GTTCCCAAAA 120
 AATTGGGGAA AATGGCCCCC CAAATTTTAA ATTCCCGGTT TAAAAATTGG GGTGGGTAA 180
 ATTGGAAAAA CCCCCAAATT T 201

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1481:

CAGTATCAAG CATAGTAAAA AATGAGGGTA GGACTGAAAA TACGGCGTTA TTGGTGGTGC 60
 ATTCACGGTA AATATGTTGC ATGACCAGCA AGTTTTGGnC TTCTGATGCA CC 112

(2) INFORMATION FOR SEQ ID NO: 1482:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1482:

CAAAAAACAA GTTCTGATAT GCAGTAGCTG AATAATTTTG CTAGTTACAC CAnAGTGATC 60
 TTCTGGTGTT TTA CTTTTTA TAAATGTTTT CATATATTTT ATATGTATAA AAATGGGATT 120
 TAGCGTA 127

(2) INFORMATION FOR SEQ ID NO: 1483:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1483:

AGTGGTGTAT TGGGTGAGTA ATGCTTAACT TCATACCTGG TGCATTGGCT GTTCAGTATC 60
 ATTATATCTG CATGGGCGAT ACT 83

(2) INFORMATION FOR SEQ ID NO: 1484:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TATTATTGAT GTTCTTTGGT TCATTCTTTG GTAATAATTT TGCACCTGAA AATTTACAAC 60
 CGTTAGCTGG AACCTAGnCA AAGGGATGGG TTTAGTGGTC TATTGTGGGT TTATTGGTAT 120
 5 TCCGTGGGCC ACCCCATGGG GCCATTATGG TTTGGGAATT TTGGGAATAA ATTAATTTnC 180
 CCAACCAAAA ACCAGGCCAA G 201

(2) INFORMATION FOR SEQ ID NO: 1485:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1485:

20 CTCACAGCAA CATCAAAGAG GCAGATATTA GTCAAGTTCA ACGTAATAAC ATCTACCTTC 60
 ACAAGTCGAT AAAGGAGCAC CATCATTAAT AAGTAGATCA ACAAGTCAAC GAGAATTTTA 120
 ATGTGCAGAA TAGAGAAGTA CACCACACAn ATAATCAAGC GATGTAATTA CTACTACATT 180
 25 TnCATGACA GAGTGAACCT CAACAGCGGT 210

(2) INFORMATION FOR SEQ ID NO: 1486:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1486:

35 CAGGTTATGT TTGCATTAGA AGTTCTTGGA AAATCTTTAT GGAACGTGGT TTACACCCTG 60
 40 ACTTTGAATT GCATCGATCT GATGAAGATA AATGAAATTG AATGGGATGG CnACATGGA 120
 ATGCAACCTA TGACTTGGAT GGAATTAGAT GAAGCGGG 158

(2) INFORMATION FOR SEQ ID NO: 1487:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1487:

TTGCAGCATA TAGAGGTAGA GGCATCGCGA CAAAGTTATT AACGTCATTA CTG 114

(2) INFORMATION FOR SEQ ID NO: 1488:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1488:

15 TGCTAAGTGA TAAAAAGAAT GATAAGCCAG GTGTACCAAT GGGTCCTGGA TTAGACCATT 60

TGGGAGATAT CGTTGTACCA CATGTTGATC AACTAACGTT nCCACATG 108

(2) INFORMATION FOR SEQ ID NO: 1489:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1489:

30 CAAnACGTAA TTTCATGATG AAAGTGGTCG ATAATTTCTT GAAACATCGC TTTCAGTAAT 60

AACGCCTGCT TTAAGGTCAC GTTCCGCATA GGTGTACTGA GGATGTTGAT GT 112

(2) INFORMATION FOR SEQ ID NO: 1490:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1490:

45 CAGAACGTTT AAAACAAAGT TGGAAAAGTT TTCTAATCGT ATTAGCTGCA TGTTTAATAC 60

TTATTATTGC AAGTGAAACG CTTATTTTCC TTTAGTCATT TGACCGATGT TAAAGAGGTG 120

AGATGGTTAT TTAGAATCAT TGTATTGATT GTTTTTCGGG TAGTGATGTT CACAATTTAT 180

50 ATCTCTTATC ATCAATTATAT GAATGACTTT TTAGTTACTA AGTTATTTAA TATTTCCGCA 240

GCGACGCCAt AGTTATTATG TCTAT 265

(2) INFORMATION FOR SEQ ID NO: 1491:

55

- (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1491:

10 CnAAATTGGC CAGGGGCTCA TCCAATATTA AAATAGGCGT ACGAGGGATT AATAGACCAC 60
 CTAATGAAAC GCGTTGGTTG TTGGACCTCC AGATAAATCC TGGGGGTCGG TGG 113

(2) INFORMATION FOR SEQ ID NO: 1492:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1492:

25 ACTAAGAAAA TCCGAAATCT TTTCCGCTTC TTTTAAATAC GTAATACTTC CTTTTTTTCG 60
 CTCTAAATGT TTGGCATTCA ACTCATAACT ATTCATTAGT TTCGTTAAGC CTTCTGCATG 120
 ACTCTCATTT TGAGAAAAAA TTTCCAAATG GTACGAAGAT GTTTCAGGGT TATTCACTGA 180
 30 GCCACCTGCC AGAAAAGCTC CTCTCAAGTA ACTGCGTCTC ATTTTCGTCAT CTTGAATCAT 240
 TGAAATGATC AATTTTCATGG CGnnAAAATG CCGTCT 276

(2) INFORMATION FOR SEQ ID NO: 1493:

35

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1493:

45 GATGACGAGC GCCAATTATG TCACTTTTAT GGCAAAAGCT GGAACATAAC AACnAGCCT 60
 GCCAGTAAAA TTGGCAATTG GGACGTTCTT AGCAGGTGCG TCATACATAC 110

(2) INFORMATION FOR SEQ ID NO: 1494:

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1494:

5 AAAAAAAGG TTTTACCC GGAATCCAA AnTTTAAATC CCTTAAAAA AATTCCGGCC 60
 AACCCCCAAA CCAAGGTTT TTTCCTTAAC CTTGGAAnTA ACCAAGGTTT TTTTCCAAA 120
 AAATTTTCCA AAAAAGGAAT TACCCAAACC CTAAAGGTT TAAAATTGG GGGGGGAAAA 180
 10 AGGCCCTTTT AGGGGGGGAA 200

(2) INFORMATION FOR SEQ ID NO: 1495:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1495:

20 AAAAAATTG GTGCATTAT CATATGGAGT ATTAATCTGT AGAAGTAAAG GCGATATAAA 60
 TGTACTTTG GTAATAAAGA TTACAGCGAA CGTTATTATT GCTCAGGTCA GATCAAGAAA 120
 25 TTGGTGTCCG GGTGACAAGA CTTGGTGGCG CGGTGTAGTT TGTCAGTTGT GTGGTCATCT 180
 TAAATAACGC TATCGTACGG TGTGTATCAC ATGAAGGGAC TCTTACTAAT TCTGCAAGTA 240
 30 CACGTCACGC nnt 253

(2) INFORMATION FOR SEQ ID NO: 1496:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1496:

40 ACGCTAGCTT CTGAAAAAAT AAGTGAActA TGGATGCAAT GAnCCTATTC CTGAATGATA 60
 45 TTAGACGTAG CGCACCTGGT GCAGAACGCC AATAAAAAGA CAAG 104

(2) INFORMATION FOR SEQ ID NO: 1497:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

AGGGAGGCGC CCAAATGGCT CTATATTAAA AAAGGACTCT CAGAGCATTa ATGAAAAGTT 60
 GAAGCTCAAA AGGAAnCGAA AGAAACAAGT ATCAAAACAT 100

5

(2) INFORMATION FOR SEQ ID NO: 1498:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1498:

TGGAACTTTG GGGAAAGTCAA ACGGTTGTAA TCGTTGAACA TAAAGTTAAA CACATTCTGG 60
 ATCATGTGCGA nCGCGTCCAT TTGATGGATA TAACGGGAAT A 101

20

(2) INFORMATION FOR SEQ ID NO: 1499:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1499:

AGTTCTGGTG CATCGTTTTT CATTGTATTT GTGACGATTA TCATTCCAGC ATTAGAATAT 60
 TATGCATTAT ATTTAGGTGT GATAGGTGCA TTTATAGGTG GTTTAACTGT TTATACACTT 120
 TCAGGTG 127

35

(2) INFORMATION FOR SEQ ID NO: 1500:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 560 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1500:

TCCCCGCTTT AATACCTTCC ACGATTTCTT TAATTGCTTG CGGTTGGTCA CCTTGAGGCT 60
 CAAAATCAGA ATGTATTTTA AAAGGATAAT GTTCAACCAT TGTCACATAT GCCTCCTCTT 120
 TCAACGTATT ATTTATATTT CCGCTCAACT CTTTGCTTTC TCATnACATA TnTTAGCAAA 180
 GTAGTCACAC AAAAaGCAAA CGTTkGTTTC TAAAAATGTC GAACAAaGAA AnACAAACAT 240

55

AAATACACAT TATATTAATC ATCATTTTGT TTCAACAAAT TTGTTTGAAA CATTATTTTA 360
 AAGTTAATCT TAGCGATCTT CATCTTGATG TTTATGAAAT TCGAGTTGAT CTATAATTAA 420
 5 ATAACCAGCT AATAATGACA CTACATCAAT AAAAATAATC CACTCGTTAT GGAAATACTC 480
 TTTATAGATT GAGGCACCAA TTAAAATTAA TGTCAGAATA GTACCGACCC ATTTACTTCT 540
 10 TGTATTACA CTAAATAATA 560

(2) INFORMATION FOR SEQ ID NO: 1501:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1501:

ATTAAATCAT ACTnACAATT ACCGATGACA TTATTCCAAT TCAATCTAAT TCCGTGATGA 60
 AAGAGCCACG TTTTGGTTAC TTCGTGGGCG TGAATTATTA TG 102
 25

25 (2) INFORMATION FOR SEQ ID NO: 1502:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1502:

TATGGTAGCT CCAAATGGTT GTATCGTCAC ACCATCATCT TCAAGTGCAA TGCGATGTAA 60
 TCGATTGGCT GTTGTCTTCTG TTACCCATAG TACTTTTCA TCTGTACTTA AAGCAATACC 120
 40 ATTTGCTACG CTAATATTTT GAATGATAGG CGTCACTGTT CTAAAGTCCG GCGAAACATA 180
 ATAAACGCCT CCTAGTGGAT TGGTAGAGTA TCCTCTAAAA TCTGTAAAAT AAAATCCACC 240
 TTTAGAATCA AATACCATGT CATCAATACA ATATGCTGTT GAAAGATCTT CAATAATATC 300
 45 TTGTAAGTTG TCACCATTTT CTGTAGCTGC AAAAATGCCT CChGGAGATT TAAAATCTCC 360
 nAAAATAACC AACGnATAAA TCGGGCAnCT TATGGAATTG 400

50 (2) INFORMATION FOR SEQ ID NO: 1503:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 base pairs
 55 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1503:

5 TACAGGTAGT TAACAGTTGA TGTTAAATGG CGTACTGGAT TCTTTACGCA CGATTTTTTTG 60
 TTAATAAGTA TGGGATAGCA CATTACTATA TCCTACTTAC GACTTATTGG ATATGTCTnTA 120
 GCTATTCTTA AGCTCGAAAA GTTTCACAGG ATACATAAGG GACCAACT 168

10 (2) INFORMATION FOR SEQ ID NO: 1504:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1504:

CTACTGATTG TGTAATGTCG TTGGTAGGCT TGGGCTGTAC GCAGTATTAG GTGTAGGCAA 60
 CTGGCTTTTT GGCATCTACC TTGTATGTGT CGTGTATCTA nGGCTGGGGC TTGCTCCTTC 120
 25 AGTTGTTAGA CAGTAGGGGG TAATCTCAGG GGTGCAATGT ACTCCCTCCG TCCTAAAATA 180
 CTnTATATGC TCGTGCCGAA TTCCTGCAGC CCGGGGGATC CACTAGTTCT AGAGCGG 237

(2) INFORMATION FOR SEQ ID NO: 1505:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1505:

CGCATTTACC ACCATATGAT GGATCCAnCG ACGTTTTAAT AAAGATAAAA GTGACAGTAG 60
 40 CGGGAAAACA GGNCCATAAT TCACATCTCT TTTGAAAAAT ATGTTCAAGC TAGGATCATT 120
 AGGAGAGTCA TATTAATAAT AAAAATGTTG CAATCAATCG ACGTGC GTTG AATCTTAAAT 180
 45 ACATAATAAA TGTGTTAGAA GATATGGGT 209

(2) INFORMATION FOR SEQ ID NO: 1506:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1506:

AAAATGTGGC TATTGATTTT GACTTGGAAC TTTTGAACA TTTCTCTCAA GGATTAAAT 60
 GTAGGTAACA GGGCAGGTAC TACGGTACTT nCCTATTTT TTATGCAAAT TTTAAAAAAC 120
 A 121

(2) INFORMATION FOR SEQ ID NO: 1507:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1507:

AATGACAAGG TCAGCATTAA AACCATTAA AAATAACGC GTTATGGTTA CTGGACGTAT 60
 ACAACGTGTT TTGTTTAAAA ATTATTTAGA TAGACATAGC ACATTTAAGC CGAATGTAAG 120
 GATATTATTA AAAGANGTAT TTGT 144

(2) INFORMATION FOR SEQ ID NO: 1508:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 139 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1508:

CCGATTGAAT CTGTGTACAC TTCACCAAAG ATATCTTCT TCGTTTCTTC AGATAAACTT 60
 TCCATTGCTT TCTTATCAAC ACTTGTTTCT ACTAATAAGT GTGTTAATTT GTGCTTnTTA 120
 ACAAACTCAA TAGCTTGTC 139

(2) INFORMATION FOR SEQ ID NO: 1509:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 155 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1509:

TCTGCCTGCC TCGGCCTCCC AAAGTGCTGG CATTACAGGC ATGAGCCACC ATGCCTGGCT 60

CAAGTTAAAA TACAGATGTA AGACTTGACT TGATC

155

(2) INFORMATION FOR SEQ ID NO: 1510:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1510:

15

ATCCCAATGC TAATGAATTT GCATATACGA TAAATAATGC TTTTATCAT CAATAAAGCT

60

ATGAATCTTT CAAGATCTTC ATTGAAC

87

(2) INFORMATION FOR SEQ ID NO: 1511:

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 217 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1511:

30

ATAGGCGTTT ACCAGTTATT TTCGAATCCA TATAATTATG TTTGTCCGTT TGGTTTAATC

60

CAATTAATTG ATTAAGTTTT TCCAATTCCT TTTTITTTAA TTAAAATTCC AATCCTTAAA

120

AAAAATTGGA AAAAAGCCTT AAAAAAATT GGTTAATTTT CCCAAGGGAA TTAAAAATTT

180

35

TGGGGTTTTT TnAGGnCCCT TTTGGGAAAA ACCCAAC

217

(2) INFORMATION FOR SEQ ID NO: 1512:

40

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1512:

TGACATTGCA TCGGATTATG TTACATCAnG GACAACGGGC CTCAAAAAGC GGTGCACAAA

60

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CGTTCCGTAA TCATATGCCA GTGCAATCGG ATGTAAAGAG A

101

(2) INFORMATION FOR SEQ ID NO: 1513:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1513:

GATTTTATTG AAATGATTTT ACCTGTGATC AATTATTGTA ACAAATCTAC AATAAAATTG 60
TCTTACTGCA TGACCTAATA AATAGCAAC AGATATCATA CACACTTGTA ATTT 114

(2) INFORMATION FOR SEQ ID NO: 1514:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1514:

ACATATACAG GTACGTGTTT AGTCCGTCGT ATACTGCAAA ATTATGTCCG ATGAAATTAG 60
GGGAAAATTG TAGAACG 77

(2) INFORMATION FOR SEQ ID NO: 1515:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1515:

CCTTATAAAG TTAATGCAAG CAACATGGAC AAATTATTAA TTGAATAAAC TGCAAGAAAG 60
ACAACAATCA TTCTTCGGAA TGCTAGGAGA ATATATTTTA GA 102

(2) INFORMATION FOR SEQ ID NO: 1516:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1516:

CAATTTTAAA TAGGATTTTT AAGACCTTGG TTGGGTTTTG GTACAATTAA TGGGGACATG 60
ACTAGGTCTT GCCACGTTTA TATGCATCT 89

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1517:

GTAAGAGTGC ATAGTTTTTA AATGTTGCTT GTCTGGTnTC ATTTTGGCAC CATACAGTTC 60
 GTACCTGGAT TAGGGAAATG CCAAATGTCC GCGTAGTGAT AT 102

(2) INFORMATION FOR SEQ ID NO: 1518:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 448 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1518:

GAGAACTCCT TACCACAATC AAAAGTAATT GATTTAAATA TATGAGAAGA TAAAATGAAA 60
 AGGTGCAAGC AGTATTAAGA ATTTAGGTAG CAAGAAAACA AGAAGTGGTA CATACGATGC 120
 TAACCTAAAA AGAATTGGAG ATTAAAAATGA TTATTAACCT TGAAACACAA CAAATACATT 180
 TTGATTTAGA ACATGAAATT CCCTATTTTC AAGCACCTGA GAAAAATAGG ATACGCTTAG 240
 ATATTGATGT TCTCAATAAA AAGCnAATTT CTAATATTAT TAATGTTATA TTTAATAACC 300
 AATCAAAGAC GAAATGTACA TTTTGTCTG AATACTTATA TCCTGTATAA TTTAGAGAAA 360
 AAACAAGAAT TGGTCGTTTT TTTAATATTA CTAAGTGGTA CGAAGAAATC CATTCTACCG 420
 ATGAGAAGTA TGTnATTGCA ACTATTAA 448

(2) INFORMATION FOR SEQ ID NO: 1519:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1519:

ATGGACGAAA GAAGATGTCA TTGCTTTTGA AAACCTAACA AATATTAAAG TAAATTTAAA 60
 AGGTAGCGGT TTTGTGTCCC ACCAATCAAT TAGTAAGGGA CAAAACTTA CTGAAAAAGA 120

ATTCAAATTC AGATGGTnAA GAAGAAATCT GACAGTTAAA ACTGACAGGG ATAAGTCGGG 240
 ACTnAACAGG AATGGGCTAC nTTTAAATTT AGGGATGGTA TTGGGCCACT ATTTGGTTTT 300
 5 TGAC 304

(2) INFORMATION FOR SEQ ID NO: 1520:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1520:

ATGACGTCGC ATGCACGCGT AcGTAAGCTT GGaTCCTCTA GAGCGGCCGC CCTTTTTTTTT 60
 20 TTTTTTTTTT TTTCTGTTGG CCTTTGATAA TTTTATTGGA TCAGTAACAA CTTTTTGTGT 120
 TTCAACTAAG ATAGCTAAAA TTCTAACACT TATATGTAAA AATTACACTC CATTTTAGCA 180
 CAAATGTTAA CAGAAATTAA CAGCACAGTG CCATGAAGAA ATGAnAAATA CACAGCTTTG 240
 25 GTAGGGnAAT GGTCTGGAA ATAATGTAAT GCCAAGTnTC TGATCATTTA ACATATCACT 300
 CACCTCCTTC TTCATCTGAT GT 322

(2) INFORMATION FOR SEQ ID NO: 1521:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1521:

40 TAAATACAAA CCCTTTAAAC ATATTTACTA AGTCGTTCAA TTGTTGATTT GATAAnTGAT 60
 GTGATGTGGT ATTTTGCATC GGTCTGCTT GATTCCAGAC ATGTC 105

(2) INFORMATION FOR SEQ ID NO: 1522:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1522:

55

GATCGTATTT CCCAGATGTA AATTCnGTGG ACAATTGGCG TCAAATAGCT TCTAGTGG 118

(2) INFORMATION FOR SEQ ID NO: 1523:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1523:

15 CnGCATATAA TCCCGCGACA TGTCTTTTAC GGGTGCACTT GTAATATTAT TACCCCCCGT 60
 ATAACCCATG TATATCTATA CTTTACCACA TAAATAAATT CCGGGACTAT TTGGCACATG 120
 TTTTGGGTGA ATTTCTTTAG TGGCACACCA CCCCTGG 157

20 (2) INFORMATION FOR SEQ ID NO: 1524:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1524:

30 ACTGAGGTAG GTTATGTAGG ACGAGATGTT GAAAGTATGG TTAGACATCT TGTGATCCT 60
 TGAGTAAGAT TAGTCAAGGC CG 82

35 (2) INFORMATION FOR SEQ ID NO: 1525:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1525:

45 GATACAAAAA AGAAGTTCAA TTTGAACTAT GAAGAAATTT ATATTTTAAA TCATATTTTA 60
 AGAAGTGAGT CTAACGnAAT CTCATCTAAA GAGATTGCTA AGTGCTCAGA GTTCAAACCT 120
 TACTATTTAA CTAAAGCTTT ACAAAGCTA AAAGATTTAA AATTGTTATC AAAGAAAAGA 180
 50 AGTTTACAAG ACGAAAGAAC AGTTATTGTT TATGTTACAG ATACACAAAA AGCAAATATT 240
 CAAAACTGA TTTCAGAATT AGAAGAATAC ATTAAAAATT AAATCAAGGT TAATTGCGTT 300

55

AAAATTAAC TAAAATTTAA ATATTGAAGA GCTTAATTAA

400

(2) INFORMATION FOR SEQ ID NO: 1526:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 125 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1526:

15

ACTGTCTAAT ATTCACTCCC TTAAAGTGTT TTTCATATTT TTCTATTAAT GTTCATATTG

60

TAGGGTGTTG AATGCATCTA AGCATTnCAA GTTATTCTCC AAGTTCATCA ATTTCAAAT

120

GGAAC

125

20

(2) INFORMATION FOR SEQ ID NO: 1527:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1527:

30

CATGTTTATT TATGTTTCGG CTTTAATGTT GAAGAGTTTT ACAAAGTTTA CCGATTGCAT

60

TTTATAATTT TAATGCATTA TTGGAGCATT GGCTATCATC TATTACTGCG nA

112

35

(2) INFORMATION FOR SEQ ID NO: 1528:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 115 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1528:

45

GCGAAGATGA GGATGAGATG ACTAAAGGAA AATATTGAAA AACAACCAA AACTGATGA

60

ACATTATTAA AAATTTACAA AATCAAATCG ACAACTTGAG CGCAAGAACH AACAG

115

50

(2) INFORMATION FOR SEQ ID NO: 1529:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1529:

5 ATGGATCTTC CGCTTCTCTT AATTGATCAA TTAAATCAGA CATTTCATGT TTTTGTAAT 60
 AATGATTCGC TTTAATGGAT TTTTACATG ACATCATGAT TGCTACATCT TCACGTAATT 120
 TTTTGATATC TACTTTTTTC TCTTCCAAAA TTAGCTCAAT CATATCTTTA ATAATTTCTT 180
 10 CTACTTCATC TTTAGGGAAC CAAACTGGAT AGCTACTTAC AATATAATCA TGACCACCAA 240
 AATGTTCTAA CATGATACCT ACTTGTTGAA GCTCATTTTT ATATTGATCA ATGACTAATT 300
 15 GTTCATCTTT TGAAAAATGA AATGTTAACG GGATTAATAA ATCTTGTAAT TCATTGGTAA 360
 CCTCACCTAT TTAATCTCGA AAATATTCAT ATTTATnCT 400

(2) INFORMATION FOR SEQ ID NO: 1530:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1530:

TAACAGTCAA CCCACCCATT AATATATATT CAACGGCTGA CTGATACGAC GAACGTCAA 60
 30 GAATATGAGA GGAATAGGA CAAGATCATC ACACATA 97

(2) INFORMATION FOR SEQ ID NO: 1531:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1531:

TCATAACGGT GCAACTTAGA GCTGACGTAT AGTTCATTCC AACTATATAC GATGTATCAA 60
 45 CACCATGTTT CAGTTTTAGG TTAACGATAC TGTATACCGT ATTATGTCAG nGGCACCTTA 120
 TCTTCACGTA CTTTACGGCG AGATGATGAC 150

(2) INFORMATION FOR SEQ ID NO: 1532:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1532:

5 ATTCAATTCTG CTAACCAGTA AGGCAACCCC GCCAGCCTAG CCGGGTCCTC AACGACAGGA 60
 GCACGATCAT GCGCACCCGT GGCCAGGACC CAACGCTGCC CGrCCTATCC TGAAGCCAAA 120
 GGAAATGAGA TCGGAATT 138

(2) INFORMATION FOR SEQ ID NO: 1533:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 460 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1533:

20 GGGGnCCnGG CAATGGAGGC GTGCTTGGAT GGTGCTTGGA ATCATCCCTT TGGCCTCGAT 60
 CATAAGCTTA AACTTTTGGT GCTGGnGCCA CTGGAGGGAA ATCTTCAATT CTGGCAAATG 120
 25 GTAATThCCT ATACCAACAT TTAAGGCATG TGGTAATGCT GGCTACTCCC GCTTCGTTAT 180
 CAGCTACATG ACAAATACAG ATGCCATCAC CTTTGCCTCC ATTTTAATCG TTGATGCTTG 240
 GAAATGTTTT TTGTAAATAT CAATGTTATC CTTGCTGTA TGTATCGCAT TTATATCTGG 300
 30 TAGCAAAAAT GTTCCAACAG AAAGCCCTAT ACCTAGTTCG GCAGCTATTT TGGCAGATGT 360
 TGCCTACTA CTTAATAACC ACATTTCTGG AAAATGATCA TGTGTGGTGC ACTACGATCG 420
 ACTTGGTTAT CTTTATTGTT AGATAATACG GAATACGnAA 460

(2) INFORMATION FOR SEQ ID NO: 1534:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1534:

45 TACGCTAATA AATAGTTCAC TTTCCATTT TGTGTAGTCA GTCATTGTA TTCTTCAATT 60
 TGCTCTTCAT TTAATGCCGC ATAAGCTTGA TCAATAATAT TTGGATTAAG TTGTCCAATA 120
 50 TACTCTAACT GGTATGATA AACAn 145

(2) INFORMATION FOR SEQ ID NO: 1535:

55

(A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1535:

10 ACGCGATTTA ATCGTTCGTT CCAACGATGT CCACTCCCCT ACTAATAATT AAAATCATT 60
 CAAATTATTT CAACTTTTAC AATTnAACT AACAGTTTTT TCAATAAAAT GCAAGCTTTT 120
 CTCATTGTGTT ATTTAGAATG ATTATGATT A 151

15

(2) INFORMATION FOR SEQ ID NO: 1536:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 86 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1536:

25

ATAATAGAAT CATTACAAAT TATTTTCAGAC TTTACAATTA AGACTAACAG TTTTCTCAAT 60
 AAAATGCAAG CTTTTCTCAT TGTTAA 86

30

(2) INFORMATION FOR SEQ ID NO: 1537:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1537:

40

ACCAAAGTGT AAAGCCATAT ACTGAACATA TTGATAGCAT ACTCAATGAG ATCAAATTAC 60
 ATCGTGAATT TATTATAGAA GTACCTTATA TGAATTCAAG GAAATTGAG CTAAGTATTG 120
 CTAACATTGA ACAACTTTCT GTCGAATGTC ATTTTAAGCG AACAAGTCGA AAGTTATTTA 180
 TAGAAAAGCT TAAAAGTGTT CAATATGATT TACAAAATAT ATTAGATGGC GTAACACnAG 240
 AGGGTACTGA TGGTTAAAAC AGTTTATGTA ACAGGTTACA AATCATTGGA ATTAAACATT 300
 TTTaAAGATG ACGCACCTGA AGTACATTAT TTAAACAAT TTATAAAACA TAAAATTGAA 360
 CAACTGTnGG ATGAAGGATT AGAATGGGnG TTAATACAAG 400

50

(2) INFORMATION FOR SEQ ID NO: 1538:

55

- (A) LENGTH: 136 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1538:

10 ATATCGTTAC TGCTGTATGT TTCAATATCT ATATTCATAA ATTTCAAATn CTGACACCTC 60
 AATTTCTTTA AAATAAGGGG CAGAACCCAC TATGACTATA GGATCTCTCA CAGGTCAATT 120
 CGCAAATCAC TCGTGC 136

15 (2) INFORMATION FOR SEQ ID NO: 1539:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 85 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1539:

25 TAAATATCTC GGCACAATGA TGCGGGATAT TTTTACAA TAGGCATAAA GGCTGGAAAA 60
 AACATATCTA GTGCTATGAT ACTTA 85

30 (2) INFORMATION FOR SEQ ID NO: 1540:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1540:

40 ACAATTTGTT TATTTCAACA AATTATCTTT ATTCCACGAT GTGCACAAGT GGTGAAATC 60
 AGCTGAAGAC ACG 73

(2) INFORMATION FOR SEQ ID NO: 1541:

45

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1541:

55

TGCAGGAATT CGATATCAAG CTTATCGATA CCGTCGACCT CGAGGn

106

(2) INFORMATION FOR SEQ ID NO: 1542:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1542:

ACATCAACTC ACCCATAATA TATATTCACG GCTGACTGAT ACGACGAACG TCAAAGAATA

60

15

TGAGAGGAAT AGGGACAAGA TCATCAC

87

(2) INFORMATION FOR SEQ ID NO: 1543:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1543:

GCTTATTCTG AAAAATATTT AAATTGAAGA AAAGAATATT CTAACACGG AAGTGGTATT

60

30

AACTAATAAC TAGTATCCTT TATAAATAAA CATAAAAATA TTCAAACGAA GGTCTACTAA

120

ATAACTATCC ATAAAGTGAG TATAAGTTTG TTTGTAAAC TGAAGTAAAA AGCATAAGGA

180

ATTACACTTT AAATACATAT AGTACTTACG AATAGAAAAT AATCCCTTCA ACAGTAATTT

240

35

TTAAACAAAA ATAAGTGTTG TTTTATGTTG ACTCTACTAG AATAACTTGA TATTATATAA

300

AAGTCGTCAA ACGGCACTAA TATTTAnnAA ACAAATGTTT TAAGTTGTTG GATTThAAAA

360

TATTGAATTA AAGTGTAAT TTGGACTATT GGAAATTGCG

400

40

(2) INFORMATION FOR SEQ ID NO: 1544:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1544:

ATAACGCTAA TCAGCCACAT TCAGTATTGT TAAATGGACA CACAAGCAGT TGATGAAAAT

60

55

(2) INFORMATION FOR SEQ ID NO: 1545:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1545:

GGCTGTTATT GTTGTGGAGT TAAAAATGAA GGAAAATTAT AAACATGGTA AGCGTGTTC 60
 TCGTATTACT TTACTIONAAC NAACGGTATA ACCATACCTA ACTTAGTA 108

(2) INFORMATION FOR SEQ ID NO: 1546:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 554 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1546:

AAATATGTTT CATATATTAT GAATCTAGCC TTAATCATAT TGCATTCAAA ATAATTTTAA 60
 AAAATGAAAA GAAAGGATTT AGCATGCAAA AATTCAAAGA CTTTTTTTAC GATGATTTAT 120
 CGGTACACG AGGAAATTAT TTTTAACTT TAATGGCAGC ATTTTTTATT ACTATCATT 180
 TATTTATCGG CATAGTTGTC AGTGAAGTAC ATTTACTTTA TAGCATGCTA ATTGTATTAG 240
 TAGGTTTAAT TCTATTGAGG CTATTCAAAA TCAATTTATT CTCTTTTAAA AAATTAACAT 300
 TGTCTCAAGT TATTTATATT ATAGGCGGTG CACTATTAAT TTATGGGTTA GATAATCTTT 360
 ATTTATATTT TCATGACGTA CCGGCAATGA ACAACAATTA GAGCAAGCAA TACGGAAATA 420
 CACCATTCTA TATTTCTATT TtCACTGTaC CATCATCCCC GCTATTGTGG aAGAAaTTGT 480
 TTTtCGCGGT ATGATAATAA GGGkTATCTT CAGAAAACAC TTGTTTTTAG GGTTAATTGT 540
 GTCTAGTTTA GTTT 554

(2) INFORMATION FOR SEQ ID NO: 1547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TAAAGCAACA CTTTAAATCC CTTTGAACCT TAGTTTATCC GCTAAATCAT AAGCTTCTTT 60
 TTTGCTACTT ACAAAAATCA ATCCTTGTA AATTTACCT GAATATCCAT AGTAATCTGT 120
 5 CTTTGAATA ATATAATTAA CTCTTTCATC AGAAGTTAAA TATCTCAGTT TAGTTACATC 180
 ATCTTCTTTA ATACCTTGAT GTACATAATC AGTCACACCA AAATAATGAA ATGGGACATA 240
 10 AAATATCACT TTCTAATGCT GCTTGTAACC TTATTTTATA TGCAATATTA TAATCAAACA 300
 GTTCAAATAT ACTTAATTCA TCTGGATCTT TCTGGTGGTA GGCAGGTCAT TCCCAGCAnG 360
 AACTTAGGGT TTGGAGGTAG GTTAAAATAC TCGGTTGGAT 400

15 (2) INFORMATION FOR SEQ ID NO: 1548:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1548:

CGCTCTAGAA CTAGTGGATC CCCCgggCTG CAGGAATTCG GCACAGCATA TCTAGTATTT 60
 TAGGACGGAG GGA 73

30 (2) INFORMATION FOR SEQ ID NO: 1549:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1549:

GTATCCAAGC AGCTTTTAAA CAATATGGCA TAAACATTAT TAACGGCTAT GGTTTAACTG 60
 ATGGCACCTC TTG 73

45 (2) INFORMATION FOR SEQ ID NO: 1550:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1550:

GTAACATGTA TAGTGAAGTG ACTACTAAGA AGnCGTATTG TGATATTGAT AGCAGCTGAT 120

(2) INFORMATION FOR SEQ ID NO: 1551:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1551:

GGTATGTATT AATTAAAATG TGGTCATGAT TGAAACAGCA ATGTAAAAAT AGCACAACAT 60
 AATTnATAAA GGAGAGAAAC GGCATGCATG AACAGATTT TAGAATTTTA GAGGGTCAAG 120
 ATATTACTTT GCCAGAATTA GGTAGAGAAT TAGAnAATAT TACAGGACAT ACGATTGCTG 180
 ATTCTACTGG CG 192

(2) INFORMATION FOR SEQ ID NO: 1552:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1552:

CTAAGTTAGA TGCTAGTATA CAAGATTTAC AACAAAAGGT ACTGGAATCG AATTGTGAAC 60
 TAGACAAACT AAATC 76

(2) INFORMATION FOR SEQ ID NO: 1553:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 135 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1553:

TGTGTTGGGG CCCCGTATAT TGAAAATTG TTATAGGTGT ATTTCTTTGG TTAACATTG 60
 TTATATAACT TGTAGTTTTA GGATGTTGAT TTTGCTTACC TTGTCTGCTA TGTAATGTCA 120
 CATCAACATG ATThA 135

(2) INFORMATION FOR SEQ ID NO: 1554:

(A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1554:

10 TTTGAnATCA AATTCAC TTC GCAAACGTGT CCAAGCGTGA GCAAAGGGCT AGATGATTAA 60

TAGTTGCCCC ACTAACGGGA TCGCCCCAGT TATCCAAC TT ATCT 104

(2) INFORMATION FOR SEQ ID NO: 1555:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1555:

25 AATAAGAAAC AnGACACTAG CTCACCACGA CGCGCACGGC CTGCGTGTAA AAATGTTGGT 60

GGCGCGGGTT GGAGATCGTG TTCAACCAGA GCAGAAAATA 100

(2) INFORMATION FOR SEQ ID NO: 1556:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1556:

40 CAATGAAATT ATTTATTATT TTAAGTGCAT TAAACCCCGA TGATGGCTGT CCGGTACCAG 60

GTGCATTTTG GTGCCCATGG TTTACC 86

(2) INFORMATION FOR SEQ ID NO: 1557:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1557:

55 GTCATGTTCC CATCAAACT AATTTGTACT TACTAAAGGC TCAGCAGCGC AACAATTAGG 60

(2) INFORMATION FOR SEQ ID NO: 1558:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1558:

AAC TGGTTAC AGAAATACCA CGTTCCTGTT TCAACTTTCA TCCAGTCACT TGATCGCAA 60
TTTACCAGTC TTCTTCCCTT TA 82

(2) INFORMATION FOR SEQ ID NO: 1559:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1559:

CCACAGCGGC ACTATAGCCA GCCCCTAATA TATACAGTAT TTGCATCTGA CTCATTGGTT 60
CATAAGTATA TGCAGTGA 78

(2) INFORMATION FOR SEQ ID NO: 1560:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1560:

ACCATTGCT AACTTTTTAG CAGCGCAATG TTCTTATTAA CTGCTTACGC CATCTATAAA 60
AATAAACGTT CAACAA 76

(2) INFORMATION FOR SEQ ID NO: 1561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TTGGAACCCA AATTTTTTTTA ATTTTCCCAA AAATTGGGGG GGGACCCCCA ATTCCCTTAA 60
GGGTTTTTCCT TGGGGGCCGG GGGTTAATTC CACCCGGGGT TAAAATTTTC CCAAAAATTA 120
5 ATTTTnGAAA AGTTTTAATT TAAGGAAACC CATTnGTCCG GAATTTTAC CCCATCCTTA 180
TGGGGGGTCC CAAAGATTCC 200

(2) INFORMATION FOR SEQ ID NO: 1562:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1562:

20 AACACAGAGA ATAACCAAGA GAAGACGTTT TCATCTGAAG AAAGTAACAG TAmGCCATTT 60
ATGGAAGAAA ATCAAAACGA TGAGATAGTT ATAAAAGAAG ATTCATATAA TCCATTCGTA 120
ACGAAAACAT CTGAAAGTTT AATAGCTGAT GATGAATCTT CTGGTTATAA TAATACACGT 180
25 GAAAAAGATG AAGACTACTT CAAAAACAA CAAGAAATTT TACAAGAAAT GGATCAAACA 240
TTTGATTCAA ATGATGGTAC AACTGTGCAA AATTATGAGA ATAAAGCGTC TGATGATTAT 300
TATGATGTAA ACGATATTAA AGGAACAAAA AGTAAAGACC CTAAACGAGG AATTCCATAT 360
30 ATGGAATTGT TGGnCAGTCA TGAACGTTA TTATTGCTCA 400

(2) INFORMATION FOR SEQ ID NO: 1563:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1563:

45 TCTTCATCAT CTTCTAATTT ACCAGCTGGA ATTTCTAGCA ATGGTTTTTC TACTGGTTTA 60
CGATACTGTT TACTAATAC GACTTCTTTT TTAGGTGTCA CTGCACAAAC ArCAACTGCA 120
CCATTATGAT AACTAATTC TCTGTGAC GTTTCACCGT TTGGTAATGT CACTGTATGA 180
50 ATTTCTACAT CTACAATTTT GCCATTATAA ATAACTGTTC GATCAATTGT TTTTTCATTT 240
AAATCCATTA TAATCACGTT CCTTTAAATT CATATTATAT ATTGATACAC TATGCTTGTT 300
AGCTAAAGTG TATCGAAAGG AGAACAGACA TGCAAAAAAA TATATTAAAA AGTGGTATTT 360

AAATTATAGG ATTGTGCTGT TGAAAATGGG TATC

454

(2) INFORMATION FOR SEQ ID NO: 1564:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1564:

15 ACATCTCGCA TCGTCACGAC TTGCTTGAAC CACTAGCAGG TCAAACAAAG CTGTACAGGC 60

AACATCTGC 69

(2) INFORMATION FOR SEQ ID NO: 1565:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1565:

30 TCCAGAACCA TTTTAAATCC CGGGAAATAT AATTACCTCC ACTAAnGTAA TATATCCAAG 60

CCAAGACTAA TCCTCCTTAA GCCGGTTTAA GTAACCAGGT TGAGAAGGAT TTTTGG 117

(2) INFORMATION FOR SEQ ID NO: 1566:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1566:

45 TATTGAGATT AACAGTCTGG GAAAAATGAA CAGCAATTGT nTAATGTGAC GATGCTGATT 60

ACTTTTTTAAC AGTATCATTT AATAACTCAG AGATGCGCTT TAT 103

(2) INFORMATION FOR SEQ ID NO: 1567:

50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1567:

5 AATGGATGGG ACAGCAATTA GTGCATAACG ACAATATATG CTCAATTGT CCGCAACTGG 60
TTAAGAATCG TATTGTCACA A 81

(2) INFORMATION FOR SEQ ID NO: 1568:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1568:

20 AATGGATTCA GTAGGTATTG GTGAAGCGCC AGACGCAGCT GATTTGAAAG ATGAAGGTTC 60
ACATACTTTT AGCATACCTT 80

(2) INFORMATION FOR SEQ ID NO: 1569:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1569:

30 TTTTAAATA CGATTTTAAG GAGGCCATTA TAATGGCGAG TAAAAGTAGC GAATTAATGG 60
35 TTTTGGTTAG GAATTGGTCG TTTAGGCATT CAGGA 95

(2) INFORMATION FOR SEQ ID NO: 1570:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1570:

CCCAATAAAA AAAGCCTGTT GTCACAATGG TCATAGACAC GTACATACTT TAAAGGTTTC 60
50 TGTAATATAA ATATTTTATA TGCCACTTTA AAGTTGGnAC GTTCGTATGT TGTACTAA 118

(2) INFORMATION FOR SEQ ID NO: 1571:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1571:

GACTTGATCA ATGAAGCATT GTGTGACAAT TGGTCTGTTT GCACACCGCA CGGATTGnGC 60
GTCATTTATT TGTACTAATT CAAAAACAT TGTGTGTTTC CTAG 104

(2) INFORMATION FOR SEQ ID NO: 1572:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 118 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1572:

CCGAAGTGTGTA ATGGTCCTAA TGTTTTACTC ATACCATATT GCGTAACCAT TGAGCGGCGA 60
TTGTGTTGCA CGTCGAGCAT TGAGACCGTT GTACTCGTAA nGTATATCTC TGTACACG 118

(2) INFORMATION FOR SEQ ID NO: 1573:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1573:

AGGGATCAAAA GGTCCATCCC CCATGCATTG GATAGTGGGG GATGACTTTT GATCCTATGT 60
TCCAGTTGCT TATT 74

40

(2) INFORMATION FOR SEQ ID NO: 1574:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1574:

AACCTTTTGA GTAAATTCAC CAATACTCAT CCCCTTATCA TTAAACAAAC TTTTATTAAT 60
GTTTTTGGTT ATATTATGAG TCTTTACTGC TTTTAGATTG TAAAAATTAT CGTCATAAAT 120

55

GTAATTAATG TAATAATAGA AAAGTGTATA TATCTCATAT CGCCACCTGC TATACAACTT 240
 ATTAAATAAT TAATTCCAAG ACATATTAAT TATCTAATTA TAACCTTAGT TnACGTTATT 300
 5 ACATAATATA AAAATATATA ATAACCTTATC CnCCGGCnCC T 341

(2) INFORMATION FOR SEQ ID NO: 1575:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1575:

ACGTGTACCA ACTTTTGGGC ACCATTGATA ATAnGTGTCA TAGGGTGACT CAGCATAACG 60
 20 GGCAAGCCTA TTAATGATAG CCAGATTAAG ACATACAGTA CATATGTTC 109

(2) INFORMATION FOR SEQ ID NO: 1576:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 79 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1576:

GCTAGATTGC GGAATTAAC AATCATCAGC GATTTAATAT TTGCACTGGA GACGTCATGG 60
 35 TAATAAAAAA TTGATGAGA 79

(2) INFORMATION FOR SEQ ID NO: 1577:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1577:

ATGATGGCTA TCATGAGATT GAGATGATAA TGACAACAGT TGATTGAAA TGATCGTGTA 60
 ACTTTTCAT 69

50

(2) INFORMATION FOR SEQ ID NO: 1578:

(i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 104 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1578:

AAATTGTCAC TnCAGGTCAT AACCAACCAG GTGGGACTGC ACGAGCGTTA CTAATGATCC 60

10 AACGGTCTTG CTTTGTGATG AGGCAACAAG TGCACTTGAT CCGC 104

(2) INFORMATION FOR SEQ ID NO: 1579:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1579:

GCTCAATAGA TACAACTATT AGGACAACGG ACTATCGTTT ACAATTTATT CCAGATAAGG 60

25 ATCGCGCAGG TCGTATGCGT AACTATGCA 89

(2) INFORMATION FOR SEQ ID NO: 1580:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1580:

TTGTCTCTAA TAATGGnTTT GGCTTTTTTCT AAAATTTTCAG ATGTGGGTGC TGGTGAAGCA 60

CCGACTGGTT AATTTTCTTG TCGTCACGGC CACTTTTGT TT 102

40

(2) INFORMATION FOR SEQ ID NO: 1581:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1581:

AAGGTGCTGT TATTAGGATA ATGnATTTAA ACCCCATGGT ATGAAGGATA TCTGGAAGTT 60

AGATTGGATA TCCCTTAACC ATGGGGGGTT TTATTTTGG GG 102

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1582:

TTCAGGGGAG CTGAACATAT TGACGACTTT TGGGTCAATT CATTTTGCAT TTTACTTTTA 60
 AATGCGTTGT TGCATGTAAT TGTATTAACG ACATACATGG TGGGGCTCTA AATnAATGCT 120
 TGACTAATTT CTTGGATGGA GACCACGATT TACCAACTCA 160

(2) INFORMATION FOR SEQ ID NO: 1583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1583:

TAAAAGCAAG TACATTAGAG GTTAGATCAC AAGCTACTCA AGACTTGAGT GAATATTATA 60
 ATAGACCGTT CTTTGAGTAT ACAAATCACT CAGGATATAA AGAGGAAGGA AAAGTGACGT 120
 TTACTCCTAA TTATCAACTT ATAGATGTAA CTTTAACTGG GAATGAAAAG CAAAATTTTG 180
 GTGAAGATAT TTCTAATGTA GATATATTTG TTGTAAGAGA AAATTCTGAT AGATCTGGTA 240
 ATACAGCTTC AATTGGTGGT ATTACTAAAA CAAACGGTTC AAATTATATT GATAAAGTAA 300
 AAGATGTAAA TTTAATAATT ACTAAAAACA TCGATAGTGT TACATCAA 348

(2) INFORMATION FOR SEQ ID NO: 1584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1584:

AGCCAGCAGT AGATAGATAT ATTAATGAAT TCTTGAGAGAA AGGTAGCTCA AATTGTCCAA 60
 TTGAGATATT GAA 73

(2) INFORMATION FOR SEQ ID NO: 1585:

(A) LENGTH: 255 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1585:

10 GTAAGGAATG GTCACGTATT CCACACTTCT ATATGAATTA TTATGTATAT CAATACGCAA 60
 mTGGTTACAG TGCAGCTCAA AGCTTAAGTC ATCAAATTTT AnCAGAAGGT AAGCCAGCAG 120
 TAGATnGATA TATTAATGAA TTCTTGAAAA AAGGTAGCTC AAATTATCCA ATTGAGATAT 180
 15 TAAAAAATGC TGGTGTAGAT ATGACAACAC CTGAACCAAT TGAACAAGCT TGTGAAGTTT 240
 TTGAACAAAA ATTGA 255

(2) INFORMATION FOR SEQ ID NO: 1586:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1586:

30 TTATTAGGTG AnTCCATTGG CAACATTGAT TGGTTTGTCA TTAGGACAAA TTTTATTATA 60
 CATTGGCGTT ATTTTACTA TCTTATCTGG TATTGAATAC TTTTATAAAG GTAGAGATGT 120
 TTTTAAACAA AAATAAATAT TTGTTTATAC TAGATTTTCAT TTTCATATGG AATCTAGTTT 180
 35 TTTTAATCCC AATTTTAGAA ATTAGCCACG CAATTGTTTA TAATGATATA TTGTAAACAA 240
 ATATTTGTTT ATTTTTTTAG GGAAATCTG TAGTAGCATC TGATACATTG AATCTAAAAT 300
 TGATGTGAAT TTTTAAATGA AATACATGAA AAAATGAATT AAACGATACA AGGGGGATAT 360
 40 AAATGTCAAT TGCCATTATT GCTGTAGGCT CAGAACTATT 400

(2) INFORMATION FOR SEQ ID NO: 1587:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 561 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1587:

55

CAAAGCGTCT ATTATTGTTT GATTTTGATG AAACATATTT TAAACATAAT ACAAATGAAG 60

AAGTGATCAC TGCTGTATTG ACAGGAAGTA CATTTCAAAG TGTCATGGAT AAaATGGATC 180
 AAGTTAATAT GACGTTTAAA CCATTACATA TCTTTTCTGA TTTGAGTTCT AAAATGTTCA 240
 5 CTTGGAATAA TGGCGAATAT GTTGAATCAG AAACATATAA AAAGAAAGTC TTGAGCGAAC 300
 CATTTTTATT TGAAGATATT GAAGATATAT TACGTCATAT TTCTGCGCAA TATAATGTCTG 360
 AATTTATTCC ACAAAGAGCA TTTGAAGGTA ATGAAACACA TTATAATTTT TATTTTCATT 420
 10 CAACAGGTAA TCACAACAAT GATAGTCGTA TCCTAGAAGC ACTnnTCAGA TACGCAAATG 480
 ACCAAACTA TACAGCGAGA TTTAGTCGAA GCAATCCATT AGCTGGTGAT CCTGAAAATG 540
 15 CGTATGATAT TGACTTCACA C 561

(2) INFORMATION FOR SEQ ID NO: 1588:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 79 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1588:

CCAACAGTTT TATCATTATG GCAAGTTCTG TTAAACCTGC TGAGAGTTAT TTTGCACTGA 60
 30 TTGCAAAACC AGAAATTGG 79

(2) INFORMATION FOR SEQ ID NO: 1589:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1589:

GCAGATATGC AGCAATTTAT AGAGGACTAG TAAACGCATA TATGACTTAC AGCTTTCAGA 60
 45 CAAATAGCTT TGC 73

(2) INFORMATION FOR SEQ ID NO: 1590:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

TCATTTTATG GTTGATCATA GCGTCGTCT TTTTCCTTGG GGATTTTATC TTAAATACA 60
CAGATTGGCG C 71

5 (2) INFORMATION FOR SEQ ID NO: 1591:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1591:

ATACAATACA ATTACACCA TATATGGATA AAATGCAAGA TGCAATTACT GCAGTTGCAC 60
AGTGCAAGTA GCAATACC 78

20 (2) INFORMATION FOR SEQ ID NO: 1592:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 168 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1592:

CCAATTAATT AAAAACCGGA AAACCAATTT TTAAACCAA TTAAGTTAAA AATTTTTTAA 60
AATTGGGCCC CAAACCTTGG AAAAAGGTTT AATTTTCCTT TCCCAATTTT CCCAAAATTT 120
TTAAACCCAA AAATCCCGG TTTTGGGTTA AATTTCCCTn GGTTAAAT 168

35 (2) INFORMATION FOR SEQ ID NO: 1593:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1593:

TGCTAGAAAG TATAGAACCT GGTTCAAACG CATGGTTTTA TGCCCTTTT TAAACnGATG 60
TTTATTAAAA AAATATGGAA ATTGGCCACG TCCGCCAATT TCCTTAGAAA AGAACGT 117

50 (2) INFORMATION FOR SEQ ID NO: 1594:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
55

- (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1594:

AGACGAAGCC AAAAAGTTAT TCGCCAAATC TGAAATATTT TCAAAGACCT TAAAGGCGTA 60
AAATAC 66

10

(2) INFORMATION FOR SEQ ID NO: 1595:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1595:

ATTTTATTTA GGCCAATAAC TGnCTACTTC TGAAATAAGT TGCTTTGCAT AGTCTGACGC 60
GGGATGTTTG GATAATATCT TCTGTGTTAT TGCATTGCAA 100

25

(2) INFORMATION FOR SEQ ID NO: 1596:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1596:

GACCAGACGG CCGTAAACCT GGATGAAACC GTCCATTAGA TTCTGAAGTT GGTATTTTAC 60
CTAGAACGCA TGG 73

40

(2) INFORMATION FOR SEQ ID NO: 1597:

45

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1597:

CTTTATAAAA TTGTCTTTGA CTAACAGGAT TTTCAACGCT ATTCACAAAC CATGGTTTAA 60
CATATT 66

55

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1598:

TATGGCACCC TCTTTGATnT TGTGACCGTT TTTGGTAATT CACCATTATT GTACGAACCA	60
TGGAATTCGC TGCCTTCCTT TAGGCAATAA CATAATTATA TTTATCCCCT TCTTGTCAC	120
AGAGGTGCTG ACAACACCA	139

(2) INFORMATION FOR SEQ ID NO: 1599:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1599:

CTCCTCTGCA TGCACATCTT GTTGTAGCAA GGTTCACATG TAATTTATTA AATCGAACT	60
CTATCCAAC TATGTTATAAA GTTCATTCTA AACAAATnAG T	101

(2) INFORMATION FOR SEQ ID NO: 1600:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 172 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1600:

TTGTACCAAG GTTCACATGT AATTTATTAA AGCGAAACGC GTATCCAAC TATGTTATAAA	60
GTTCATTCGT AAACAAATAA GTATAAAAAT TCAATATTTT TATTACTAGA ATATGGTTAA	120
ATACATTTAT TTCTTATAAn AATTTGATGT TTAAGATATT TTGCCAAATT GA	172

(2) INFORMATION FOR SEQ ID NO: 1601:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1601:

5 TTGGCACTGG CCGTCGTTTT ACAACGTCGT GCACTGGGAA AACCAAAAnCA CGACGTTGTA 60
 AAACGACGGC CAGTGCCAAG CTTGCATGCC TGCAGGTCGA CTCTAAGAAG GA 112

(2) INFORMATION FOR SEQ ID NO: 1602:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 679 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1602:

20 TGCAATGGTT AATCATCTCA TATAACAACA CATAATTTGT ATCCTTAGGA GGAAAACAAC 60
 ATGACAAAAC ATTATTTAAA CAGTAAGTAT CAATCAGAAC AACGTTTCATC AGCTATGAAA 120
 AAGATTACAA TGGGTACAGC ATCTATCATT TTAGGTTCCC TTGnATACAT AGGCGCAGAC 180
 25 AGCCAACAAG TCAATGCGGC AACAGAAGCT ACGAACGCAA CTAATAATCA AAGCACACAA 240
 GTTTCTCAAG CAACATCACA ACCAATTAAT TTCCAAGTGC AAAAAGATGG gCTCTTCAGA 300
 GAAGTCACAC ATGGATGACT ATATGCAACA CCCTGGTAAA GTAAATTAAAC mAAATAATAA 360
 30 ATATTATTTT CAAACCGTGT TAAACAATGC ATCATTTCTGG AAAGAATACA AATTTTACAA 420
 TGCAACAAT CAAGAATTAG CAACAATGT TGTAAACGAT AATAAAAAAG CGGATACTAG 480
 AACAATCAAT GTTGCAAGTT AACCTGGATA TAAGAGCTTA ACTACTAAAG TACATATTGT 540
 35 CGTGCCACAA ATTAATTACA ATCATAGATA TACTACGCAT TTGGAATTG AAAAAGCAAT 600
 TCCTACATTA GCTGACGCAG CAAAACCAAA CAATGTTAAA CCGGTTCAAC CAAAACCAGC 660
 40 TCAACCTAAA ACACCTACT 679

(2) INFORMATION FOR SEQ ID NO: 1603:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1603:

50 CATTTTAATT GATATAATTT AGACTTTAAC ATTTTCATGCT GTTCACGGTT TTAATTTGAG 60
 55 ACGTCATTTG GTATAACAAC TATAC 85

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1604:
 ACTGGTGTGA ATAGCTCCAG CAATTTCTTT AACCGCGATC ATAATCAACG TCACCTTTTA 60
 ATTTGCCA 68

(2) INFORMATION FOR SEQ ID NO: 1605:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1605:
 TGGGGGGTnT TTTTGGGTTG GGTAAAAAA AGGGAATTGG CCCAAGGGGG GAATTCCTT 60
 AAAAAAACCC CCAACCCCCT TGGGAAATTA AAAATTGGGT TAACCGGGA 109

(2) INFORMATION FOR SEQ ID NO: 1606:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1606:
 GCTTATATAC ATGTTCCATT ATAAAAGGAG TACGAACGAA AGTAACGCAT GACGTTAATT 60
 TAAAAATATT GTAATAATTA TGGATTAAAT TAAAAACCA GGGGTATTCC AT 112

(2) INFORMATION FOR SEQ ID NO: 1607:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1607:

GTTCAAGTTG GTAACCTAAC AACACGnAAT TAGTTTAAAC GTTTGG

106

5 (2) INFORMATION FOR SEQ ID NO: 1608:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1608:

15 CACACTGATA CCATAGGATT TATGATAGAT CAACAGCATG ACCAAATGTA TGACCTAAAT 60
 TTAAAAATTT ACGTACACCT TGT 83

20 (2) INFORMATION FOR SEQ ID NO: 1609:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1609:

30 AAAAGAATAA AGTCACTGAA CAATGGTCTT TCACAATGAT GTTGGCTCAA TGCACAAGCG 60
 CATTATGTnT GTGACTTGGG CATTTTGGCT TATCAGCTGA ATATTATACG CATTACATC 120
 CCAATTAACG TA 132

35 (2) INFORMATION FOR SEQ ID NO: 1610:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1610:

TTTAATGCAT ACGCTTCTCG CTTAGCAATT TCTTTGCACG TCTAACAAGC ATTAACGCTC 60
 TTAnTACTAT AATCACAACA AAACCAGCGA AATATAACAT GCGTATA 107

50 (2) INFORMATION FOR SEQ ID NO: 1611:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 55 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1611:

5 TTCGCACCTG GTATCGTTCA AACCACCAAT GATGGCCCGT CTCGCCGTGG CAACAGCCGA 60
AGACCGCAGG TAAACCCTGA ACGC 84

(2) INFORMATION FOR SEQ ID NO: 1612:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1612:

20 ACTCACATGT ACGATAACAC CCTTCGTAAA TCCATCTTTG GTTTGCCAAG TTCGTCGTTG 60
TAAACTGTCT ATACTCGTTA AACCGCTACA TGTTTTCTTA AAnCCTGTGC CTAAATGCTT 120
TACTGAA 127

25 (2) INFORMATION FOR SEQ ID NO: 1613:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1613:

35 CGTTCAACTT TTTCAATTTT TAACGGCGTT TTACTATCTT TATCTGTAAC TAATTCAACT 60
CCAAACATTA AGCCTCGTCC TCTTACATCA CCAACATTTT GATGACGCTT CAGCGCATGT 120
40 AACTGTTTC 129

(2) INFORMATION FOR SEQ ID NO: 1614:

(i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 348 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1614:

nCAACTAGTG GATTTAAnAT AnACATAATT ATAAATGCAA ATGCTAATAG CTGAATACCC 60
55

GCACTAGGTG CATAATTTGT GTATTGAGCA AATAAAGCTA ATACAATGAT TGTAATTCCT 180
 TTAATGACAA ATAAAGGTAA ATTTAATCGT TTAAAGGTT GGTAAATTAA AAATACAATT 240
 5 GCAGCTATAT GCGAGCCACT AACTGCCAGC AAATGATATA TACCTATCTC TTAAACACGT 300
 TCCTTAAATT GCTCATTAAAC TTCTTTTACG TCACCAGTAA TCAATGCC 348

(2) INFORMATION FOR SEQ ID NO: 1615:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1615:

20 GAGCTCCACC GCGGTGTCGC CCGCTCTAGA ACTACTGGAT CCCCCGGGCT GCAGGAATTC 60
 GGCACAGCAT AT 72

(2) INFORMATION FOR SEQ ID NO: 1616:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1616:

35 CATCACGTTA AATCATAACG CGTGACGTGC TTTTGCTATT TGTCTCTCGG TATCTCTATA 60
 TCT 63

(2) INFORMATION FOR SEQ ID NO: 1617:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1617:

50 ATTGAATTCA AGGGTGGAAC TCATGAATTG GCTGGAAAAA GGTAGATTTA ACTGGATGGT 60
 TGNAGCCATA TATCGGTGCG TTTATTTTATT TGGTATTTTA AAAATCAACC TCG 113

(2) INFORMATION FOR SEQ ID NO: 1618:

(A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1618:

10 GTACAATAAA GTGGTAAACA ACATGCCAAT GGAAAAAGGG ATTAAAGGTG TTTATGTCAT 60
 TCTTAAAGAT AGTAACGGTA 80

(2) INFORMATION FOR SEQ ID NO: 1619:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1619:

25 ATCTTATGTT TTTTCCTAA AACTTCTGCT ACITCATTTA TTTGATGTAT GGTAGATAAT 60
 TCTGTTTGGA TACTCATATC AACTTTTTCT ATCATATCTG AAATCTCTTT TnTGGCA 117

(2) INFORMATION FOR SEQ ID NO: 1620:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1620:

40 CGATAAACCC TTCGTAATCA ATCTTTGGTT TGCCAAGTTC GTCGTTGTAA CAGTCTATAT 60
 CGTTAAAAGC TACATGnTTT CCTAAGCCTG TGCCTAATGC TTTACTG 107

(2) INFORMATION FOR SEQ ID NO: 1621:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1621:

55 AATATCGTGT CTCTGTCCAG TGCTGTCCAA TCAATTTTGA TCCACCGATT GTCATACGTA 60

(2) INFORMATION FOR SEQ ID NO: 1622:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1622:

ACCATCTGAC ATCATCAATT ATGAATTAAT GATGATATTA AAAATAAATT TGAAACATTG 60
CCAATTGATA GTGCC 75

(2) INFORMATION FOR SEQ ID NO: 1623:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1623:

TACCTGTGTA TCAGCTCTAT TAACAACCTA ACATATGTGA ATAATTTGCG ATCCTTGTTG 60
ATAATGCTGT AATTGAC 78

(2) INFORMATION FOR SEQ ID NO: 1624:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1624:

GCAAGCTTTT GCGGCTTCTG ATGCACCATT AACTTCTGTA ATTAAACACA CAAAGTGAAA 60
CAGGTAGGTA ATGCAAAACT GCAACGGACA ATCGA 95

(2) INFORMATION FOR SEQ ID NO: 1625:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

ATTGCGATTA CACAGTAGTG AATGAGATAT TTGACATGAA AGCTCCTGCA GCTTCTAAAG 60
AAGAGTTAGC AGGTTT 76

(2) INFORMATION FOR SEQ ID NO: 1626:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1626:

AAAAGCTAAA AAAGATTATC AGGTGTATCA CAAACTCAA TTCTCATTAC CATTTATCTC 60
AGTGTGAACG TCTTAATTGA GAACTAATCT nAATTGAGAT ATTAGTCATA TAAGGATGGA 120
CAAGCA 126

(2) INFORMATION FOR SEQ ID NO: 1627:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1627:

TGATACGATA GAACATAGTT CAGCACATTG TTGTTGAAA TTGGATATTA CCGCCATTTT 60
TTCACAATAT CAATAATACC TGAACGTGTT GGTnTTCCA CATTATGATT GTACAT 116

(2) INFORMATION FOR SEQ ID NO: 1628:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 91 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1628:

ATTTGTCCT ATCTTGAACA AATCCGATTT TTCTCAGACA CTGAATCCAA AGTATTCATG 60
TACCATAAAC CATCTGCATG TTGATTTATG C 91

(2) INFORMATION FOR SEQ ID NO: 1629:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1629:

	ACAGAAAGTC AAACAGTAAA AGCGGCAGAA TCAACTCAAG GTCAACACAA TTATAAATCG	60
10	TTAAAATACT ACTATAGCAA GCCAAGTATA GAGTTAAAAA ATCTTGATGG TTTGTATAGA	120
	CAGAAAGTGA CAGATAAAGG AGTATATGTT TGGAAGGATC GAAAAGATTA TTTTGTGGC	180
	TTGCTTGGTA AAGATATTGA AAAATACCTT CAAGGTGAGC ATGATAAGCA AGATGCATT	240
15	TTAGTCATCG AGGAGGAAAC TGTTAATGGA AGACAATATT CAATTGGTGG TTAAAGTAAG	300
	ACAAATAGTA AAGAATTTAG TAAAGAAGTC GATGTTAAAG TAACAAGAAA AATTGATGAA	360
20	TCATCGGAAA AGTCTAAAGA TAGTAAATTT AAAATTACTA	400

(2) INFORMATION FOR SEQ ID NO: 1630:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1630:

	GCTTTCCTTT TCGAAATCTA TAAATCTAAT CCATTGAAGT AAACCTAATTA TGATAATTAT	60
	TAATTCTATA ATTGTnGTTA TCTTTAAATA ATTGGAAAC CTTTCATAAT CTAAACCAAA	120
35	AAAGAAAGTT AGACATGAAA AAAGTATCAT AAATAATGAT GCTAAACTTA AGGCTTGTGC	180
	ACCTGGCTTT CGAAGAATGT CTATATTTTC CTTAGTAGTC ATATTTACCT ATCTCCTATA	240
	CATTGATTTT GTAATAGCAT ATTAAGTATT TAAAGTTATA AGTACTTAGA TTCTTTTCGA	300
40	TTAAAAGTAT AAAAGCCTAA AATTATCTTT ATATTATTAT TTGATGACAA CTTTATGGTC	360
	TCTATTGTTT TTTACTTAAA CGCTAAAAAG CTAnACAAAG	400

(2) INFORMATION FOR SEQ ID NO: 1631:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1631:

55

TCTAGAGCGA

70

(2) INFORMATION FOR SEQ ID NO: 1632:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1632:

15

CAACGAAGAT ATTCAAGTGT TCAGTCATTA TTTTGGACTG CTAATGAAAC TGATTCTTGT

60

GG

62

(2) INFORMATION FOR SEQ ID NO: 1633:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1633:

30

CTAATGATTA GATTCAAAC AATAAGACT AAAAAACAA GTTGATAATG GTAAAGATAT

60

TATCCAACCTT GACATCTAAA G

81

(2) INFORMATION FOR SEQ ID NO: 1634:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1634:

45

AATTTACCTT TTGTCTAGTA ATTTATTTGT GTAGTGTAAT CATTAAATTGT TTTAATATCT

60

AGT

63

(2) INFORMATION FOR SEQ ID NO: 1635:

50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 579 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1635:

ACCAACTAGC TAAATGCCAG CGCGGnATCC ATCTCAnAAG TGCACAGCAA GACCGTCTTT 60
 5 CCAACTTTTG AACCATGCGG TTCAAAATAT TATCCGGTAT TnAGCTACGG TTTCCCGAAG 120
 TTATCCAGT CTTATAGGTA GGTATCCCC AGTGTTACTC ACCCGTCCGC CGCTAACATC 180
 cAGAGAAGCA AGCTTCTCGT CCGTTCGCTC GACTTGCA TG TATTaGGCac GCCGCCAGCG 240
 10 TTCATCCTGA GCCAGGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA 300
 TACTAAATAA TGTTTGTAAC TAATAGTTAC GTTTTTGGAA TTAACGTTGA CATATTGTCA 360
 15 TTCAGTTTTC AATGTTCAAT AATGTTCAAT CTCTTTTATT CTACTTCATT TATTTCTTGA 420
 AGTCAATAAC TTTTGAACG ATTACTTTAT TTATTCTATA TTGTTTTTAT AGTTATTTCa 480
 ATGGTAAGTn TTACACTTTT GaaATTCTTC TTTAAAAACA ACTGCGTCGt TTTTGaCGcT 540
 20 TTATCaTATT ATCmACTTTG GGaATTAAAA GTCAATAAC 579

(2) INFORMATION FOR SEQ ID NO: 1636:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1636:

TCGACATTAA GCAACGTTCT TCGCAAAAGG TAGCGAGCGA CACGAGTTAA CTTTGCACGT 60
 35 TTCATTATT 69

(2) INFORMATION FOR SEQ ID NO: 1637:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1637:

CTGTGACTTC GTCGCGATGA CCTTCGCCGT TGTTCTCATG GTAAGCTTTA AGTATCGTCG 60
 50 ATGCAGTCnG TTCGCCATGT GCGCCAGCAG ACTGGTTGTA ATGTCGCCTC GTCCGT 116

(2) INFORMATION FOR SEQ ID NO: 1638:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 71 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1638:

ACAACATTTA GGTACTTTCA CGCATATCAC TACAGCTCAA CGTGATGATT TACCAAATCA 60

10

AATTTACAA G 71

(2) INFORMATION FOR SEQ ID NO: 1639:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1639:

GCGTGGCTTT GTGATTAACA TTGACAAGCA CGTGCAACAA CATATTCGAC GCGATAAAGC 60

25

GACATCTAAT ATT 73

(2) INFORMATION FOR SEQ ID NO: 1640:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1640:

CGCGATCATT TTCATTTCTA ATTAATCTTC CAAGTCCTTG TCTAAAACGT GTAACGTCAT 60

40

CAGGTAATAC ATATTCCTTG AAAGTTGAAG TGAATTCAGA ATCCATAAGC CAATATTTTG 120

CATTATGCTT GTTCATAAAC GGTAACCTCG CTATCATCAC ACATTTAATA CCATTGCTT 180

GAAAATCAAA ACCTTCAAAA AATGTTGACG TACCAAGCAG TATGGCCTTA TCAAAATTAT 240

45

TAAACTGTTG TACTATTTTA TAATTTTGGT TCTGCTGTTG TGTTAATACA ACATAATCTT 300

CAAATTCTGG CAATTCATTT AAGCATATCT TGTACCATAT GCATCATTTT ATAACGTA 360

AATAAGACTA AACATTTTGA TGACGTTATA GTCGTATATn 400

50

(2) INFORMATION FOR SEQ ID NO: 1641:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1641:

ATTGTTGTAC CATGTATACT AACAAATTGTA ATGTCTCATT TCAGTAAACA AAAAGCGAAA 60
 GACATT 66

(2) INFORMATION FOR SEQ ID NO: 1642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1642:

ATTTTCGTCGG GAATAAATTT TGCCATTACA TAGAAATATC TAATAGATAA CGAAAAAGTA 60
 TCGTATGTAT TTTTAATATA GTGTAAAATA TTATATGTAA AATAAAATGT AGGTTTTTTAG 120
 TTAGAGGCAT TATAAGAnAA TTTTGAGTAT AGGTTAGCTT TTAATTATGA ATCTTATTGA 180
 AATTTGATTA ATAAAAATAT GATAGGGGAT TAAAATGAAA CTATTTTATA TCGTATTTCT 240
 TATTATTATA TGGCTGAATA TATTTTTTAGG AAATGAAATC ATCCATACAC TGA CTGTTTTT 300
 AATAACAACA TTGTATATTG TTAATTCACG AnAGGGGATT AAAAATGACA GAGTTGAATA 360
 ATATTATAAA CGCGCnTGCA ATCnTTGTTT GAGTCCGGAA 400

(2) INFORMATION FOR SEQ ID NO: 1643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1643:

AACTAGAGGA GGACATCCTA ATGGAAGCAA AACCCGTTGC TAGAACAATA AGAATCGCAC 60
 CTCGTA 66

(2) INFORMATION FOR SEQ ID NO: 1644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1644:

TATCAATTTTC ATATGCGATT TGGCCTTGCA ATAATTAGGT CTCACCTTGC CATATCTTTA 60
5 CCTAAGCAAT ACTTG 75

(2) INFORMATION FOR SEQ ID NO: 1645:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1645:

CATTCTCCTG CATCATAAAA ATCAACAATT GTATCATCAA AGTGTATCAA AATATTTTAA 60
20 TATCCCAATT 70

(2) INFORMATION FOR SEQ ID NO: 1646:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1646:

AGTGACACTT TCGTTCCACC ACATCGTAAA GAAGTACTTC AAGCACGTGA AGATGACATC 60
35 AAAGAAAAAG TTG 73

(2) INFORMATION FOR SEQ ID NO: 1647:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1647:

CTGTGATTGG TGTGTGATT GTCTTGCTTC CTGTTGTCC TTCTTGTTTC GCTCGCTCTT 60
50 CGCCGGGTTG T 71

(2) INFORMATION FOR SEQ ID NO: 1648:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 115 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1648:

AACTATAGAA AAATTCGGAA TTATACCAGA AATGGAATAT GAAATGGAAG AGGTAAACA 60

10

AAACGAGCAA TATATTAGAG AGCAAGAAGA AGCTGGAACA ATAGAGCGA TAACA 115

(2) INFORMATION FOR SEQ ID NO: 1649:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1649:

TGTTGTCATG ATCTGAAAAG TCAAAGTCAA TAGAACATTG GCTTTGGCTT TTTATTTGG 59

25

(2) INFORMATION FOR SEQ ID NO: 1650:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 125 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1650:

35

ACCGATAATA GTACACGGCA TAATGnAACA ACTTGGCATG CACCCTTTT ACGTTCCTTT 60

ATCTCTGCAT GATTGTCATG TTCATCATGG TTTGGCTTGC ATTAATAGAG AGGGTTGACG 120

40

CAGAA 125

(2) INFORMATION FOR SEQ ID NO: 1651:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1651:

TGATTAACGC GAATGCCACT TTTACTACCA ATGTTCCCAA AGCTGCTTCT GACAAACGCC 60

ATTGTACTCT G 71

55

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1652:
 TCACTACATG CACCATAAAT ACAGTATGAA CGTATTGAAA TGGGCATTAC ATGATACAGA 60

(2) INFORMATION FOR SEQ ID NO: 1653:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1653:
 TTAATTGAAA CAATTGACAA ATGCAATTTG ACGCCAAACT TTGAACTTTG AATGGATTAT 60
 CACATTATGA TTGTTTCATCC ATGGnCAATT AGCATGGACG TATTACATTC TGGATTATCA 120
 AGC 123

(2) INFORMATION FOR SEQ ID NO: 1654:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1654:
 CTATGACGTC GCATGCACGC GTAACCTGGG CCCCTCGAGG GATCCTCTAG AGCGGCCGCC 60
 CTTTTTTTTT TTTTTT 76

(2) INFORMATION FOR SEQ ID NO: 1655:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1655:

TTTTAAATTT TCGTGAAATC GGAAATGTAC GATTAGTTAT TAAGCGTTAG AATGTGTGAT 120
ATGTGAACCT GGTATTGACG GCGCT 145

5 (2) INFORMATION FOR SEQ ID NO: 1656:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1656:

TTTAGAATTC CAATACGCTA TTGCCAGCGA TTTAGCCACT TGTGGGTAAT GATATTGAAG 60
GTGTTAGTCA AGT 73

20 (2) INFORMATION FOR SEQ ID NO: 1657:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 93 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1657:

CTTCTGAAAA GTAGTAATGT AACCTATTGG ATGCGAATGA ATCCCCAAAT TTAGTGGACG 60
TATGTGGCTT CATCTTCAGA ACCTGTATCT GGT 93

35 (2) INFORMATION FOR SEQ ID NO: 1658:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1658:

AAGTTAACAT GCAAGTTGAC GATGTAATGA CTCAAAAAGA GTGGAAACAA AAACACGA 58

(2) INFORMATION FOR SEQ ID NO: 1659:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1659:

TTAATCCAC AAACAAATGT ATGAAATTGA GTCAGTGATA TTAAATATGG GCTTGAAAGT 60
 5 GTCTA 65

(2) INFORMATION FOR SEQ ID NO: 1660:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1660:

TGCATTTTGT TAAGAACGCA AAGCATGTGA AATTAGTTTT TATAAATTAG GATATTATCA 60
 20 TGTGTATTGA AAACAATGAA GTGTGCTATG A 91

(2) INFORMATION FOR SEQ ID NO: 1661:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1661:

ACATATCTGT CCACACAACA AGGACCATTT GTCTGAAGGG ACAGTGAGTG GGGAAATATGT 60

(2) INFORMATION FOR SEQ ID NO: 1662:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1662:

TGGGGTTTTA ACCAGGGGAC CTAAACCAG CCCCCATTTT CCAAGTTTGG ACCCCAAATT 60
 CCCCnAAATTT AAAAAAATT TGTTTGGGGT CTAAGTTGGG CCGGTGCCTT CCTGCCTAAA 120
 TTTAGCCCAT GTCTAACATA GTACTTTGGG AACGTAAAAG TTAAATTTA 169

(2) INFORMATION FOR SEQ ID NO: 1663:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 677 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1663:

TGGCACAATT GCACCAATTA AATGAATAAC TTTATCATTT TTATATACAG GTACAACAAT 60
 10 CGCTTCTTTT ACGAACTCAG ACTGGCGTAA TTGTGTTTCA ATTTCTTCTA ATTCCATTCT 120
 GTAGCCATTC AATTTGATTT GGAAATCAAT ACGACCTTGA ATGAACCATT GACCATTTTC 180
 AACTTCGCT TTATCACCAG TGTGATATGT ACGAATACCG TCATCGAAAT TAAATACTTC 240
 15 AGCTGTTTTT TGGTCATTTT TTAAGTATCC TAAACTTACA CTTTGACCTT CGATAACAAG 300
 TTCACCTTCA TCTGTAGTAG ATAATCTTGC GCCTGGTCTT TCAACGCCAA CAGGTAATGT 360
 CGGATATTGA TCTAAGATTT CTTGTGTAAT TTGAATACTT GTAACGCTA CCGTAGCTTC 420
 20 AGTTGGACCA TATGTGTTGT AAATCGTCGC ACTTGGGAAA CGGTTTACTA ACGCTTTTGC 480
 TGCTCTGTGA GGTAGAATTT CACCACAGAA GAAGAATTCG TTAAGACTAC CATATTGTTC 540
 TTCATTAAGC GTTGGAATA ATAAACACAT TTCCATAAAT GATGGTGTG ATACCCAAAT 600
 25 GTTAATCGGT GTTGCTGTTA GCATTTTCAAT TAATAATTTA GGTATTATTA TCATGTTTTT 660
 ATCTACAAGA nTnAAnG 677

30 (2) INFORMATION FOR SEQ ID NO: 1664:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1664:

40 GTTACAACAA TAGTGGTATA AAACGGGAGC AATTAGAGAT CAATATATGA TTATTAAGAG 60
 CA 62

45 (2) INFORMATION FOR SEQ ID NO: 1665:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1665:

55

GTTTACGCAA ATGATAGCTC GGTAACAT GAGCAACATG TTGAAGCCAA TTTGGAAATG 120
 TGTTTATCGG AAACCACAAT CCACCTAATA CTGCTAAACC AATTGTTACG ATATTAGCTA 180
 5 AAGCACTTGT TTTTGAATA TCATTTAACA AAGAACCATA ATATGCCAAA AGTTATTAAT 240
 AGAGACGCAC CTAACCATAA AAATATTCCT GACTCTAACC ATTGAAGTGC ACTCATTGCA 300
 ACACCTTTAT AAAAATGTCC AACCATAAAA ATAACATA TC 342

10 (2) INFORMATION FOR SEQ ID NO: 1666:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1666:

GTCCAAGAAT TCAAAAACGT TTTCAACTTC GGCCAAAGCC CAATTTnTCT TTGTGGTTTA 60
 ACTTTTTAAT TTTGAACGTT TTAGGGCATA AAAAAAAAAA GG 102

25 (2) INFORMATION FOR SEQ ID NO: 1667:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1667:

TTGATAGTAG CCATAATCAT ACCACTTAAA TAATATGTTT GATCATCGGC ATAATTTTTA 60
 TTTATTGTCT GTTCGCAATA TTTTGAGCAT TATCATAATT ACCACTAGTC ATATCATCTT 120
 40 TG 122

(2) INFORMATION FOR SEQ ID NO: 1668:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1668:

AGAGATGAAA TTAAATCGC AATTGAAAAT TTCAATCAC GATGAGAGTG GGACAGA 57

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1669:

AACTACTGCC AATATTAATA GCATTGGTAC ATCTTAGAGG CATTGAATTC CTTACTCAGA 60
 CTCATAATGC 70

(2) INFORMATION FOR SEQ ID NO: 1670:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1670:

TTGTCTGATA TAATCCATTT CGATTGGACT CCACACGTTA CACCGATACC TTCTTTACCA 60
 GCCCCACCCG TAC 73

(2) INFORMATION FOR SEQ ID NO: 1671:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1671:

GAAGAATTGT ACTGTTAAAG TGA CTCTAAA CTATCGCGGA AATAACAGTG AAATCACCAA 60
 TTAGACTAGC GACACTGAAG TCATTAAAAA CAGACATTTG TAGTGGTGCA CTTATCACCG 120
 CAAATACAAG AGAGTTTCTC 140

(2) INFORMATION FOR SEQ ID NO: 1672:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AACAACGTTT ACTATTGGCA CAGAACGGTT GGTACTTAGT CTAATACCAT TGTCATCAA 59

(2) INFORMATION FOR SEQ ID NO: 1673:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1673:

ATCTCTTTGA CTTGAAGGAT TGGATTTAAA TCTTGGTGAT TTGGGCCGTG AAATATTTCC 60
 AGAAAATTCC TCAGACGTAT TAGTATAATT GTAACGnTAC ATTCTAATAT ACCTTTCTTC 120
 GATG 124

(2) INFORMATION FOR SEQ ID NO: 1674:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1674:

CACCACCACC ACACACACAC ACACAAACAC ACAACCCCCC CACACACAAA CCACACCACC 60
 AACACACCAA CACAnCACAA AAACCCACCA CACACACCAC ACACCAACC 109

(2) INFORMATION FOR SEQ ID NO: 1675:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1675:

TnGTCAACTG ATTTATGAAA TGGCAGAGCA TATGGCGTCA AAGGTTCTTA ATCGTTAAGC 60
 CAGACCACTG GAGGACCATT AGATGCAGCG TTGCTTTCAA G 101

(2) INFORMATION FOR SEQ ID NO: 1676:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1676:

TTTTAAAAAT TTGAAAAATT TAGACCTTAT TTCACGTGCG ATTTAATCGA TGTGTTAATA 60
 5 AAACAATACT GGCATTCAAC ATGTAATCCG ATAATAAAAT AAGGTTGCAA TTATGTTATT 120
 GCATATTTTG TTTATTACTT AGAATAATAC GATGGTTAAG ATGAAATATA TGACAAAGAT 180
 AAATAATGAC ATTAAATTCA AGATGTTTAC GCCTTTTAGA TCTTTTAA GCATTTTAAA 240
 10 TCCTGTCACT TCKACATTAC CGACTAAGAG TAATAAGACG ATAAATACCC ACCAATTsTC 300
 TTTTGAAAAA CTCATCGTCG TTAATGCTAA GACGAATAAT AACACACAC CCATAATAAT 360
 TCTCAAAATG CGAGTAAATA CAACTTCCAT TTTAAAAATA 400
 15

(2) INFORMATION FOR SEQ ID NO: 1677:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1677:

TCTTACTCAT GCATATGAGT GCAAGGGCCT GAGCATTTCAT CAGCAAGATT AGAGCGATTT 60
 TTAC 64

30 (2) INFORMATION FOR SEQ ID NO: 1678:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1678:

ACAGCTGATT TATTAAATGA TACTAAGTCC AAAGGCATGC GCATTATATC AGTTGGTACA 60
 TTCA 65

45 (2) INFORMATION FOR SEQ ID NO: 1679:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1679:

5 AGCGCCACCA ACTGACGAAT TAGGTGGTAG TTGGACACTA TGGAAAAATT TAGCGCGACA 60
 AAGTCCTGAA TTTGGTAATC CTGATAAGTT TTGCCAAAAT ATTCCTA_nAA AAAGTTGGTT 120
 TGT_{TT}CAGCA ACTTCTACAA CAAACAATAA AGAGATTATC GATACAATAG AAAGTATTTG 180
 10 TAAACGTGAC CCACTTGGCA GGCAAAACAG TTACAGGCGG TATTATTACA ATCAATGATT 240
 CTGcATGGCA AATGAGTTTT ACAATCAATC GTGCAGCAAC AGTTTGAAAG ACCAACCTGG 300
 AAAATGGAAA TATCTACATG GGGTTTGATG CCTTATGATT CnGGnGTAAA CGGCGGTTGA 360
 15 TG 362

(2) INFORMATION FOR SEQ ID NO: 1680:

(i) SEQUENCE CHARACTERISTICS:
 20 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1680:

AGATACTTCA GATTTAGCAT CATGAAGCAA CTTTAAAGC AATCGCTGAC GCTGGTATTC 60
 30 AGCCCCGAGG 69

(2) INFORMATION FOR SEQ ID NO: 1681:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1681:

TAACCATTTT TTTTGACGTT TTATGTTGTT TTAAGAAATA AATACCAGTT AATGTA 56

45 (2) INFORMATION FOR SEQ ID NO: 1682:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1682:

(2) INFORMATION FOR SEQ ID NO: 1683:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1683:

CCCCAACACA ACAAACAACA CCCCCACCAC CCAACCCCAC CACACCCACC CACCACCCCA 60
 ACCCACCACA ACACCACnCA CCAACACACA CCACACAACA ACCCCACAC 109

(2) INFORMATION FOR SEQ ID NO: 1684:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1684:

ATTATGTTTCG CGATAATTTA AGTAAAAGAA GCACAGATAT TGAATTTGAT AGGAGTAATT 60
 GT 62

(2) INFORMATION FOR SEQ ID NO: 1685:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1685:

CATAAGGTAC TTAAATTAAG GCATATCTGC TGTCTAGCAG TCGCATAAAT CATTAGA 57

(2) INFORMATION FOR SEQ ID NO: 1686:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1686:

(2) INFORMATION FOR SEQ ID NO: 1687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1687:

CTTTATAGTA TATTGCTTTT TGTTTTTCTT TTTCGTCATA TTCACTTTT AAATAGATAC 60
 CTGCAACACT AATTAATATG ATTAACATAA TACTAGTTAA TATTAAATT 110

(2) INFORMATION FOR SEQ ID NO: 1688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1688:

AATTACTAGT CTGCTTGTC AAAGATTATT TATATTCTAG CTCAACATTA ATTTCTTTGA 60
 TTTTGGTACC ATCTATCGTG TCACCCATGC GATGCGGTTG TAGTTTTTTT GTAAGTTCGA 120
 AAGTATAAAA CTTATCATCT TCCATTTTAA CTACAATTTT ACCTTTTCTA TTATTAAACAG 180
 CACCATATAA TTTTCTTCT TCCATCAATT TTTT 214

(2) INFORMATION FOR SEQ ID NO: 1689:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1689:

GCTAGTTGTA ACGTGCTTTT TCACCACCAG ATAAATCATA ATATCTTTTA ACATCTCTG 59

(2) INFORMATION FOR SEQ ID NO: 1690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1690:

CCAAACTTTA TAATATGAAA TGCTTGGTAA TTACAAAGAT AAAATCATAC TCACG

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(2) INFORMATION FOR SEQ ID NO: 1691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1691:

TAGACAGCAA TCCATTGCTA TAGGGGTGGA TATCTCATTT GCGTTTGGAG CTGTGCTTGT

60

TATG

64

20

(2) INFORMATION FOR SEQ ID NO: 1692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

25

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1692:

TGCATGGGAT TGCAGCTAAG AGAATCATAA AAATATATTA CTTTAATAAG TG TAGTA

57

(2) INFORMATION FOR SEQ ID NO: 1693:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1693:

CGATGTGTAC GTCTCACCTG ATTTGCGACG GTAAGCTAGT GCATATTCAG CACCGCTACT

60

CGCCCAGCCT AGAC

74

(2) INFORMATION FOR SEQ ID NO: 1694:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1694:

AACTTTTCAG ATGTTGATAG CTATAGATTT AGGCGCTATT CACCA_nGTCT ACATGCAATA 60
 5 CGTACGTTAT AATGCACTGC AACGAATCGC GCGTTATGAG TTGGTAATTG TTGTTCAATA 120
 TTGGGTGTAT AGTTTTC AAC GTGGTTACAA GCAACTACCT AA 162

(2) INFORMATION FOR SEQ ID NO: 1695:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1695:

20 AATTATCTCT ACACCTTTTC TTTCACATAA TTGACGCAAT ATAATCCCTA TATCT 55

(2) INFORMATION FOR SEQ ID NO: 1696:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1696:

ATGCAACGTT GGCATTGGGA AATGGTCCTG CCTAAATTAA CACGCAATAA AATGTG 56

35 (2) INFORMATION FOR SEQ ID NO: 1697:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1697:

45 ACTGTGTAGA AGATGCTATT ATTGTAAAAC ATAGTTTTAA TTTTATTTTC TGATATA 57

(2) INFORMATION FOR SEQ ID NO: 1698:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1698:

AAAATTTTCC CCCGGAACC CGGTTTTTTA AACCCCCCGT TTAAAAAAA TTTTGGGGGG 60
 5 CCCAAAATT CCCTAAAAAA nAAAAAATTT TTTTTTCCC GGGGAAAAA 109

(2) INFORMATION FOR SEQ ID NO: 1699:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1699:

GTGTTAACGT GGATTATATC AAnGAGGCGG TCAGGTACAG TCCACACGCA CAGCGCACAG 60
 20 AAGTATCACA TCCAGTAAAC AAGGCTAGTA CAGCATTGCA 100

(2) INFORMATION FOR SEQ ID NO: 1700:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1700:

AAGGTAAAT GAATTAGGT GATCAATGCT CTATACTCAT TGCTAAGTCA ACGCACCTTT 60
 35 ACCACCTTTT CCCAACTCAG TAAGGCATTC GACGTATTTT TTAGCCAAGn TTACATATCT 120
 ACTCTGCAC 129

(2) INFORMATION FOR SEQ ID NO: 1701:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1701:

CAAGAGGAAC AACTCGGTAC TCGCATCAG CAGAGATGGC GAAATCACAC TTAGAAGACA 60
 AGG 63

(2) INFORMATION FOR SEQ ID NO: 1702:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1702:

10 TATTTAATAA ATCTTCAATA CCTGTTCAT CAGTTTGTG ATAAATAAGA CCTCTCCATT 60
 TTAAATCTTC AATTAATACA TTCGTCATTA TTATTTCTC CTATTTATAA TTATTTATTG 120
 AATACTTGTT AAAATACTTT AAAGKTTTTT GAACGTAAAA AAAACCCTTA CAACAAATAT 180
 15 GTAAGGGCGC GATTGCACGT TACCACCAAA CTAAACATA ATCATAAGAT AATGTTCACT 240
 CTATTAATGA TACGTTCAAT AATAAACGTA GGACATGTTA GTTATAAAGG TGTATTCATA 300
 TTATTAAAAA CACTAGTTCA CAGCGACCAC TAGCTCTCTG ATGATTTCAA ATAATATTAC 360
 20 TTGTCCTTTT ATCCTATTCT GTATGCATTT TCCCTAATTA 400

(2) INFORMATION FOR SEQ ID NO: 1703:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1703:

TCAATATTGA TATCGAAACG CTTTGCAGAT TGATATAAAT TATCAGAATC AAGTAATTCA 60
 35 TTTATTTTCT TTGGTGAAAG TACTTGAAA ATACTATACT GATGAAAAC TAAAAATGAA 120
 ATGAAGTATG GAAGTTGTTG CTTTGGGTAA GCNAAAATTC TAATACATAC TGATTAACT 180
 40 GTTTGTTTAT TGnGAATTGC AACGCATC 208

(2) INFORMATION FOR SEQ ID NO: 1704:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1704:

AAGCCGATGT AATTATTTAT GCAACACCTG TTCTAATGCA CAAAGAAATA TCTTAGCGAG 60
 55 CTTATAG 67

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1705:
CCAAGTTGCA TGTTATTTTA AGCTGACTTT CCACCAACTT CTGAGTTTGT GGCC 54

(2) INFORMATION FOR SEQ ID NO: 1706:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1706:
CAACTACACG AAAGGGTAGT GCTTCAAGAT AATAACGTCC AATTATTAGG AACTGTGGCG 60
A 61

(2) INFORMATION FOR SEQ ID NO: 1707:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1707:
ACCATTCCAA ATGAACCTAA ACCACTTGAT ACGTTGACGA CAACAGGTTG TTCA 54

(2) INFORMATION FOR SEQ ID NO: 1708:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1708:
AAATTTGAAT AACTGTACAC ATTTTTTTGA TCATAGTCTA TATACTTTGT GAATTAATT 59

(2) INFORMATION FOR SEQ ID NO: 1709:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1709:

10 GCACAATAGC CAATTAGATG GGGCCGGTGC GGTAACATTT TGCTTCATTC CTGCATTAT 59

(2) INFORMATION FOR SEQ ID NO: 1710:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1710:

TTACAATTCA ATCAAGTTCT TCATTATCAG ACGAAGAAAT CCACCGTATG GTAAA 55

25 (2) INFORMATION FOR SEQ ID NO: 1711:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1711:

35

TTTCTGCTTA TTGTCATTCG ATATCGAATT ATTAGAAAGT GCAGATTTTCG CATCAG 56

(2) INFORMATION FOR SEQ ID NO: 1712:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1712:

TAAACCTTTA GGATTGCTGG CAATAGTAGT GCAGTTGGCT GGACTTGTCA TGCCC 55

50

(2) INFORMATION FOR SEQ ID NO: 1713:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 207 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1713:

5 CAAGAGGATT CGTGCAnTGA ATTCATGGAG ATATTTAGAT CTTTCACTGG AGAGAAAATA 60
 AAAAGAAGAA AAGAGTAACC TTTAGATTGC TGGATnTGTG CAGTGGCTGC TTGCGTGCCT 120
 TTAGGTGGCA TAAGGAGGCT ATACGCAGAC AACCACCGTC CCGGGGTTTT ATTGTACACT 180
 10 GTGTAGGACG CAGACTTTAT GTGGTTG 207

(2) INFORMATION FOR SEQ ID NO: 1714:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1714:

TGGTTATCGA CTGCTCGTAT ATTTTGACTG TTTTGACTGT TGTTCGGTA GCAATACTAT 60
 25 CTCCTAAGCC TTTCAATTGCC ATTG 84

(2) INFORMATION FOR SEQ ID NO: 1715:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1715:

GTTTGAATTG ACTGACTTCG TTTTACCGCG TGTTTAATAT TGTTATACAT ATAT 54

(2) INFORMATION FOR SEQ ID NO: 1716:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1716:

50 GAAGCCTGTC AGTGGATCAA ATTATTGAAG ATAACCTGGG TGGCATTTTT GGAAAGTCCA 60
 AATGCTGGGA ATGGTCA 77

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1717:

GGGCCCTTTT TTTCCCAAAA AAAAAAACC CCCTCAACCC AATTTTGGnC CCCCTTCCCC 60
 TTTAAAAATT TAAAAATTGG GCCAAAAGGC CCCCCCAAAA AAAACCCCCA ATTGGAATTG 120
 GAAAACCATT GGAACCAATT CCATTGAACC AGGA 154

(2) INFORMATION FOR SEQ ID NO: 1718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1718:

ATTGTCTACA CTGCCACTTT ATTTTCATTA ACCATTTCAC AAATGTGTTT ATCATTCAAC 60
 ATGAACATCA ATTGTTCAAT TACATCGACA CCTGATGCCT AAnCAGGCAC CTTTTCACA 120

(2) INFORMATION FOR SEQ ID NO: 1719:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1719:

TTCAATTGTT TGTAAAAGTG GCATTTCTAT GTCTTAAAAG TGACGAAACT TCAC 54

(2) INFORMATION FOR SEQ ID NO: 1720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1720:

(2) INFORMATION FOR SEQ ID NO: 1721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1721:

TTTGGATTAT AAATTGACAT GTAAGTACGA GGCAGCTGTA CCCGATATAT AATTGCTAAG 60
 AGTTAGGGCT G 71

(2) INFORMATION FOR SEQ ID NO: 1722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1722:

TTTTATCTTT ATTACTAAAA CCAACTGCAC CAAAGTTTGC AGTCATTACC ACACGTTTAA 60
 CACCCGCATG TTCTGCAGCT CTTAAAATAC GTTGTATACC TTCAATTGCA GGCTTCGCCA 120
 TCACTTCTGC ATCGTCTGTT TTACCGAAAA ACACCGGAGA TGCTACACTC AAGACATACT 180
 TGCAATCTTT CATTGCTTCA TCCCAATGTn CATCTTGTGA TAAATCCGCT TCGACAAACA 240
 TTAAATCGCT CTGTGGAAAT GCCCATGTCT TGCATTGTTT nAATTACTTT ATCAGCTTTA 300
 CTTAAATCAA GnATCGTCGT TTGTA 325

(2) INFORMATION FOR SEQ ID NO: 1723:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1723:

CAGTATTGCA GTCACGACAA TGTGATGACT AAATTATCCA AAGTATGAAT TCCATGCGGC 60
 ATTAATCCTA G 71

(2) INFORMATION FOR SEQ ID NO: 1724:

- (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1724:

10 TTGCAACGAT ATTAGGCTAT CTAGTCGGCA TATTTGTAAA ACAAGATCCA ATT 53

(2) INFORMATION FOR SEQ ID NO: 1725:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1725:

ATCTATTCAT CTTCGTACAC GGACAGGAAA TGAGTCCAGT AGATGCACAT TGGGAATTAA 60

25 TCGAAGCTAG C 71

(2) INFORMATION FOR SEQ ID NO: 1726:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1726:

CATCTTGCGAG GTCTACATTA TAAAATGTGA AGTTTCTAC GATAACAATT GGGAAACTCA 60

40 GGGGCATCTC C 71

(2) INFORMATION FOR SEQ ID NO: 1727:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1727:

TTCnTTTTTA AAAATTCCCC ATTCCTTTTT AAATTTCTTT CCCGCTGGAT TAAATGGATT 60

TTAAAAATTC CACCCCAACT TAnAATTAAA TGGCTTGTGG AAAATTAACG GGATTGGCAT 120

55

TCCAGCTTAA ATGGTTTTTT TGGAGGCTTC CACGTTAAAA ATGGCGGGTG GCTTT

235

(2) INFORMATION FOR SEQ ID NO: 1728:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1728:

15

TAGAGTGGCT ATAAAGCTAA GTTCAATTGA CCAATTTACA ACAGGTTATT GAGGACAATA

60

A

61

(2) INFORMATION FOR SEQ ID NO: 1729:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1729:

30

ATCACCAAGA AGTTCTAATG CTTGGTATAA ACGTTGAATA CGACGTTCCG TATT

54

(2) INFORMATION FOR SEQ ID NO: 1730:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1730:

CGTCCCGAAG CGTTGGAGGC GGAACATCC AGAGTAATTG GCACAGATTA TGACCATAT

59

(2) INFORMATION FOR SEQ ID NO: 1731:

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1731:

55

(2) INFORMATION FOR SEQ ID NO: 1732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1732:

TATGTGGTGT TCAATGCAGT GGTCAATTATG GTGCATCTTA CCAGATTCGG CATTCTTATT 60
ATAACTATAC TTGTAATAAA TGGCGACATG CAGACACGnC AATAC 105

(2) INFORMATION FOR SEQ ID NO: 1733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1733:

TTTACGTTCC ATAGCAAAGT GATACAAACG TCAGCATCAA TGTAAGGCAT AGATCATAGT 60

(2) INFORMATION FOR SEQ ID NO: 1734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1734:

TTCCATCATA CATTGCGGTT TTACTTTTCT TCTGGTATGA TCAAATATTC ACATAA 56

(2) INFORMATION FOR SEQ ID NO: 1735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1735:

AAATGGGGAT GAAACAGTTA GTGTACAGGT GAAAGCTTAA CAGCAGCTAC AATTGCA 57

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1736:
GATTGCAAT TAAACTTAAA TGTAATTTT CGGAATGTGT ATTTGGTTTA CTAAAGTAA
A

(2) INFORMATION FOR SEQ ID NO: 1737:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1737:
AAAGAAGCTA AAGAAAAAGT TGATAAAACA GCAAAAGTGA TTATTAGCTA CAGCATT

(2) INFORMATION FOR SEQ ID NO: 1738:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1738:
CAATAATATC GCTAAAACCG CCATTGTGAC CAAATGAATT TGATAATGCT GCAG

(2) INFORMATION FOR SEQ ID NO: 1739:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1739:
TAGAGCCCAA CCGGCAACCC ATCCATGGAA ATTCACCAAA ATAATACATT GACCCCAAG

(2) INFORMATION FOR SEQ ID NO: 1740:

(A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1740:

10 CCTTTTGGn AATTTAAGGG GGTTCCCAAC CAAATCCCC CAAATTTTTT TGGGTTAAAA 60
 AAACCCGGCC CAAAAATTTA AGGGAATTG GAAAAAGGT TGGTCCCTT TTTTCCCAA 120
 GGCCCAAAAT TTGGAA 136

15

(2) INFORMATION FOR SEQ ID NO: 1741:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1741:

25

CATTCAACCA ACGACTGACA ACAGAACATT TAAGAGTCTA GGACATTGAT TGA 53

(2) INFORMATION FOR SEQ ID NO: 1742:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1742:

40

GCTCGTCTGA TTCAGTCACA AAATTGTCTT GTTATACTTG TCACCTATCA TC 52

(2) INFORMATION FOR SEQ ID NO: 1743:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1743:

50

TGTTATTTAA AGAGGCTCAA GCTTTCATAG AAAACATGTA TAGAGAGTGT CAT 53

(2) INFORMATION FOR SEQ ID NO: 1744:

55

- (A) LENGTH: 94 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1744:

10 TCTGAGTTAA AGACGTCTCA CTTAAAGCTT TAGCAATTCC AACAATCAGA TATCTTCACA 60
CGTGTTATAT GTGTCCATTA ATATATCCTG TGGC 94

(2) INFORMATION FOR SEQ ID NO: 1745:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 212 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1745:

25 GGAAAAAAnn TTTTAAAAA AAGGGAAAAG GGAATTGGGG TTCCCGGCCC CTTTTTAAAG 60
CCCCCAAATT AAGGAAATTT TAAATTTTGG GGAAGGGGAT TTTCCACCGG TTAATAAACC 120
GCCGATTTTG AGGGGGTTGA ATTAATTGGC CCAAATTTAA AAACCTGGAT GCTGGGTCCA 180
30 ATTTTTTACC GGGACCAATT GGTCTGTCAT GA 212

(2) INFORMATION FOR SEQ ID NO: 1746:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1746:

TATCTTCCGA TGAAGAACAA GATGCACAAG AAGTACGCCA ATGATTTAAG AAAGTGGT 58

45 (2) INFORMATION FOR SEQ ID NO: 1747:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1747:

55

AAAATTAAGn CCTTTTTTAA CCTTCCCTT CCCCAATTGG GGCCT

105

(2) INFORMATION FOR SEQ ID NO: 1748:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1748:

15

AGTGCCTATT ACTTTGATTG ATGTCCAAGT TTCCTATCAC ACAACTTAAT TT

52

(2) INFORMATION FOR SEQ ID NO: 1749:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1749:

AAAGCATCAT CCGAACTCCA ATGATTATAC TCCCTAGATA TTATTATGTG ATGCTTTGAG

60

30

CATTAAATTAG AGATGGGACG ATTCCATGAA AGATA

95

(2) INFORMATION FOR SEQ ID NO: 1750:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1750:

TTGACACATC TACTCACATT AAAAGTAGAT GAAGCGTTGA GATTAACATT TCCACATTTA

60

45

CAA

63

(2) INFORMATION FOR SEQ ID NO: 1751:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

TCGATATTTG AGACACGCTG CTGTAATAAA ACATCCTATA AAGTATATAC CAAGATCTAC 60
CAATATAAAC AGCGGCTATA TGATATAAAT GCTCAGACAC ACCCnCTGCG ATCCAT 116

5 (2) INFORMATION FOR SEQ ID NO: 1752:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1752:

TATGATTAAG CTTAGTGCAG ATTTGATTTA TTnAACAAAG CTTCACTACA TTAAAAATAG 60
GGCACTCGCA CATATAGTTG TATCAATAGC CTTTATCAAT TTTTGGGAA GGTT 114

20 (2) INFORMATION FOR SEQ ID NO: 1753:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1753:

30 AACTTCAAAT GTGCCAAGTG TTGAATCACA TCAAATCAT TTTTATTTAA CG 52

(2) INFORMATION FOR SEQ ID NO: 1754:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1754:

ACTAATCCCT TCGTGTTTC CAATCAATTG CATTATTAGT GGCCATTGTG TTGATATAAC 60
45 TGACAAGCTT TAACC 75

(2) INFORMATION FOR SEQ ID NO: 1755:

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1755:

GTGAACAAGG GTAGATGTAA ATAGTTGATG CATGTGTACA CATCATAACA AAA

53

(2) INFORMATION FOR SEQ ID NO: 1756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1756:

TTATTTGGGC AGGCAAATAC CCTTAATATA TTCAAATCAT GTTAATATCA TTGCTATTGC

60

TAAACC

66

(2) INFORMATION FOR SEQ ID NO: 1757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1757:

ATTAATCGGA GCACTTGGGT TCGCAATTTA TGCTGAAATG GATCATTCTA CATCATC

57

(2) INFORMATION FOR SEQ ID NO: 1758:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1758:

CGAACAATAA CTCTAAGTAT CCAACAAATG CTGCAAGTGT ACCTACTGTG ATTGATCCAG

60

AAATAGCAAG ATATGCACCA ACACCGATGA CAATAATTGG TCCAATATCT GTAAGTGTAT

120

TAATTGCGGC AAAGGAATAg GCATTCCATC TTGTATGTTT CAACGCACGT GTTAGGAAAT

180

TAGTATTCTT TTTATCAAAG TTTTTCGCTT CATGTGCTTC AATCGCAAAA CTTTAAACGA

240

CTGAAATACC TTGAACACGT TCATGCAAGA ATCCTTGAAC CTCAGCTAAT GCTTGAGATC

300

TTTCAnGTGT CAATTTTCTT AATCTTCCAA AGAAAACGTA CACCGTTAAA ATGTAAAATG

360

(2) INFORMATION FOR SEQ ID NO: 1759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1759:

ATTATGTCA TGCTAGGTCA CTGTCATCAT CCATTTAGTA TAGAAGACGA CAAAATTAAA 60
 TTATAGTGGG CTCCTTGATT GGCAGTATTC ATTTTCGGGA AGCGGGGTCC AGGCTTAAAG 120
 GGTATTAGAC GTGGTTACC 139

(2) INFORMATION FOR SEQ ID NO: 1760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1760:

TCGCCCCTCC AGGCTATTAT TTCATCTATA TCATTGTCAT CAGTTAAATT CAGCCTCGAC 60
 ATTTCCATTT CAATAGACTG TTCATTCAAT TCTAAGTCAT TATTGTAAGT TTCTAGTTGA 120
 TTTTCATAAT GATTAGATT ATTTTGCTCA ATTAACTTTC TTTGAGACAA TTGCATTAAC 180
 TTATCTTCAA TCTCCTTTGA GAGTTCTTGA TGCTGATTCA CATCTTGAAC ATACTTCTTA 240
 TAATCCACCT CAAAATTAGT GATATTAnTA TATnTCGAGA GTGTTTCAAA TTCAGTGATG 300
 AGATCTCGAC ATAAT 315

(2) INFORMATION FOR SEQ ID NO: 1761:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1761:

TAAATCCTCG AGATTCTTAA TAGGGTAGAT ATCTAACGTT TTCGCAAAGC TCTTTTTGAT 60
 TTGTTCTTCT TTTGAATCTC CAATGATCTT ATTATCACCA TCACAAGATG TAACAAAGAT 120

CCATCCTCAT CATTTCATCAT CTTCATCTAC CTTCGCGGCT GGAAATTCAA aGAaTCTATT 240
 ACTGACAAAT CGCTTTTTC ACCTTTTGAA AAGTCAATT CCAACTTTT ATAACCCACA 300
 5 GAACCTCCTT TCAAATTACC ATCAATATGC ATTTTAAATA CCGGTGCTTT ATCAGTAGGA 360
 ATATTATAAC GACTTCTTAA TTGCTTAACA TTTTCATCT 399

(2) INFORMATION FOR SEQ ID NO: 1762:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1762:

20 GTATAGAAGA CGACAAAATT AAATATAGTG GCTCCTTATT GCAGTATTCA TTTTCGGAAG 60
 CGGGTCAAGC TAAAGGGTAT AGACGTGTAC AATTAATGAT GGCATTATTA ACGATGTATT 120
 TATTCCTCTT AAGCCACTTA GACAATTGGn AATTATCTCA GCGGAATATA ATGATGTTAT 180
 25 TAATGAAAAA GTTCATGTGA AAAATAAAGA TAATTATnTA CATT 224

(2) INFORMATION FOR SEQ ID NO: 1763:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1763:

AGCAACCAAC GCCAGATAAA GCAGAAGATA ACGCATTTC CCCCATCACC ATAT 54

(2) INFORMATION FOR SEQ ID NO: 1764:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1764:

50 ATTCCCTTAT CGCATTCTGT AAAATGATCT TCATCAGAAA TTGCTTCGAT ACGTTTATG 59

(2) INFORMATION FOR SEQ ID NO: 1765:

(A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1765:

10 GATTCAATTC ATCTGTATAG ACGATATATC CTGATATGAA TTGGAAATGG AATA 54

(2) INFORMATION FOR SEQ ID NO: 1766:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1766:

ATCGCATAGA AGCATTAGAC TCAAAC TATT TTCGGTTATG AGAATAACTC TGACATCCAT 60

ATGGATACTT AGTTTCCAAG TTAGA 85

25

(2) INFORMATION FOR SEQ ID NO: 1767:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1767:

CAGTACTGCT GAATGATGCT ATTGATTTTC TCATGAGACA TGGCGATAAC ATCG 54

(2) INFORMATION FOR SEQ ID NO: 1768:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1768:

50 GACACTACTA ATCGTATCAG GATCACTAAT TAAGGCATCC AGCATCAGAT ACGAGCGCAC 60

GTCAGACTAA TCTACTGTCA TGATAAAGCA GCTGCTAACC TTGTAAGTTC GTGAAA 116

(2) INFORMATION FOR SEQ ID NO: 1769:

55

- (A) LENGTH: 82 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1769:

10 GTTCTATCCA ATATGGAAAT GAGGACATTA TGC GTGAAAG CTATGGACGA TGGACGATGG 60
 TACACGCATG TTGTGTAAGC AG 82

(2) INFORMATION FOR SEQ ID NO: 1770:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1770:

25 TATCTGTATT GTAGTAATCC GCTTCTCCCA TCTATATAGG GATCTTTCGT AGATATTCAC 60
 TTTATGCCTA GGATCCAAGA TGTGTAAGCA GCAC TTTGCA TTATCTAATG CAAAGGGnAC 120
 ATGCGGCTGT AAGCCCTGTT CTGATAATCA TA 152

30 (2) INFORMATION FOR SEQ ID NO: 1771:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1771:

40 TGGAGGCGAA GTAAATGAAA AGTATTACGT TTGAAGAACA TTATGTCATT G 51

(2) INFORMATION FOR SEQ ID NO: 1772:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1772:

nGAAACAAAT ATCTGATGAG ATATGCAATG ATGACTATAA GTAACATTAA AATGAAGCCC 60

55

CGTACACCAA TTATATCTTT GTGGnTGTTA TATTAAATCT ATATTATGTT CATTTAACAG 180

CATATGTTAA AAATTGACAG TTAACACATG TAGCTATTTG ATGTGAATGT GC 232

(2) INFORMATION FOR SEQ ID NO: 1773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1773:

TAATGTCCCC CAGAATGTAG GCAAATGCAG AACCTGGTTT TAGGGTCAAC TGTTTnTTCT 60

CCAAGCAGAA ACAAAGTTCT TGTGTCAGTG CACTTTTGGT CCACCATT 108

(2) INFORMATION FOR SEQ ID NO: 1774:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1774:

CGCAATTGAA GGATACACTA TTTTAAGAGC TGCAAACATG CGGGTGTAAC GTGTGGTATA 60

CTGCAACTTT GGTnATTGGT TTAGTATAAG ATAAAATCAT CACAATGAAT C 111

(2) INFORMATION FOR SEQ ID NO: 1775:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1775:

CAGGTTATCA GCTAATAGAT ATGTTGAAGA GGCAGTTGCA GGCCAAATGA AACTGCAGAT 60

GTAGTTCAGT ACC 73

(2) INFORMATION FOR SEQ ID NO: 1776:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1776:

5 TAGACACAGT GCAAAATCTG GTACAGCTTA TGAATTAGA CGGGTAAAGC AAATTACTGA 60
GTACCCA 67

(2) INFORMATION FOR SEQ ID NO: 1777:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1777:

GTATGCCAGT GTCATTGCTG AAAACATCAA CCATTCCCTG CACCAAAATT TTTTGGTAGA 60
20 GTTTGATGCT GGCCATCCTC CAAGGGACTA AGGGTAATTT TGnTTAAAAA GAGCCAAAGG 120
CCCAATG 127

(2) INFORMATION FOR SEQ ID NO: 1778:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1778:

GAACCCAAAA ATTAGCAACA GTGGCTACAA TAGTTGGGCA CTGAAAGCCA GCCAAGTGGG 60
35 ATTTTTAGCC CTTGATTTGA AAGCGGGGTC CCCAGGATTA AAAAATTAA ATTAGCCTAA 120
TAAGCCCAAA ATTCCCATTT GGAAAAGGAA ACCTCCTTAA ATTGGGTTGG AAAAAAGnTT 180
40 AAAAAAAGAA AGGCCAGnC CTTGGAATTT TTTGGAATTG GAAAAAGGAA TTAAAA 236

(2) INFORMATION FOR SEQ ID NO: 1779:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1779:

55

(2) INFORMATION FOR SEQ ID NO: 1780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1780:

GACGACTCGC TTCTATTTTA AAATCCGGCG TACTTgGTTA TATAAATATC ATAATGGTTA 60
 AAATTAAAAA GCAATGTCAG TTCACACTAT TACTGACATT CTTTtagTTA TGTGTATATT 120
 ATTCATTAC AAGCTTTTGG TCTATAAATC GAGTGATTG CTTTGTTTGT ATATAACCAT 180
 CTGCTACATA TTCATCGTTC ATTGTAATTA ATGGATAAAA TAGTTCATCn n 231

(2) INFORMATION FOR SEQ ID NO: 1781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1781:

GTCTCCCTGC CCCACATTTA ACATTGTAAT TTTGTGATGT GAATTTGTTG GAAACGTTAT 60
 TAATAATGTC AGAATAATTA TAGTCCAAAA CGTAACCAAT ATATATTTAC GTTTAGCCAA 120
 TAACCAAAAT ATGTAATAAA CAGAAATTAT AAATACTATA AATATCCAAT CATTAAACTT 180
 GGGAACAGAA AAATGTGATT GCTTGATTG 209

(2) INFORMATION FOR SEQ ID NO: 1782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1782:

GTTAACCTTA GTTAGATAAA ATGCAAATCA CATTATTGTA GATAGTCTCT TTTC 54

(2) INFORMATION FOR SEQ ID NO: 1783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1783:

TCTGGAATGT CTCCTTGTCT CTCTATATAG CTATAGTCCG TCGCAAGCGG ACGTAATGTT 60

10 CATTTTCATA ATGATTATAG TATGAAAGCG CTTTCTTGTA TATGTGACAT GTGCGTGtng 120

(2) INFORMATION FOR SEQ ID NO: 1784:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1784:

CTACCATTTA CATAAAGACC GTCTAATTCT TCAGTTTCAA TGGCATTTTG GAGCAAT 57

(2) INFORMATION FOR SEQ ID NO: 1785:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1785:

35 TCATAACCAT TACCAAGTAT CCAAGCAGCT TTAAACAAT ATGGCATAAA CATT 54

(2) INFORMATION FOR SEQ ID NO: 1786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1786:

GGATGGGTGA TTTTAGCAGG TTTGGCTATG AGTACCGTAT TTGCATTAGG ACCGATTICA 60

TTTAACAAAA TCATAATTTT GGGC 84

50

(2) INFORMATION FOR SEQ ID NO: 1787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1787:

CCGGTTTACC CTAAAAATTA TTTTTTGGGG GGTTCATTA AACCTTCCAA TTCCCAATTA 60
10 ACCCCnACCC CCCTGGGTTT TCCTTAAAAA CCAAAGGCC CTTTTTTTTC CCAACCCAAC 120
CTTGGGGGAA TTGG 134

(2) INFORMATION FOR SEQ ID NO: 1788:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1788:

TATATCAACT AAAAAGCGCA TCTGCAACCG ACGTTGAAA ATTTGGACAG GAGACAGATA 60
25 ATGTAATATA 70

(2) INFORMATION FOR SEQ ID NO: 1789:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1789:

AATATCCAAT TATACAAGCA GGTATGGCAG GAAGTACGAC ACCGAAATTA 50
40 (2) INFORMATION FOR SEQ ID NO: 1790:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1790:

50 TGATTACTA GCTGAATCCG ACATGCTTGA TGATACACTA TGTGAATTCA 50

(2) INFORMATION FOR SEQ ID NO: 1791:

55

- (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1791:

10 CCGGACGCTT TACTTCCAAC TTTAGGTGGT CAACACAGGT TTAAACATGG CGATGTCA 58

(2) INFORMATION FOR SEQ ID NO: 1792:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1792:

CATCATCCTC TAATTTAGTC CAAACTCCTG GATGATATCC AAATGAAGTT CCAATTGA 58

(2) INFORMATION FOR SEQ ID NO: 1793:

25

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1793:

35 CACAAGTTTT AGAAGGAAAC CAATAACAAA TGACGAGATT AATTGCCACA AACATTAACG 60

AC 62

(2) INFORMATION FOR SEQ ID NO: 1794:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1794:

50 AAGGCCCGGG GGGTTTAAAA AAAAAGGTTT AAAAAAGGTT TTGGCCCTTT AAACCCAAAG 60

GGAAATTTTA ACCCCAAAAA AAAAAACCC CTTTGGGAAA GGG 103

(2) INFORMATION FOR SEQ ID NO: 1795:

55

(A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1795:

10 TATCGATCGA TCATGTCGAA TCGATCTGTC GATCGATCGT ATCGATCGAA TCGCGTCGAA 60
 TCGAATnCGT CGAATCGATG CTATCGATCG AATGCTATCT GAGTCGAATC ACGTCGATCT 120
 G 121

15 (2) INFORMATION FOR SEQ ID NO: 1796:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1796:

25 AATTCATGTT AAAATCCTCC TGATATTAGA TGGCCCATTT TTATTTTTTTT CGTTTCCATA 60
 TA 62

30 (2) INFORMATION FOR SEQ ID NO: 1797:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 397 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1797:

40 CATACTCGAC AATTTAGATG GTGAaTACTT ATCATTTAAG TCCTTTGAcA CCTCATCTAA 60
 AATTCTAGGA CTTTAAACAA TTTCTTTATA CGTATTTACA AGTTGAATAT TACTTTGAAC 120
 CTCTTGC GCC ATAACTGAG GATTGTCACC CTTAGTTTGA TTTACTAAAA TTTGAGTATT 180
 45 AGCTTGATAT TTAGGTGATA AGACGAAAAA TGTAACAATA GCGCTAATAA TTAAAAATAA 240
 TAGCGGTAAA ATAATTAAAA TCTTCAAGTT TTTTGTGAAT ACTTCTTTAA TTTTGTGTTAA 300
 TTCTAATGTA CTTTCCATTA TTTACCTCCC TTAAAAATTT TCATTAAAAAT TGGTATTATA 360
 50 TATATAGTAT TTACATATTA CATATCGTTT AAACAAT 397

(2) INFORMATION FOR SEQ ID NO: 1798:

55

(A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1798:

10 CGGGTAACAG CGAATGGTGT GTCACCGTAT ATAACCTTAC TATTTAATAT TTGGCCTGTT 60
 GCTTTC 66

(2) INFORMATION FOR SEQ ID NO: 1799:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1799:

25 GTTGCTAAGT TTGTATTACA ATTTAAATGA TTTTtagCTT GAGTAAGTTT ATTTAAAGAT 60
 GCAGTAATTT CGCTAGG 77

(2) INFORMATION FOR SEQ ID NO: 1800:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 172 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1800:

40 TAATGCTATT TAATTTTCTA CTTCCTAAGC TTCCACCCAT AACGAGTAAn ACTTTTTTTAT 60
 TTTCATTAAA GCCTGTTAAT TGATAACCAT TATGTGCATT ACCATTTTTT AAATCTTCTC 120
 GAATTGTTGC TCCAATAAAA TCAGCTTTCT CTTTAGGTAA GTAGTTTAGC GT 172

45

(2) INFORMATION FOR SEQ ID NO: 1801:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1801:

55

AGTAAAAATTT GTCATCACGA TCAGCAAAAG CTTTGTGATC TGACGTATCT TCCATAAATG 120
ATCTAAAAAT TGGTAGITCG 140

(2) INFORMATION FOR SEQ ID NO: 1802:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1802:

ATCCCCCGTA CAGACTTCAG CTTACGTAAA CATGCTGAAC ACTCTAGTGA AGATTTCAAA 60

(2) INFORMATION FOR SEQ ID NO: 1803:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1803:

CAATTTAAAT GCATCTTTCC CATTAATTTT ATTGTGTGTC GCTTTAGCTG TGTTAATTAA 60

(2) INFORMATION FOR SEQ ID NO: 1804:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1804:

ACTTGATCGA AAAGGTTTCA TACCGGTAAA CGATAAAGTT GAAACAAATG 50

(2) INFORMATION FOR SEQ ID NO: 1805:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1805:

(2) INFORMATION FOR SEQ ID NO: 1806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1806:

AAGAACTGTC TATGAATATT GGATGACGCT TTGATGAGAA CATTAGTAAG CCATTTGTTT 60
 AAGGAGTACA 70

(2) INFORMATION FOR SEQ ID NO: 1807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1807:

TAGCATTCTTCT AATGGAATCC AATCTTACCG AATGACAATT GGAATATAAC TGGTGATAAT 60
 GTTGAATGGT CCTGTGA 77

(2) INFORMATION FOR SEQ ID NO: 1808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1808:

CCCGGCCCAA AACCCCTTTT TTGGGTAAAA AATTTTTTTT AAAAAGGGAA AAATTTCCCC 60
 TTTTTTGGTT CCAAATTTT AAATTAGAAA GGGCCCCCCC TTCCCCCCA AATTTTTCCC 120
 A 121

(2) INFORMATION FOR SEQ ID NO: 1809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1809:

AAGTTTGGTG AAGGAACCAC GTGCATGATG GTGTTCAAAC AATGCGTTAC GATGTTGACG 60

(2) INFORMATION FOR SEQ ID NO: 1810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1810:

TGGTTGAGAA AACACAGCGT TAAAGTTGAG GTATTTCAAA AGACAAGTTG GAACATTA 58

(2) INFORMATION FOR SEQ ID NO: 1811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1811:

CTTAAATAGC AAGTGGTTTT ATAACAAC TT TGAGTTATCT CAATATAGTT ATCGC 55

(2) INFORMATION FOR SEQ ID NO: 1812:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1812:

TAAGTCTTCA ATTTTTTCAG TTGATACACC TAAGTGATAC AGCCATTCTT 50

(2) INFORMATION FOR SEQ ID NO: 1813:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1813:

(2) INFORMATION FOR SEQ ID NO: 1814:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1002 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1814:

TGGTCATGCG	GGAAATACTA	GGACATGAAA	ATTATGCTAA	AGGCATCAAA	GTAAGTGAAG	60
ATAATGGCGT	AGTGGATATA	GATATGTACA	TTATTGTAAG	TTACGGTGTG	AAAATATCTG	120
AAGTTGCCAA	TAATGTACAA	TCAACAGTGA	AATATACTTT	GGAAAAATCA	CTTAATGTAT	180
CAGTAAATTC	AATCAATATA	TATGTACAAG	GTGTACGTGT	GAATAATACA	GGCAAGAAAG	240
CTTAGGAGGA	CAACTTGAAA	TGATTAGCAA	AATTAATGGT	AAATTATTTG	CCGATATGAT	300
TATACAAGGG	GCACAAAATT	TATCTAACAA	TGCAGATTTG	GTAATTCTT	TGAATGtGtA	360
TCCAGTGCCA	GATGGtGATA	CAGGAACAAA	TATGAATCTT	ACTATGACTT	CAGGTCGCGA	420
AGAAGTAGAG	AATAATTTGT	CGAAAAATAT	CGGCGAATTA	GGTAAAACAT	TCTCGAAAGG	480
TTTACTAATG	GGTGCAAGAG	GTAACnCTGG	TGTCATCTTG	nCACAAATTAT	TCAGAGGATT	540
TTGTAAAAAT	ATTGAAAGTG	AATCTGAAAT	TAATTCAAAA	TTGTTAGCTG	AAAGTTTnCA	600
AGCTGGTGTT	GAAACGGCAT	ATAAAGCTGT	TATGAAACCA	GTTGAAGGTA	CAATACTTAC	660
AGTTGCAAAA	GATGCTGCGC	AAGCTGCAAT	AGAAAAAGCA	AATAATACTG	AAGATTGTAT	720
AGAATTAATG	GAGTACATTA	TTGTAAAAGC	CAATGAATCA	CTTGAAAACA	CACCAAACTT	780
ATTAGCTGTA	CTTAAAGAAG	TTGGTGTtGT	TGATAGTGGC	GGTAAAGGTT	TGTTATGCGT	840
TTACGAAGGA	TTCTTAnAAG	CGCTTAAAGG	TGAnAAAAGTT	GAAGCCAAAG	TTGCAAAGAT	900
AGATAAAGAT	GAATTTGTAC	ATGATGAACA	TGATTTCCAT	GGTGTAATTA	ATACTGAAGA	960
TATTAAATTA	TGGCTATnGT	ACTGAGATGA	TGGTTCGTTT	TG		1002

(2) INFORMATION FOR SEQ ID NO: 1815:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1815:

5 GACAACGCTA TTATTTTTAG TTTTCAATT CTATTATGTC ATAATTATGT CACTCAAAAA 120
 CTGTTTTCCA ACATTGATTT ATTGTTGGAA AATCTCGAAA ATCTAGTCTA TTTCTCCAAC 180
 AATCGAAGAr TTATGCCCTT TTTTCTCCCT TTAATAAGT CATAATACGA GGCATACATG 240
 CAACATTTAC AATAAAATAT GTTCCTACAT CGTATTATAC GAATGCTCAC ACTTATAGTT 300
 10 GTTTAGTAAA CCCAGATGTA TTGCTAACAT ACCCATnAnC nCTATATAGT T 351

(2) INFORMATION FOR SEQ ID NO: 1816:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1816:

ATATCGTATC CCATGCGGA AGGGCTTTAT TTATACTGTG CACGATGAAT GCGCACAACG 60
 25 GG 62

(2) INFORMATION FOR SEQ ID NO: 1817:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1817:

AAAGGGGGGA AATTTTTTTT TTTTGGGTTT GGGGGGAAAA TTTTTTTTGG GTTTGGGAAA 60
 40 TTAAATTAA 70

(2) INFORMATION FOR SEQ ID NO: 1818:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1818:

CAAGTTCGGA ATGCGAACGC GTCTTAATCT ATATACAAGT GATGCACTCC A 51

55 (2) INFORMATION FOR SEQ ID NO: 1819:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1819:

10 TCGCCATACT ATCGACAGCT GCTAAAATTG CGCTCTTCTT GTGTCGCAAT CG 52

(2) INFORMATION FOR SEQ ID NO: 1820:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1820:

CAAATTGGGG AAATTACTAG AAATGAAGAT ATTTATAAAG ATGACTGGAC GTCAACTT 58

25 (2) INFORMATION FOR SEQ ID NO: 1821:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1821:

ACTGCTTCAG CACCTGTATT CATTGGGGAA AGCTTTATCG TTGACCGGCC AGTTTACA 58

(2) INFORMATION FOR SEQ ID NO: 1822:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 190 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1822:

ACCTGTTGCT CGTGTCTATAA ATAGGTGACT ATAAATCTCT GTTCAATATA CTTTTCGTTT 60

50 TTCCAATCTT AAAGGTCGAT GTTCGTGAGT AATCTTATCT CTGGnCCAAT TTAAATGTCA 120

TGATATGTTT ATAGTATCAC CCCTTTGTTG TGTAAATAA ATCAGGTGGG TGGTTAGAAC 180

55 GGTGTGAATA 190

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1823:

AGCnTTAGCn TATGGTTTtag ACACAActGn TAAAGATGCn AAGTTCTTGT 50

(2) INFORMATION FOR SEQ ID NO: 1824:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1824:

AAAAATTGGA AAAAAGGGGC CCAAAGGTTA ACCCAAATTG GAAAnAAACC CAAATTTTTT 60
 GGAAATTAAC CCAAAAATTG GCCCCCAATT GGAACCCAAA AT 102

(2) INFORMATION FOR SEQ ID NO: 1825:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1825:

ACGTACCAAT GTCATAATCA GTCATTTTAC CACTCTTAAT AATCTGCTTC CGGGCAA 57

(2) INFORMATION FOR SEQ ID NO: 1826:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1826:

ACCATCTTGT ACAAAGTGA TGTCATATGC ACCATCTTGT GTTTtGAGCT GCATTTAATT 60
 G 61

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1827:
ACCGTTTCGC CAAGCCGACC TAATTTCTCA GCAATATTTT TTTCTACGCC ACCAAT 56

(2) INFORMATION FOR SEQ ID NO: 1828:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1828:
ACTTATAGGG CGCACTTATT TTTCGCTTCC ATAGCGAAAC TAGTGTCAC TATACGTATG 60
TG 62

(2) INFORMATION FOR SEQ ID NO: 1829:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1829:
GCTACACACG ATTTACCTTT CTTGTCACGT TTGCGACCA TCATTGTGAT GATA 54

(2) INFORMATION FOR SEQ ID NO: 1830:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1830:
GTAATGACCA TCGCTGATTT ATGACATTGT TAGATCTCAT GTGCCATTTA GTCTGCTGAA 60
TCTTGGG 67

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1831:
 ATAACTCTTC G_nCAAACTCC TCAACAAACT TCTTGTGTTC CATCTTCTGG 50

(2) INFORMATION FOR SEQ ID NO: 1832:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1832:
 AAACGTnAGA ATATTTAATG GAGCCAAGAA TGGTTTACAG ACGGAGAAAT GGGATATGTT 60
 GAAGCGAGGC GTACGCGGAA AGCGTACTAG GCTAGAACAC T 101

(2) INFORMATION FOR SEQ ID NO: 1833:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1833:
 TCGTCATCAT GTCTGTGTTA CCAACGTTTG ACGATTTAnT TCATGCnGAA 50

(2) INFORMATION FOR SEQ ID NO: 1834:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1834:
 ATAAGTTAAT TGATTTATTG ATAAAGAGAA GCCAGATTTA AATATTATTA AACGT 55

(2) INFORMATION FOR SEQ ID NO: 1835:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1835:

10 AAACAAGAAC CCCCATATGG TTAAGCTGCG CGTTTCAACA TACGGGGGGT TTTCATAT 58

(2) INFORMATION FOR SEQ ID NO: 1836:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 125 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1836:

TACGTTTTAT AAAACAAGA ACTAAAGTAT GCAGTGTGAA TTGTTCACTT TcTGGCGTT 60

25 GGAATTGATT AAAACGAGAT ATGGTGTGTG GGAAGTTGTT TGTGTTTGCA TATTTTAAAC 120

CGATT 125

(2) INFORMATION FOR SEQ ID NO: 1837:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1837:

40 AATCTACAAT CCTGAATCAC TCGTTAAGAT TAAAAGTATC GACAATGAGT ATCTGAACAT 60

GAGCTCATCT GCCGTTTTTA ATGChAAAAA CCGGCGGCGG GATATTTTIG ACCACGGC 118

(2) INFORMATION FOR SEQ ID NO: 1838:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1838:

55 ATTTGGGGTT TTGGGACCCT TACCCAAAAA TTGGGGTTTG GTTATTAAAA AAAAGCCATT 60

GTCCCAAGTTT TTGGGATTGC C

141

(2) INFORMATION FOR SEQ ID NO: 1839:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1839:

15

TCTGGGGACT AAGTATGTCT CAGGCTTTAT GCTGTTATGT TTGAAATGA AAGG

54

(2) INFORMATION FOR SEQ ID NO: 1840:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1840:

30

ATTAAAAAC CTTTTTAAAC CGGGAACCCA AGGAAAAATT CCGGGTTTTA ATTAAACCT
TTTGTTAATT GGTTCCAAAC CAACCTTTTG GGTTAATTTT AACCAGGAAT TTTGAAAAC
nGTTTTATTT GGA

60

120

133

(2) INFORMATION FOR SEQ ID NO: 1841:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1841:

45

AAAGTATGGA TTGATCGTGG AGAAGTTCTT CCTACTAAGA AACTAGTCG

50

(2) INFORMATION FOR SEQ ID NO: 1842:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

GCGTTTTCTT GGGATATGTT TGATGAATGG ATGTTGTAAC ATGTTAATAA ATCGTTGGTA 60

(2) INFORMATION FOR SEQ ID NO: 1843:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1843:

CTGAGATGAA TATTGTGTTT CGCCATACAT ACTGGGTAAT ATCCCAACCA TTGCTGTAAA 60

(2) INFORMATION FOR SEQ ID NO: 1844:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1844:

CATTACCTGT AAAAGGAAGC TAAAGACGAT GAGTATTTAT AGAAACCAAT TGCCGACCAT 60

TTGCAGCCAT TAGGAGGGTA GGAGGGCAAT CGCGnCCAAA GGTTATTAAC CGTCAATTAC 120

CTTGA 125

(2) INFORMATION FOR SEQ ID NO: 1845:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1845:

ATCCACCTGG GTTGTCTT AATTAACT GtTAATTAAT TGGGTTGGGT CCGGCAAAAG 60

TCCGGACCTG CAAATCGGAT TTTATCGTTA AATCTTGAAT TCTATTGCCC ATATTAAATC 120

GCAAAT 126

(2) INFORMATION FOR SEQ ID NO: 1846:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1846:

5 TTTTGGGAAT AAACCAATTA ATCATGGGCA AAAAATAAGC AATCCAAGTA CTTACTA 57

(2) INFORMATION FOR SEQ ID NO: 1847:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1847:

TGATAAATAT TTCATCTAAA GAGAGGGAGT CATTATGACA CTA CTTACTG 50

(2) INFORMATION FOR SEQ ID NO: 1848:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1848:

30 ATCTAGGCAA TGAATGGACG GACTTAATAT TGATGTGCAA CAAGAAGAGG AGAAGCGAAT 60
CAATA 65

(2) INFORMATION FOR SEQ ID NO: 1849:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 244 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1849:

45 CGTGTGAAGT CATTACTTTT AATCCCATGA TGATGGTGAT GGATGAGACG ATATCTCTCT 60
GTCTTTAACA GTTAAGTCCA ATTCTTCCAA CGAAACTTTT CCATAGGTTG TTTTATAAGT 120
TGGAATACTT GCACAAATCA TaCCTAATTG CTTATCAATT TTCTCAAGAC TGTCATCAGT 180
50 TATAAGATCA ATTTTATTAA TAATAATCAT GTCACCTAGT TTCAACTGAT CTTCCATCAG 240
GCGA 244

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1850:

TTTAAAGGTT CCCGAAAGG TTTGAAACCA AACCTTTGCC CCGGCCCCCC GGGAAAAAAA 60
 AAAnTTGGTT TAACCCCGG GGGGGGGGC CCTTAAAAA ACCCAA 106

(2) INFORMATION FOR SEQ ID NO: 1851:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1851:

TTTTTAAGG CCCTTGGGGG GCCAATTTTC CCCCCCCCC AACCTTCCAA AGGTTGGGG 60
 GCCTTTTTTT TAAATTGGG GGA 84

(2) INFORMATION FOR SEQ ID NO: 1852:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1852:

TCATGATTAA AATTCAACAA TTACAACATC ACTTTGGATC ACATAAGAGT AA 52

(2) INFORMATION FOR SEQ ID NO: 1853:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1853:

ATAAACATT TCAAGATGCG CTTGTAATTG TATGTGATAC TGCCAATGCT CCACGA 56

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1854:

AAAAGATCAT GCGCATAATG ACATGGTGAT GATATGAGTA TGATGGTGGG TACA

54

(2) INFORMATION FOR SEQ ID NO: 1855:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1855:

ACAACAAATG GTAATGCATA AACATACAGC CAATAGCTAC AATTGCACGA CG

52

(2) INFORMATION FOR SEQ ID NO: 1856:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1856:

ACGGCTGCAC TCATCATGGT CTGTGGCGTG ATTGTTAATG TTTTAGTTGC CCGCTTC

57

(2) INFORMATION FOR SEQ ID NO: 1857:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1857:

GCAGATAACT TCCTTGATCC TAACAAAGCA AGTTCTCTAT TATCTTCAGG GTTTTCACCA

60

GACTTCGCTA CAGTTATTAC TATGGATAGA AAAGCATCCA AACAACAAAC AAATATAGAT

120

GTAATAnACG AACGAGTTCG TGATGACTAC CAATTGCACT GGACTTCAAC AAATTGGAAA

180

(2) INFORMATION FOR SEQ ID NO: 1858:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1858:

CGCTGCACTT CCTGAACGCA GTGAGACCAG AACGTGGTGT CACTTTCGGT CTATTCGGT 60
TAAGTGTTGG TCTCGGA 77

(2) INFORMATION FOR SEQ ID NO: 1859:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1859:

TTTGCGCTTC GTGATTTTCT CTAGACGTAG TAACTTTCCC ACTCTTTGCG TCC 53

(2) INFORMATION FOR SEQ ID NO: 1860:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1860:

TTTCTCACTC GCGCAATTCA GTTTGTTTTG ATTTACCCGT CTCTTCTATT TGTCTTAAT 59

(2) INFORMATION FOR SEQ ID NO: 1861:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1861:

AATGAATGTA TGCACATTAA CATCATCAAT TAATCCTTTT AATAAATTGA GTTGTAATTT 60

(2) INFORMATION FOR SEQ ID NO: 1862:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1862:

ATTAATACTG AGCAAATGTG CATAAGACAT CATGAATTAG CACCAATTTA CAGG 54

(2) INFORMATION FOR SEQ ID NO: 1863:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1863:

TTTAACCATC ATTCTATGTC AAAGTTTGA AATGATGGTT ATTTTTTATT GCTTAAATTT 60
 ATTATTGCTA CTACTATACC AATGAAAGT 89

(2) INFORMATION FOR SEQ ID NO: 1864:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1864:

AAAGCTGGTA CGCCTGCAGG TACCGGtCCG GAATTCCCGG GTCGACCCAC GCGTCCGGAA 60
 CCAAAATTGC ATCTGATGGT CTCAAGGGTC GTGTGTTTGA AGTGAGTCIT GCTGATTGTC 120
 AGAATGATGA AGTTGCATTT AGAAAATTCA AGCTGATTAC TGAAGATGTT CAGGGTAAAA 180
 ACTGCCTGTA CTAACITCCA TGGCATGGAT CTTACCCGTG ACAAATGTG TTCCATGGTC 240
 AAAAAATGGC AGACATGAT TGAAGCTCAC GTTGATGTCA AGACTACCGA TGGTTACTTG 300
 CTTCGTCTGT TCTGTGTTGG TTTTACTGAA AAAACGGCAA CAATCCAGAT ACGGGAnGAC 360
 CTCTTnTGCT GCAGCACCAA CAGGTnCCGC CAAATCCGGA 400

(2) INFORMATION FOR SEQ ID NO: 1865:

(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1865:

10 AAATGGCGTA TCTTTATGTA TCAACTAAGT AATCACCAAT TTCTTTGGA T 51

(2) INFORMATION FOR SEQ ID NO: 1866:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1866:

GTGTTGCGGA TAATCCGTCG ACATTAGCGT CTGAAGGTAT CATGAGGCAA CTGCGCAA 58

(2) INFORMATION FOR SEQ ID NO: 1867:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1867:

35 ACAGCAACTG ACCCAGTTTA CTACCGTCAC TCAAATCACA CAGGTGGTAT CAAATCAATC 60

(2) INFORMATION FOR SEQ ID NO: 1868:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1868:

CAATCTCTTA CCATTATCT CAGCTGGTGA AACGGTCCA TTACACTTAG AATAAA 56

(2) INFORMATION FOR SEQ ID NO: 1869:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1869:

5 GCTATAGACT AGAGGTACAG CAAATTCATG TGTACAGTGA TTAGAAGGCG ATGAGCAAAA 60
GTAAT 65

(2) INFORMATION FOR SEQ ID NO: 1870:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1870:

20 GCTACTGGCG GGGGATAGTA ACACCCAATG TTACACGTAT ATACGTACGG CTTCTTGATA 60
AAAAGATGAA GCCnTTACAA GTAGAGAGCG TAAGAACGTG ATCATCTAAA TGGTAAGGGT 120
AGACTATCCC ATGCCATTGT GGGCGGTTGC ATAGGTACCA CGGCACATAG CGG 173

25 (2) INFORMATION FOR SEQ ID NO: 1871:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1871:

35 GCTGTGGGAT TGTCTTTTGG CATGGGGTTA GGGAGAGCGT TTCTAAGGGG CGTTTGAAAG 60
CCATTGATCC GTAAAAGGAC CATGTGTGGA AGCnGCCTTA AGAA 104

40 (2) INFORMATION FOR SEQ ID NO: 1872:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1872:

50 CCATTATCTC AAGAGGTTCT AGTAAGGGGA TGGCATTTC TTCTTATGAA TTTGACCAGA 60
ATAA 64

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1873:

GACAACCTAT TGTTCCTTA CCATACTGTT GTCCGGTTTG ACAAACGGC GTTCCACAAT 60
 CCATACATCG TGCACCTTGG ATAGAGGCAT CTTCTTTAGT AAATCGTTGT TGATATGCTT 120
 TATGATGCTT CAAACGGTCT ACCAGTGATA ATTCACCTAA GTACTGTTTG TCATACTTCA 180
 TAAATCCTTT AAATTCACCC ATCGTATCTC CCCCTTTCCT TAATACACAA CGGCTGGTTT 240
 ATGTTTAGCA TCGATTGTTT TGACTGTnCA TCGTAAATG CAGCTAACAT CGCTTCATCT 300
 TCCATTGTCA TGTGAAGATT TTGTGGCAAA nGGAATTTTT TGCATCAATG AATnGGTGAA 360
 CCTTTGGGGG TGACCTT 377

(2) INFORMATION FOR SEQ ID NO: 1874:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1874:

ATTATCTGAA TACGCAGCAG TTGCAGCACT TGATGGATCA GCAGTATTTA AAAGAGGTTA 60
 ACACATTACC CAATAGTG 78

(2) INFORMATION FOR SEQ ID NO: 1875:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1875:

CTAAAAGAAG TTAAAGAGTG TGATGGTAGA ATTATATTAT TTATTGATGA AATgCCATAT 60
 GCTTGTAGGT GsTGGTAAAA CAGATGGTGC CATGGATGCa GGCAACATGC TAAAACCAAT 120
 GTTAGCACGA GGAGAGTTAC ATTGTATTGG TGCAACAACCT TTAAATGAAT ATCGAGAATA 180

TGTGAAGAT ACAATT

256

(2) INFORMATION FOR SEQ ID NO: 1876:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 286 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1876:

15

AGCGCGAAAT TGAGCAAGCG GAACATGCGA CTGATGAAGA AAAACAAGTT GCTTTAAATC 60

AATTAGCGAA TAATGAAAAA CGTGCATTAC AAAACATCGA TCAAGCAATA GCAnATAATG 120

20

ATGTnAACGT GTTGAACAA ATGGCATTGC TACTACTAAA GGTGTACAAC CTCATATTGT 180

AATTAAGCCT GAAGCACAA AAGCAATaAA AGCAAGTGCA GAAATCAAG TAGAATCAAT 240

AAAAGATACA CCACATGCAA CAGTTGATGA ATTAGATGAA GCGAAT 286

25

(2) INFORMATION FOR SEQ ID NO: 1877:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1877:

35

ACTTCCAAAC ATGATAAAGA CAGACTACTT CACAGGTTTA AGGGAAGCAA CCACATTAGC 60

GGGATTCCACC CTAT 74

40

(2) INFORMATION FOR SEQ ID NO: 1878:

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1878:

50

TTTCATTAAG TTCAAAAAAT CTCAATAACT TTAAGGATTG GTCCGCATAT TA 52

(2) INFORMATION FOR SEQ ID NO: 1879:

55

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1879:

ATACCCCTGA GATTAAATTAC TTGTCCTTTT TTTAGAACAA CATCTCCTGG CTTTGTTTCG 60

10

(2) INFORMATION FOR SEQ ID NO: 1880:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1880:

20

AATATCATTATAATATCAT TGATGCAAGT CCTATTGTGC ACAACTGGGG TGATTGCCTT 60

(2) INFORMATION FOR SEQ ID NO: 1881:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1881:

ACAATGGCAC ATGGACTTAT GCCTGGGGTG TCCTGTTCGT CGCAGCATCA AAATGA 56

35

(2) INFORMATION FOR SEQ ID NO: 1882:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1882:

TGCAAAGCAT TGGCACATGG CCAGTCAGTT TTACAACGTC GTGACTGGGA AAACCCGAGA 60

45

ngcgacgttg TAAAACGACG GCCAGTGCCA AGCTTGCATG CCTGCAGTCG ACTCTAGAGG 120

50

A 121

(2) INFORMATION FOR SEQ ID NO: 1883:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1883:

ACATTTAATG TATAACCAAGT TTCAACATTG CCGATTTAGT GGCAGCAGTT GCAGGA

56

10

(2) INFORMATION FOR SEQ ID NO: 1884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1884:

20

TGCATCCATT TGATTGAATT TTATGTTTTG ACCAAAGCCG GTTGCAATGT AC

52

(2) INFORMATION FOR SEQ ID NO: 1885:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1885:

TGAAAAGTGG TGGAATGGTG TTAAAAGTTG GTGGGTAATT TTAGAGAAGA G

51

35

(2) INFORMATION FOR SEQ ID NO: 1886:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1886:

TACACGAACC ATACTCACCA GGTTTTCGTG TCATGAGGCG ATATTTTTTG TCATTTTATA

60

TACATTTATC CAAATTCATC TTTTAAATGT TGAGT

95

50

(2) INFORMATION FOR SEQ ID NO: 1887:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1887:

GCTACCAAAG GCGTTTACC TATTGCTAGT CACTGCAAGT GGCTTAGCTA TGCAGATCAA 60
5 CTGGT 65

(2) INFORMATION FOR SEQ ID NO: 1888:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1888:

GTGGGACCAA CTGGCCGGTG ACGGTGGTAA AGGTGCTTCA GTCGTATTGA AGTGGGATGA 60

20 (2) INFORMATION FOR SEQ ID NO: 1889:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1889:

TGTTGGAGAA ACAGTTAACG AGGTTTAATG TTAAAAAAGC AACGTATCAT GGGTATA 57

(2) INFORMATION FOR SEQ ID NO: 1890:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1890:

45 TGGGATCTGC TTGCAAATAC ACAAACCTTT CTGGATTTTA TTACAATTGC AATATAATCA 60
AACA 64

(2) INFORMATION FOR SEQ ID NO: 1891:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1891:

GGCATCCACT CAGATAAAAT AAAGATGTCA AAAAGGCCAA GATGGTGCTA AAAAAACAA 59

5

(2) INFORMATION FOR SEQ ID NO: 1892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1892:

GGTATCTCAA CGATCCTTTA GGTTAATTCG GAAATTTCTA CACGTGAGTT AGCA 54

15

(2) INFORMATION FOR SEQ ID NO: 1893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1893:

TTGTCTTGGC AATGGCAGAG CAACAGAAGT TTAAAGTGCT TGCTGATCAT AT 52

30

(2) INFORMATION FOR SEQ ID NO: 1894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1894:

TAAACCTATA CCCTGTAAAA AGAAAAATCG TGGATCGAAA GAACATGTAT GTGGCATTTA 60

40

TGATTGATGC TCAAGCAGA 79

45

(2) INFORMATION FOR SEQ ID NO: 1895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1895:

TTATAAAGGA GAGAAATCCT TAATTATGAA TAAAGCATCA TTTGATAAAA AAGTTAAAAA 60
 5 GCAATTATGG TTTTGAACA AGAAGGAGAA ACAAGCATTG GATCAACGAT TGTCTTCTAT 120
 ATCTGATGAT GACAGCGTTA ACTTAAATAA GCCTGTTACC TTTGCTAATG CTTACTTAAG 180
 ACAAATGTA TTTCGAAATA AAGAAACAAA AAGTTATAGT ATGTTTGTGA CATTAGTAGT 240
 10 GATGATGTTT GCTTATGTTG CTTTATTAGG TTTGTnTTTA TTTGGGCTAA TTACAAGTCT 300
 ATCTGGCGTA CAATTTTTTCG TTAGTCCTAA GGTAGATTTA TCTACnACTG TTGTTATTTT 360
 AACAATnATT GGAGCGA 377
 15

(2) INFORMATION FOR SEQ ID NO: 1896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1896:
 TTAGGATCCG TCTTTGCCGC AGCGTGGGTG TTCCGCGAGC GCTTCTTAGA GGTTTTGC 58

(2) INFORMATION FOR SEQ ID NO: 1897:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 445 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1897:

40 ATCGCTCAAA CCGAAATTGA AAATGCATCT ATTACTTCAT TAAGCCGTTT ACCAGACGTT 60
 ATATTAGCAT TGAAAAGTGG AAAGGTTGAA GGTGCTGTAG TTGAAAACC TGTAGCAGAA 120
 GCATATTTAA AACAAAATCC TAAATTAGGA ATTTCCAATG TGAAATTTAA TGAAGAAGAA 180
 45 AAAGATACAG TGATAGCAGT GCCAAAAGAT TCACCAAAAT TATTGTCACA AATTAATAAA 240
 ACGATTAAGG AGGTTAAAGA TAAAGGATTA ATCGATAAAT ATATGACTAA TGCTGCAAAT 300
 50 GCGATGAATG ATGACAGTGG TTTTATTTCT AAGTATGGTA GTTTTTTCTT GAAAGGAATT 360
 AAGATTACAA TATTAAATTC ACTTATCGGT GTTGCAATTAG GTTCTATTTT AGGTGCATTG 420
 GTTGC GTTAA TGAAATTAAG TAAAA 445

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1898:

ACCTTTTCAA TGTGCTTTG ATATAAATTC ACAAAGTTGA CTTTnAATT CTTCAATAGA 60
 TTCTCTACTG CGATAGCTGA ATTGCCATCT TTTCTACTAC T 101

(2) INFORMATION FOR SEQ ID NO: 1899:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1899:

TGCCCTGGAT GCCTTTAACT TGATTCATGA CCTGTGGTTT TATTTC AATT TAGATGAGCT 60
 ACCTTCAAGA CCTTC 75

(2) INFORMATION FOR SEQ ID NO: 1900:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1900:

AGCAATACGG AACTGATGAA CGGAATTGTA ATACGAGAAT ATGAAGCATC AACG 54

(2) INFORMATION FOR SEQ ID NO: 1901:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1901:

AGTACCTGAG TATCGCAGAC CGGCTTCAGG TCGTAGAATT TCTATACGTG GAGCTAGAAG 60

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1902:
 GTCTAACTAC AGCATGCCGG CTTATTGTTG CACTTTCTCA ATATTTCCAT A

(2) INFORMATION FOR SEQ ID NO: 1903:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1903:
 GGATTnAAAC GTGCATTAAC GCGTGnTTA AATAGTTATG GTTTAAGTAG

(2) INFORMATION FOR SEQ ID NO: 1904:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1904:
 ATCGTATTTA TTTCAGCGAG TAGCGGTAGC CTTCAATACA CAAAGATTTT ACC

(2) INFORMATION FOR SEQ ID NO: 1905:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1905:
 ATAAGACGCT AGATCTGGTC AATTTATTTT CGATTTTTTC AACACTATTC

(2) INFORMATION FOR SEQ ID NO: 1906:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1906:

TTCATCTGAA TCGTCGGCTT TCGCGATTAC TTCTTCGTCA GGGTTGCTAT C

51

10

(2) INFORMATION FOR SEQ ID NO: 1907:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1907:

20

CAATTGCTAA TAATCCTTTT AAGTCATTAA TGATTGATC TTCCGTAATG TTGAA

55

(2) INFORMATION FOR SEQ ID NO: 1908:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1908:

TTGCCAAACA GACATGACTT AAATTTCAAT ATCTTCTTTG ACTGCATCGA TAT

53

35

(2) INFORMATION FOR SEQ ID NO: 1909:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 94 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1909:

45

TGAATTTCTA TACAATTATG GGGAAGGGTA TTGGTGAATT GGAATGGGCT CCTAAGTTTA

60

CAAGCCCCCA TCGATGGCC GTTAAAGTTT TTAA

94

50

(2) INFORMATION FOR SEQ ID NO: 1910:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1910:

5 AACATGATCG TGGGGGGATG TTATGTTTGT TCATATATTT AGGAAGTCGT TTGTAGTTAT 60
TGTTTG 66

(2) INFORMATION FOR SEQ ID NO: 1911:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1911:

20 ATCTTCGCTC CACTTACTGC AATAAGGATT TCGGCAATC CTAAACCGTT TTTCA 55

(2) INFORMATION FOR SEQ ID NO: 1912:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1912:

30 AACCAATCGTA ACGATACAAC GCAATCTTCG AAAAATAATG CAAGTGCAGA TTTCCGAAA 59

(2) INFORMATION FOR SEQ ID NO: 1913:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1913:

45 ACACCACACA CACACACACA ACACCCACA CAACACACAC AAACACACAA A 51

(2) INFORMATION FOR SEQ ID NO: 1914:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1914:

5 TGTTCAGACT TGGTCGACCT GGCAAGCGCT TCGCGCACGT TCTGCAGCnT CTCACCTATT 60
GGTATCGCGA TCGGACGTTA AGAAATTTCTG GAGTTCTGGT CACCTTATGT T 111

(2) INFORMATION FOR SEQ ID NO: 1915:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1915:

TGGTCCGCTC TCAATCGCAT CTTCAGGTTT TACTTGGCAA AAGAGCGCGG TGCTCA 56

20

(2) INFORMATION FOR SEQ ID NO: 1916:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1916:

GCCGACAGTA AAATAAAGGT ACTTGATATA ACATATAACG GAAAGCAACA GTTACTGTCA 60
CA 62

35

(2) INFORMATION FOR SEQ ID NO: 1917:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1917:

ATGATATTTA TTTGATTGAA GAGATGTTGC TTAAACAAGA AGACGTACAA TTGATAnAAC 60
GTAAAGATTA TATTCAGCAC CCTAAAGAAA ATGGTTACCG CAG 103

50

(2) INFORMATION FOR SEQ ID NO: 1918:

- 55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1918:

CAGTGTAGCG TGTGTCATGC CGTTTTACCA CAATTGAAGA CTGAGCTCTA TCCCTGTGCC 60

(2) INFORMATION FOR SEQ ID NO: 1919:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1919:

TCAAATTAAC TTCCAACAAA AACAAATGCA AGGTGAAGAA ATTGCTGAAG AAGATTTACA 60

AAAAGCGCAA GAACAAGCGC AAGCAATTGA AAAAGATGAA AACATCTCTn CATTAAT 117

(2) INFORMATION FOR SEQ ID NO: 1920:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1920:

TGCCTAATGA AACATTTAAA AATATTTTTA AATATATCTA TCAACACATC GTTCTATTAA 60

TTGGGATTGT TAGTTTTCTC AAAGGATTTT TAGGATTTTT CATGGAAAAA AATGGAAGTA 120

ATTTATATTT TGTTTCATTC CCGTTTTTCAG TAGTCGTTGG ATTCCTTATT GTCTTTTTAT 180

TTATATGGTT TAGTTTTAAA ACAATACAAC TGCAGTGTTT TAACAATTCA AATTGGATAT 240

GGATATTCAC CTATTTAGCA ATCATTCTAC TAATTGTAGG ATTTTCTAT GTATTCTTTA 300

TTCCACAATC ATTACTTGCC TTTGGACCAT ATATTCAGGT AAGCAATTGG GTATTTATTA 360

TATTTTCATT TATAGTTATG CCTATnGGAT TACGCATTGA 400

(2) INFORMATION FOR SEQ ID NO: 1921:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TCACAGTCAT CATTThATTT TCGATTTTCA ATAATTGTAT TTTTAATTTA TCTTGATATT 60
 CATTAAAGATT TATACAAGCT ATCTTTAACA TTGCCTTATC TTTGATATAT TTCTTGCAATT 120
 5 CG 122

(2) INFORMATION FOR SEQ ID NO: 1922:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 410 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1922:

AGAAGATACC ATACACATTT aATTAGTTAC AGCATAAATC AATTTATACC CTTAATTATT 60
 20 ACATTGTTTA TATTTTAAAT TCGGGGGAGT AATTTTAAGT AATATCTTGT TGCTGCTAAT 120
 TCTATTGTTA ATAAATTGAT ATTAGATGTA GAAATTGAGT GTGAAAGTTA ATAATAGATG 180
 ATTTAGCTAG TAACATAATT AATTCATATA TAGTCAAAAA GTTCTGTTAG ATACTGTTCT 240
 25 TGATGAATAT TCTTTGATGT TAGGTGTTAG CTATTCTAGA TGAGTTTCTT AGATGTGGAT 300
 GCCTGTCTTG ATGAAGTTAT CTATGATGTT AATATAATAC TTGATGTTGA TTCTTAGATG 360
 TTAGTGCGAT TTCAAGATGC TGATTCTTTG TTGTTGCACT ATCTTGGTGA 410

(2) INFORMATION FOR SEQ ID NO: 1923:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1923:

TTTCTATGGT TTATCAGGTG ATTTTACGGA AAACAGTGAA GATTATGGCG TATACCGCTT 60
 TAAACGTGGA TTTAATGTAC AAATCGAAGA ATTAATAGGG GATTCTATA AACCAATTCA 120
 45 TAAAGTGAAA TATTGGTTGT TCACAACATT GGATAAATTA CGTAAAAAAT TAAAGAAATA 180
 GATGTAAATG ATGTTAGGGC TTATAGThAT TGATACTATA GGCTCTTTTT TATATGTTTT 240
 TTAATAAAGC CTCGAATAAT GATATATTAA ATGACAAGTT TAACAAGTGA TTGCAATAAA 300
 50 TATAAATnTG AATTGCACAA CCGATTTGnA AATGATTGAG TTGAGGAA 348

(2) INFORMATION FOR SEQ ID NO: 1924:

(A) LENGTH: 253 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1924:

10 AGGGCAGATT TAAGCTAACT TGGAAATGTTT TCGAGTTTTT GAGTTAGTTC TCTATCCATT 60
TTTTCAGTTA CATGAGTATA TATGCGAATG GTTGnTTGTT CATCTACATG TCCTACCCCTT 120
TTCATAATTG CTTTTAAAGA AACATTCATT TCTACTAATA AAGTTATGTG TGTATGTCTA 180
15 AATGTGTGCG TGGTAACTTT CTTATTCATA TTTAAAGCTT TTGTACGTTT TCTTAACGCA 240
CACCGGCCAT TTC 253

(2) INFORMATION FOR SEQ ID NO: 1925:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1925:

30 GGTATAGGTG CAAGTCCTAT CTTCCGCTCC ATGGTTTAAT GATAATGCGG GA 52

(2) INFORMATION FOR SEQ ID NO: 1926:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1926:

TGGTCACTGT TCCTGATGCT TACGTTAGAA TGTAAGATTC CCGATTTATC AGTTATATAC 60
TGTTTGCTTC ACTTTGGAGA TCTG 84

45

(2) INFORMATION FOR SEQ ID NO: 1927:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

CTTCTCTAAAT AATTCTAGTA TAGTTTTTAT TCAAATACGC TAGGCTCAGA GCTATT

56

(2) INFORMATION FOR SEQ ID NO: 1928:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1928:

15

GCAAATTGTC ATTAGACGGA GTATTATTTA GAATTTTCGG TGATATCCAC CGGCACAAGA

60

TCGATGTTGG ACAATATCTA ATATACTGAT ACGCATTTAA ATAGAAGAAG GGAATTAGAG

120

TTTGGTThTG AATGCAAA

138

20

(2) INFORMATION FOR SEQ ID NO: 1929:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1929:

30

ACATCTTTAT ATGCTTCAAC ATCAAATACA CCACATATTG GTAAACAACA AA

52

(2) INFORMATION FOR SEQ ID NO: 1930:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1930:

TTTAATGTTT ACAACACCGG AATAATAATA ACTAAAGCGC CGCTAATAAA T

51

45

(2) INFORMATION FOR SEQ ID NO: 1931:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

ACGAAAAATA AATAATCATT TCACCTTTAT AGCCAGTATT TTAAATTAAT ATATTTTCAT 60
 CTATTAGCGC TTCTAAAAAT CTATTTGACT TTTGAACATA CTCCTTAGCT ATATTATTAA 120
 5 CAACAGTATA GGATTCTCTA TAATTTAGTT GATTAAATTC TGAGTCGTTT ATTAATTCAA 180
 CTAATCCTTT TATTACTTTT TGTACAACAT TAATATTTTT ATCAAAATCA AATTTATCTT 240
 CCTTAGATAA ATTAATAnnn AAAGTCTTAA GAACATTTGT AAATAGCTCT GCAACACTTA 300
 10 TAGTTTGGnC AAATTCCTTA AATTTATTTA CACAGTACTC ACACATTAGT TTTAAAAATA 360
 ATGGATTGTT GAATTCTGGA TTAAATATAG GTAACCTAGG 400

(2) INFORMATION FOR SEQ ID NO: 1932:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1932:

25 ACTTGCGGAA nGACGCAACG TTTATGTACG TTGGAAGAAA AATTCAGGAC TTACGTTCAA 60
 AACTACCATA GCAATATGCA TTGAAAGATG ACAGTATGCG 100

(2) INFORMATION FOR SEQ ID NO: 1933:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1933:

40 CGCTCTGCTT TAAGCGTTGG GACTTTGTCA ACGGTAGTGG ATGGGAAGTG GTTCTGCTTT 60
 G 61

(2) INFORMATION FOR SEQ ID NO: 1934:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1934:

55

(2) INFORMATION FOR SEQ ID NO: 1935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1935:

ATGTATTACG GTTTAATTAA GCCACATACC AACAAGATTG CATTTATGGT ATCTCA 56

(2) INFORMATION FOR SEQ ID NO: 1936:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1936:

TCGCACCAGA AACAAGGGAT TGTTAAATT GCGTAAATCC TTAAATTTAT TTGTAAATAT 60

A 61

(2) INFORMATION FOR SEQ ID NO: 1937:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1937:

ATGAATAATC ATATTTCTAA TCAAAGTAAT AGCATTIATA TTGTGTTTAA A 51

(2) INFORMATION FOR SEQ ID NO: 1938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1938:

TTGCTGAAGA TAGAGGCTTC ATGAAGGTGG AGAAGTTAGC TGATTTCTGG AACAGG 56

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1939:

10

ATCTCAATGT ATTCCTCTAG TGTAAGTTCT TCATAAATAA CCGGTGATT C

51

- (2) INFORMATION FOR SEQ ID NO: 1940:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1940:

CTCAGGTCGA CTCTAGAGGA TCCCCTGTTA AATAAACTT CTTAAGCACA TACTTATTC 60
 ACTATGCCTT TTACGTTCCC CTTATACTTT TCTCACATCT TTCTCTTAGA CTACTCCCTT 120
 ATACGCCCCG CTCAATATCT TTAATCATTT CATCTACAGT TATTTTCGCA CTCGTTAAGA 180
 CAATAGGAAC GCCTGGCACC TGGATGCGTA CTGACCTG CAAAATATAW ATCTTTATAA 240
 TCTCGCGATA CATTYTGTTG ACGATAATAA TTAAGTTGCG CTAAAGTTGG GCATTAAACC 300
 GAATGCCGAA CCAAATTC 318

35

- (2) INFORMATION FOR SEQ ID NO: 1941:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1941:

45

CCGGGAAAAT TTTTGAATT AAGTGAAAA AAAATCCCCT TAAAATTCCC CTGGCCA

57

- (2) INFORMATION FOR SEQ ID NO: 1942:

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1942:

5 TGTTCTTCTT TTGAATCTGT TTTATTCGTT TGTTCTCTCT TTTTCTGTTT ATCTTTCATA 60
 TTCCACATC CCCCAATAAA AATGATTAAA AGTAATACAC TCATGTACAA AGCAATTTTT 120
 TTTATATACT CCATCATTTT ACATCTCTCT GTTTTAATTT TATAAACATT TGAATATTTT 180
 10 ATACAACTTA TTAATAAGT GATTATTCAA CTTTATGTT ATCAAACAAA ACTAACTTAT 240
 TCAATTTAAT ACATGTAATT CATTTTAACT TTATTATTAA ATGTTCTAAC GThATTTTTT 300
 ATATTAGTAA TTATATTTAT TTATCCTCGC TTGGATTAAA GTAGATACTA TCTGTGAAGT 360
 15 AnATATTTTC TGCCTTGn 378

(2) INFORMATION FOR SEQ ID NO: 1943:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 394 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1943:

AAGAAGAAGT CAAAATTCAG CTAAGTAAAA GCTCGAGTTA TAAAAAAGTC TAAATTGATT 60
 30 CAACAGGAGT AGAAAAGGAA ATTAGTCTTG CATATTTTAG AAAATGAATA AAAACAGTTA 120
 CTATATGCAA CTCAAGAATT AAATATTATT TAAGCCACAT ACCTATTAGA GTACAAAATA 180
 TACAAGTTGT ACTTATATCT AGGTATGTGA CTTTGTGATT TAAGCGTAAA GTAAAAGTTT 240
 35 TTATGTTTGT ATTAGTTCTA AATTATTTTG CACTTGGATG ACACGTATTT TTGAGTTTAA 300
 GTGGTGACTC AAGTTCAATA AATAAATAT CAGATAGGAT AATTTGAnAA TnATATGAAA 360
 40 GGGTTATCTC CAAAATnATC TCCATATTAT AAGG 394

(2) INFORMATION FOR SEQ ID NO: 1944:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1944:

50 TATTCGTGAT GACGATTGTC GGTGACATGA AGTTCTATTT GCTGGCACTG AT 52

(2) INFORMATION FOR SEQ ID NO: 1945:

55

- (A) LENGTH: 82 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1945:

10 CGTTTAAAAA ATGATATCAA TCTTTATTGT GGATTGCAAC ATCCGTGTGC TCCATAAAAC 60
 GTGTGGCGAG ACTTGGGAAA GG 82

(2) INFORMATION FOR SEQ ID NO: 1946:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1946:

25 GTATTATTGA TGAAGAAACA GCTCTCCAGT TGTAGATGCA TGCTACGTTC ACGTTACCAC 60
 TGTATCAATT 70

(2) INFORMATION FOR SEQ ID NO: 1947:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1947:

40 TATCACCAGC ACCAAGGnTA ATGACATGCT GATCTTTTGC AGTTATGGTn 50

(2) INFORMATION FOR SEQ ID NO: 1948:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1948:

ATTGTATGAA TCTTTGGGGA ATGAACTTTn AACGAACGGA CATCTTGCAA TGACGCATCA 60
 55 AAATGGTTTT AACACATGTA ATCGGCTCTC GGTACTATTC GTGTGATGTA CACATGG 117

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1949:

10

TTTGATGATT TCGGGATGGA TTGGTATTGT GGTGAATGAA TTTTITAGCT CATCATCAAA 60
TTAG 64

15

(2) INFORMATION FOR SEQ ID NO: 1950:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1950:

25

CTCTAGTGGC CATTCAATATT TGTCGCTGAA TGATGTTGGT ACATCCATTG CTGCTGT 57

(2) INFORMATION FOR SEQ ID NO: 1951:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1951:

40

CTGTCCTTCT GAAACTTGGG TATTTAATTA GGAATAGTTA AAAAAATCAT TCACAGAAAC 60
ATTTAATA 68

(2) INFORMATION FOR SEQ ID NO: 1952:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1952:

55

TTAAATTAAC CTTAAGGTTG GnATTTTTTAA CCCCCAAATT TTTGGGGTGG TTAAATTC 60

(2) INFORMATION FOR SEQ ID NO: 1953:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1953:

GACATTTACA CCTGCTTCAA TCTGGTCCAG TGCAGCATCT AATTCTTCGA 50

(2) INFORMATION FOR SEQ ID NO: 1954:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1954:

ATTTGGCCAA CTGTTTCAGCA CGGTATTGGT TCAATGCAAC ACTTTATCAT TGCTTCAGGG 60

CTATATCGGT GGTATGGGnT GTATCACTTC TTAGAACGTG GTATTAA 107

(2) INFORMATION FOR SEQ ID NO: 1955:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1955:

GAAGTGAATA TGAAGCTGCT AAAGACTCCG GAATGCTACC TCAGACAACT GATG 54

(2) INFORMATION FOR SEQ ID NO: 1956:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1956:

ATGATTATTT TAGTTCATT TGTTGAGTCG ACTGCTAAAG TTCCATTAA ATGTTGTACA 60

ATAAGCAGTA ATTTATGATT GTTTACAGTT TTTAATTTAC CATGAACTTT TGAAGCATT 180
 GCATGTTTAA TAACATTATT TATCGCTTCA CGCGTAATCA TAACTAACAT AGATTGTTTA 240
 5 GTAGGACTTA ATACTTGCGC TAATTCTTTA TTTTCAAATG TAAAATCAAT ATCAGCATCn 300
 nTnAAAACTT TACGTATACT ATCAATCTCT TCAATAAATG ATGGTAATTT TACATCATCA 360
 ATAAT 365

10

(2) INFORMATION FOR SEQ ID NO: 1957:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1957:

AAATAATGTC ACAAAGTTA AAGATACTAA TATTTTCCA TATACTGGTG TAGTTGCTTT 60
 TAAAAGTGCA ACTGGATTG TAGTTGGAAA GAATACTATT TTAACAAATA AACATGTGTC 120
 25 GAAAAATTAC AAAGTGGGCG ATCGTATTAC TGCACATCCA AATAGTGATA AAGGTAATGG 180
 TGGTATTTAT TCGATTAAAA AGATTATTAA TTATCCAGGT AAAGAAGATG TATCAGTCAT 240
 30 TCAAGTTGAA GAGCGTGCAA TAGAACGTGG ACCAAAAGGC TTTAATTTTA ATGATAATGT 300
 AACGCCATTC AAATATGCGG CAGGGGCTAA AGCTGGTGAG CGAATT 346

30

(2) INFORMATION FOR SEQ ID NO: 1958:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1958:

TTTTCCAGTT AATTTTCCA GTTCACTAAA TACTTTATTG ACTGTACCAG ACCCAATAAT 60
 45 AATTTGGTAT TGTCCCCCAG TAGAAAACGT CCCTTTAACT ACATCCATAT TGTTTAGCGC 120
 CTCTTCATTT ACTAACTTT CATCATTTAA AACTAATCGT AGTCTCGTTG CACAATGCGC 180
 50 CATTGCATCT AAATTCTCTT CTCCGCCTAT CGCGTTCAAA ATTTCTTCTG CGGATTGCTT 240
 ATAATTCATA TATTTAGCCT CCTAATTAGA ACCGGTTCCA TTTATTCCAC TTTATTGTAA 300
 CCGGTTCCAA AAATATTTGC AACACTCTAT TATCATTTTA TATAAACACC TACACCATTT 360

55

(2) INFORMATION FOR SEQ ID NO: 1959:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1959:

GATTGCATAT AATAGTAAAA ACATTACATC TTGAACAGTA CTCGTTTTGT

50

(2) INFORMATION FOR SEQ ID NO: 1960:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1960:

AATTTGAACC AGACACTGAT ACAAGTCACA CCCAGAACT TTTAAGGACG TAAATGT

57

(2) INFORMATION FOR SEQ ID NO: 1961:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1961:

AACGCTATAT TAGCGATATA CAATGATGCC ATTATCAATA nTACAnCTGn

50

(2) INFORMATION FOR SEQ ID NO: 1962:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1962:

TACAACGTCA GTTGGCAGAC ACCAGAAGAA GGATTCATAA GTATATTCAG GAACTTGTTA

60

(2) INFORMATION FOR SEQ ID NO: 1963:

- (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1963:

10 AATTTTCCC CCTTTTAAA TTTCCCAAAA AAAAnCCCCC AAnAAAAAAA 50

(2) INFORMATION FOR SEQ ID NO: 1964:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1964:

CAACAAGTAG ATGCATCAGA GAGTAGTGT CAAACGTTAA TAGATGTGGC ATG 53

25 (2) INFORMATION FOR SEQ ID NO: 1965:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1965:

35 AGCAAAGGCA TAACTGCTAA TGACCATGTA AATGAGACGA GTCGATCGTG GCCA 54

(2) INFORMATION FOR SEQ ID NO: 1966:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1966:

CTCAAATAAC TGGCTCAACT CAACCGGTCT ATAACACCAT AACACCGCAT GCCACTCTAG 60
 50 CATACTCAAT CGCTCTGGTA CCAGCnCTCA AATAACTGGC TCACGCCAAC TGTCTATAAC 120
 ACTAACACGC ATGCACTCTA GCCTACTCAG AGCTCTGGTA CAGCACTCAA TAGCTGACTG 180
 55 TCACAGTCCA CACACACTCA ATACTGGCTG ACACAGTTCA CACACnGCTT ACTCGCTCTC 240

(2) INFORMATION FOR SEQ ID NO: 1967:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1967:

CAGTTTAAAC TCGATGTTGT GTACTACTGT GCCAGCTGGA ATGTTTTATA ATGGTGATG 59

(2) INFORMATION FOR SEQ ID NO: 1968:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1968:

GTTACATGGC ATCACGCCAA ACCTGTCTAT AACACCATAA CACGGCATTG CC 52

(2) INFORMATION FOR SEQ ID NO: 1969:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1969:

ACAATTTTAA TTATATAACT CCAGGGGCTA CAGTAATACG ATTTCTCCAG ACTCCAAA 58

(2) INFORMATION FOR SEQ ID NO: 1970:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1970:

TGACGTATAA TGGATGAAAG TCTATTAAGT TTAAGAAGCT AATACTGTGA AATCTTTCT 59

(2) INFORMATION FOR SEQ ID NO: 1971:

(A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1971:

10 TATCATGTTA TCTTCAATCG TTCACCAACA GTCATTGCT GCATCAGTAA CG 52

(2) INFORMATION FOR SEQ ID NO: 1972:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1972:

TTGCTGGTGC CATAGACTAC ACTTGTTTGA TATCAGAAAT GGGATCTGTT CCATTACC 58

25 (2) INFORMATION FOR SEQ ID NO: 1973:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1973:

35 AGTTAAACCG AGTCCAACCC AAACCTCCAA TCCACCTAAT GGTAAAAATT CCAAACCATT 60

ACCAGGGAGG GACCAAAAAA CGGAATGGGG CCTATTGGTA GGGTACCTAT CCCATTAAAA 120

40 AATCCATCCA AAAGCCCAAA TTATCGGACC ATTTTCGCCA AAAATAATTT AAGCGGAAAT 180

TGAATACCTT AAAATTCTCT GGGCCCACT 209

(2) INFORMATION FOR SEQ ID NO: 1974:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1974:

55 ATCTGAGTAT TTATAACATA AATCACTAAT ATCGTTATTA CATAGGGATA GGGTAAAAGT 60

(2) INFORMATION FOR SEQ ID NO: 1975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1975:

TTCCTGCATC CGAGTCTGAA TCGCTGTCGA ATCACGTCGA GTCGATCGCT ATCAGGTCGA 60
 GTCGCGTCGA ATCGnTCGCT ATCGAGTCGA TCGCGTCGAA TCGAATCACG TCGAGTCG 118

(2) INFORMATION FOR SEQ ID NO: 1976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1976:

TTGCAACnTT TGATCTAGAT ACTACCTTAG TTGGATTGTA CTA CTGATT CTA CTTCACC 60
 TTTAGTTGGT TTTGTAGCAG GCGTTTTGTC TTTACCTGAC TCACTAGATG CGTCATTTTC 120
 TTTTCAACA CTTGGTAATT GTTTATTGTC ATCTTTTGG CTGTCTTGTT TTTGTGATTC 180
 TTTTCAACA GGTGATGGTG TTGGTTTGCT AGGCGTACTG GAGTAGCTTC CTTCTTAGCT 240
 GAGTTATCCT GTTGTTCCTT TTTGTTAGAT TTATCGGTAT TGGCTTTTGT AAATGCTTCT 300
 nTATCAACGA TTCTGACATG GTATTGTCCA TCATAATCAA TCGTTTTTAC GTGAACTTTA 360
 ACGATAGCAT CATATAGAGT TTACCTTCAA CATATGGGAA 400

(2) INFORMATION FOR SEQ ID NO: 1977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1977:

TAGACAAAGA CAGTAACAGT AAAGTACGCT TCAGAACTGA TGGCTCACTG CGAGTATAAA 60
 AACTTGTAGT GTCC 74

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1978:
 ACTCAAAAAC TCGGAAAACA TTCCAATTGA GCTTAAATCT GACCCTTTTT TTGACCCTTA 60
 TATTTTTTAC AA 72

(2) INFORMATION FOR SEQ ID NO: 1979:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1979:
 ATGTCATTGG CTTTGAACCT TATCTTCAAG CACCCAATCG TTTTAACTTT TCAAAATTTG 60
 GCACCATAA 69

(2) INFORMATION FOR SEQ ID NO: 1980:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1980:
 CAGAGAGTTG TCGCTCATTA AACGCCACnT GATGAGTTTT CGCTTACGAA GTGCCACGCG 60
 GTATGGATAA TTTTCACCTG TTGCTGAGTC TTTGATAAGC CTCGACTGT 109

(2) INFORMATION FOR SEQ ID NO: 1981:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1981:

(2) INFORMATION FOR SEQ ID NO: 1982:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1982:

GAATCTGTTT AAGTTAGAAT TATCCCGGCA TAATGATAAA GGCGAGTAAA TGG 53

(2) INFORMATION FOR SEQ ID NO: 1983:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1983:

GnCTTTTGAA TAAAGAAAAA TTCATCAATA GAAAAACCGT CTTTATCGTC TATTTTITTA 60
 ACTAGTAAGT TCGGCGTTCT TAGAGACTCA AATATTGATT TTACGTTTTT CTTTGTTACA 120
 CCACTAACAC TAAATATTCT TCCATCTAAA TCTACTAATT CTGGTACCGC AAAGACATCT 180
 AAACCATGTG TTTTTCCTTT GTATTATTTT TCATCTTTTC CCAATAAAAA CACTTGGAAC 240
 TTTTGATTn GT 252

(2) INFORMATION FOR SEQ ID NO: 1984:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1984:

CGTGTTAATC AACTAATTCT TAGTTTTAAC TGTCGTAATA ATCAACTGAA CACTTTCAAT 60
 CTA 63

(2) INFORMATION FOR SEQ ID NO: 1985:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1985:

5 TCCTAAAATG ACCGCTAATG CCTATGGATT GTTATCACCG ACCGCAGGGA CAGCACGACC 60
TAC 63

(2) INFORMATION FOR SEQ ID NO: 1986:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1986:

GGCATATAAA AATTAGAGAA ATTATTTCAA ATGAACAGAT AGAGGCACAA GATGAATTAG 60
20 TTAAACGATT AAACGATTAT GntTTTAAATG TCACTCAAGC AACTGTTTCT CG 112

(2) INFORMATION FOR SEQ ID NO: 1987:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1987:

TTTATCAATT TGTAACGAAC ATGAATTACA TGTTTCAGGA AAATATATTT CATCCCATTT 60
35 TTAAAAAGTA TAAGATTTTA TGAAAAATTA AACCAATTnA GTATAA 106

(2) INFORMATION FOR SEQ ID NO: 1988:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1988:

AATGGCGTAG TTACAGCATT TATGATTGTG TTAATCTTTT CTTCTGATAA ACATAATCTG 60
50 TTTGACCAAA AGTATTTAAG TGTTC AATTA ATTAGTTTTTA TTATTTACGT CGTATGGCAA 120
GTTTTATTGA TAATGTTTTA TTATCATTCA AAACCAAAAA ATAATTCATT TTCAAAATTT 180

55

TGGTTAGGTG GACATCAGAT TCACTTCCAT GAAAGTAAAT TAATTGAATT TGTGGTTTC 300
 TTAGGAATTT CTTATGTTAC ATTCAAAAGT GTGCAGTTAA TTATGGAAAT TCGTGATGGT 360
 5 TCTATCAAAG AAATTAAAGT ATGGAAATTA ATTCAATTTA 400

(2) INFORMATION FOR SEQ ID NO: 1989:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1989:

TTCAGCTTAC AATAATGAGC AGGTTGGGGT GGGCTCCAAC GCAGAGAATT TCGATAAGAA 60
 20 ATTCCACAAA TAATACAAGT TGGCCCACTC CCATTCTGTA ATAAATATAG GAGGTCATTG 120
 TTATGCAAAT AGAACTTACT GATGCAGCAG TAACTTGTT TAAAAATGAA CTTGAGTTGC 180
 CTGAAAATAA TAAAGTGCTC GTGTTTTTTG TAAGATATGG TGGCGAATTC CAACTCAAGC 240
 25 AAGGATTAG TCCTGCTTTT ACAGTTGAAC CAAAGGAAGA TGTTGATATT GGCTATGAAC 300
 AACAAATATGA CGATTTAAAT GTTGTCTAG CGGAAAAAGA TTTGTGGTAC TTTGAAGATG 360
 ACCACATTAT TGTAATGTA GTTGTACGA AGATGAATTT 400

(2) INFORMATION FOR SEQ ID NO: 1990:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1990:

CAATTTATTA TGTAATAAT TATAGCATTG ATGAACAAGG CGCTCAACGT AATAnTACAA 60
 TTAATGGATT GTTTCACAAG ATGGTAAAGC TAGGATGTCT TTTTATTAAG A 111

(2) INFORMATION FOR SEQ ID NO: 1991:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TAAACAAATT CATCAATTGT TAGTGGCATA TCCTAATGTA ATTAGAGAGG AGTT

54

(2) INFORMATION FOR SEQ ID NO: 1992:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1992:

15

GAACGATAGA TTGATGAAAA GTTTAAAAAA GTACGTATAT GTTTATTAAG TTTGAGTTT

59

(2) INFORMATION FOR SEQ ID NO: 1993:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1993:

CGAGACCAAA ATATTCGAAC GAATAATTC AGTGTTTGC TCCTTTATTA TAGATTCAAG

60

CTATGGATAA TAG

73

30

(2) INFORMATION FOR SEQ ID NO: 1994:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1994:

ATCCATACAA ATGTAACAAG CACAATTGCh GCCATACTTn GCATGACAGT

50

(2) INFORMATION FOR SEQ ID NO: 1995:

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1995:

55

(2) INFORMATION FOR SEQ ID NO: 1996:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1996:

TCaNTTAAnA TTAATGTnCG TTGGGGCTCT AATAAAATTT GTTTACAACG 50

(2) INFORMATION FOR SEQ ID NO: 1997:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1997:

TCATGATTTG AAATGACTTT CAATGACTTG GGTGGGACAC TTGTTGCACA GCTGGATGTG 60
C 61

(2) INFORMATION FOR SEQ ID NO: 1998:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1998:

CATGCATTGA TGnTCTCAAA GAACATGATG AAACAGGTCA nCACATGnCA 50

(2) INFORMATION FOR SEQ ID NO: 1999:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1999:

GGTTCGCTAC TGATTGGGTA TACATCTGAT TTAGCAATCT TGCGCACTTG TT 52

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2000:

ATGTGGTTAG ATATCTGCAC ACTTGAACGT TATTGTGGGA TATACTTGGC CAT

53

(2) INFORMATION FOR SEQ ID NO: 2001:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2001:

ATCTCAGTAA GGGTAAGCGT CAAAGTCTGC ACGGATGCTA ATGTTTACCA GGTT

54

(2) INFORMATION FOR SEQ ID NO: 2002:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2002:

CTAAAGATTG TAATGCTTGA ACAATTGGTT CAGTGAATTT TTGGAAATTG TGGAAACTGT
 TACCATCATC ATCTGTTATA AACTAAAGT TTAAATTGCC AGTATCATGA TAAACAGCGC
 CACCACCAGA AATTCTTCTT ACTACATCGA TGTTGTGAGC ATCGATATAT GTCTGATTTA
 CTTCCTCTAT CGTATTTTGA TTCTTTCCAA CAATGATAGA TGGTCTATTT ATGTAAAATA
 AAAAGTAACT TTCTTCTGCT GGTAATTTT TTAAACATA TTCTTCCATT GCTAAGTTTA
 AAGTTGGATC TGTAATATTA TTATTACTAA TGAATTCAT TACAATCTCT CCCTTATATC
 TATATATATn CTCTACTTAT TTATGCCTTA ACTTTGCTCA

60

120

180

240

300

360

400

(2) INFORMATION FOR SEQ ID NO: 2003:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2003:

CCGAAATAGG ACGGGCAGTT GGATTTATTC GAAATGGGTG GCGTTAATAT ATACAGT 57

5 (2) INFORMATION FOR SEQ ID NO: 2004:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2004:

DAGTAGTTGA AGGCGACCGC GGTCCACAAG CTGCAAACGT TGTAAACTA TAATTCTTAG 60

ATTGGAATCA TTGATTTTAA CTAACACCTT ACCAAGAAGT AAGGTGTTTT TA 112

20 (2) INFORMATION FOR SEQ ID NO: 2005:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2005:

30 AAATCTTGAC ATAGGCACAG GAATGTATAT TGATCTCGAT CACTTAAGTC 50

(2) INFORMATION FOR SEQ ID NO: 2006:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2006:

AAGGTGGGTT TAAATTTCCC AAAAAAAAAA GCCTTTTAAC CTTTGGGGG GTCCCCTTTC 60

45 CTTGGAATTG GAAAGGGGCC AAAATTGGAA TAAGGGGnTT GGAAAAACCC AAGCC 115

(2) INFORMATION FOR SEQ ID NO: 2007:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2007:

TGAAGAAATA GCAAATGAAC TCAATATTTT TATTGAACGT CAATATTTCA ACCAATTATA 60
 5 TCGCTTCAAT AATCAAGATT TAAAGCATCT TGAACAAGAA TTTGA 105

(2) INFORMATION FOR SEQ ID NO: 2008:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2008:

ATTGGCTACT AAAGTTAAGG ACATGATGGA TTGGATTAGT GGTATGCGCT TTGAAAAGAT 60
 20 CAATTAT 67

(2) INFORMATION FOR SEQ ID NO: 2009:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2009:

TAG CCG TCAAT ATCACAACGA TGATGCTCTG TGCGAAGATC TGATTTATTT 60
 ATGCGCGC 73

(2) INFORMATION FOR SEQ ID NO: 2010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2010:

CTTTGTTTAT GTTTCGTTTA ATTTGTAACC CTCTCTTTGG ATACCGAGGT T 51

(2) INFORMATION FOR SEQ ID NO: 2011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2011:

TAACGACCAA GCTTAAAGAG ATACGCTCTT ATGCGATTGG ATAGGTCGTT AAAGTTAACT 60

10

ACAATACCTC ATAAGTAGAT TTAGAATC 88

(2) INFORMATION FOR SEQ ID NO: 2012:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2012:

GTCAACCCCTT GCCAAGCTTA TATCAGGATA CTGGGATGTG ACTTCCGGTG AATTAC 56

25

(2) INFORMATION FOR SEQ ID NO: 2013:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2013:

35

AGCTTATAGT ACTTGTGACT TCATAATGGA TGAAGTTGAA GTACCAAAAG AATTAACACA 60

ATTACACGAA TAATTTAAAT AGAGACTGTG ATAGTAGGTG GAATTATTAA ATAGTTATAA 120

TTTGTTTTTA TTCGTATTAA CTCAAATGAT ATTAATGTTT ACAATACCAG CTATAATTAG 180

40

TGGTATTAAG TACAGTAAAC TTGATTATTT TTTCATCATA GTAATTTGGA CATTATCGTT 240

ATTTCTATTT AAAATGTTTG ATAGCGCGTC CTTAATCATA TTAAC TTCAT TTATTATTAT 300

AATGnATTTT GTCAAAATCA AATGGnATTC nATTTTGTTG ATTATGGCTT CGCAGATTAT 360

45

CCATACTGGT GCCAACTACA TGGATATAGT TATATATGCA 400

(2) INFORMATION FOR SEQ ID NO: 2014:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2014:

TCTTTCGAGG ACAGTAGAGG GTCCACCCTA TTGGACGTGG TACTGTACTA CTTTTAAA 58

5

(2) INFORMATION FOR SEQ ID NO: 2015:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2015:

TCTACCTGCA GGCATTCAAG CTTGGCACTT GCCGTCTTTT TACAACGTCG TGACT 55

15

(2) INFORMATION FOR SEQ ID NO: 2016:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2016:

TACTCTTAAG CTAACAACGG CGGTTATGAG TCCTTTGACA AGGTATCGGA GGAAAGACCG 60

30

TAAAGC 66

(2) INFORMATION FOR SEQ ID NO: 2017:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2017:

CCAATAAGCA CACTGCCATT ATTGAGGACG GTACATnTAC GGTTAGACCC AATTGTTTCAT 60

45

GGCGGTGGGC ACATAGTGTT TGGCTTTGAG GAGGTTACCA TTGCC 105

(2) INFORMATION FOR SEQ ID NO: 2018:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2018:

CCTTCCAATA GTAATTGATT GATGTATGAG TATATTAGGT GTGAAATCAA GAGGATTC

58

5

(2) INFORMATION FOR SEQ ID NO: 2019:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2019:

TTTCCTCGTA GGTGGTTCTT CTTTCATCTTC GTTGTTTTGT CCGAAGTTTG GA

52

(2) INFORMATION FOR SEQ ID NO: 2020:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2020:

30

ATAGTTTAGG TGAGGATGTT GnGGTACGAC AGGAAGAAAG ACGGCAAACA

50

(2) INFORMATION FOR SEQ ID NO: 2021:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 300 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2021:

TTGTCACAAT AATTTCTTCA GGATCATAGG AAAAATGATA ACGATTTTTG AAGTATTGAC

60

45

TAATTGCTTC GCGAGTTTCT AATAACCCTT TATTGTGAGA GTATGATGTC TTGTCATTGT

120

TAATAGCATC AATATATGCC TTTTTCACAA CATCAGGCAT CGGGAAGTCT GGTGGCCAA

180

TAGTTAAATT AACACAATCA TCCAAATTAT TCATACGATT TGAAAATTGG CGATACTTGG

240

50

GTGGCTCCTA AAATAATTAG GAAATGAGGA nTtnAAGGAA GGTttCCATT TnGTGGACAC

300

(2) INFORMATION FOR SEQ ID NO: 2022:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2022:

	TCATCCAAAT TATTCATACG ATTTGAAAAT TGGCGAATAC TTGGTGCTCT TAAATATTTA	60
10	GAATTAGAAT TTAAAGAAAG TTTCAATTGT GACACCTCAA ATATAAATCA AATATTGTCT	120
	AAAAATTTAG AAATTAATAA TATCATAACA TACTTTTAAA GCAAAAAAGG GTAAATTACT	180
	TAAGCTTTAT TTGAAAAACG AAAAATGTCT AAATACACTG TAGTAACTAC TTTTCAAAAT	240
15	GAATAAGTG GTTACAGTTA ATGTACTTAG ACAGTATAAA ATTATGAATC TTAAACTGT	300
	GATGGTCTTT GTAAATTAAT TATTGGATTT GTCCATTAC AAACAAAGTT TGTAATAAT	360
20	ACATATACGA TGATTACAGA TATACTTATT AAATAAGAT	400

(2) INFORMATION FOR SEQ ID NO: 2023:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2023:

	TTTAAATATA CCAATCACGT TCATCCACAG TGATCCTAGA CCAATCCAGA	50
--	--	----

(2) INFORMATION FOR SEQ ID NO: 2024:

35

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2024:

45	TTTTTAATGG TTAAAAAAT CCCTAATAAA ATTTTGGAAC ACCTAAATTC CAAGGGGTTA	60
	AATTCC	66

(2) INFORMATION FOR SEQ ID NO: 2025:

50

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2025:

GTAAGAGCAA TGGCGCAAAA TGCCTGTAAT GATATTGTGA ACGTAATTGA ATCAGTAGAG 60
 5 GACC 64

(2) INFORMATION FOR SEQ ID NO: 2026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2026:

CTGTCGCTGC GTGACTTAAT TCTTTTGCCC CGTTGGCATA TGAGGAAATG TCA 53

(2) INFORMATION FOR SEQ ID NO: 2027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2027:

CATTTCACTA TTATTGGTTT AGGGTTGTTC ACGTTCATCA TGACCGCACC ACA 53

(2) INFORMATION FOR SEQ ID NO: 2028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2028:

CAACTAGACA TAGTATTGCT GCATTAATCA AGTCAAGCTG CCACACTAAG AATCGATGCA 60
 45 AACGGAATCG TCA 73

(2) INFORMATION FOR SEQ ID NO: 2029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2029:

AATAATAATT CTGGAATAGT GTTTAATACT TATTnTCCGT TTAAGATTTC AACTTAATAT 60
 5 GGTTTACAGC GCGTAGCTCG TCTAATTCAT CATCACGTGT AGAGTGCTCT GCCTTATCAG 120
 ATCAGTT 127

(2) INFORMATION FOR SEQ ID NO: 2030:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2030:

GCAAGTGAAT TGAAGTGACA TGTGGCTGGT GCTTCATGGT AATGATAAAC CAACACCATG 60
 G 61

(2) INFORMATION FOR SEQ ID NO: 2031:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2031:

ATAAATATCT ATTTAGATAT AAGTATTGAT AAGTTGCTTG AATTTATAAA GTGAAGGAGT 60
 35 AGGTGTCATT AGTATAGT 78

(2) INFORMATION FOR SEQ ID NO: 2032:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2032:

GAATAGTGTT TATAAAATGT TGACACTGTA GTGGCATATT GTAAATTAAA TATTATTATG 60
 50 TGATCATTTT GTTTAAATAT TAGTTATAAG AAGTGAAATA nTCATTTTAA AAGGAGACTT 120
 AAAACTTGAA ACGATCAACG AATCAAGAAA AATTTCTTGA TACACTAATT AGACTTAATA 180

(2) INFORMATION FOR SEQ ID NO: 2033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2033:

TTTTGTCATC TGTATAGGTA TCGCGCCCGG TGTCTTTATT CACTTTGAAC TGTGCGT 57

(2) INFORMATION FOR SEQ ID NO: 2034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2034:

AAGGCATTGG ATATAAGACT TGATGTTGCA TGGCAATCAC ACTGCCTAAT CCTTGCATAT 60

AA 62

(2) INFORMATION FOR SEQ ID NO: 2035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2035:

ATGGCAAATA CTATACATCG TCCAATTGAT TGAAAAATAT GGTATTATAA GA 52

(2) INFORMATION FOR SEQ ID NO: 2036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2036:

AAGGTGTTTT TATATGCTTA TTACAAATAC TTAACGCGAT GAGTTTCTCA ACCAAATTGA 60

(2) INFORMATION FOR SEQ ID NO: 2037:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2037:

TACCCACCCC CAAACCCAAG GTTTTAAAAA ACCCCTTCCA AAAGCCCGGA AAAACCAAAA 60
 GGAATTATTT T 71

(2) INFORMATION FOR SEQ ID NO: 2038:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2038:

GAATCCCGGA AGTACAATTT GGTACGTGAA GAAAATGGTA GTGGAATTAC 50

(2) INFORMATION FOR SEQ ID NO: 2039:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2039:

CAGTATCTCT TGGTATTTTA ATTGGTGCTT TATTAAACGT AATTTTACCT TTATATATCG 60
 ATGGAGCGAA GAGTATTTTC GTATACGTTT ATAGTGCCTC TATTTTACCA GGTATGATTC 120
 CTTGGTTTAT GATTTTATTC AGTCATTTAC GTTTTAGAAA ATTACACCCT GAAGAATTGG 180
 AAGGTCACCC ATTCAAAATG CCTGGTGGCG CAGTAACTAA CTATTTAACA ATCTTATTCT 240
 TAATATTAGT ATTGGTTGGT ATGGTATTTA ATGTTGAAAC TAGAATATCA GTGCTTATTG 300
 GTGTCATCTT CTTAACGATT GTAACGATTT ATTATTTTAT TAGATATAAT AAAAnTAATG 360
 TAAAGCAnAA TAGTATGTTA TAAAGAGCGn TACTTATGAC 400

(2) INFORMATION FOR SEQ ID NO: 2040:

- (A) LENGTH: 79 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2040:

10 AAGCTGATTT TTCTAAATGT TGAAAATCAT AAAGTCTTA ATAATAAATA ACGAGATCTA 60
 AGTAATAGTG CTCCATTAA 79

(2) INFORMATION FOR SEQ ID NO: 2041:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2041:

25 AATTGAACGG ATCGTTCCCA ACCGTTATCA ACCCAGACCG GTGTTTGAAC CCAA 54

(2) INFORMATION FOR SEQ ID NO: 2042:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2042:

AATGGGATTG GTTCAAAGTG AAATGGGCTG TTAGTCCCTG TAAAACCAAG 50

(2) INFORMATION FOR SEQ ID NO: 2043:

40

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2043:

50 ATTGGnATAA TCAAAGCATT GAATCATACA TAGTCACATT GATTGTTTCC TCAGAGTTTC 60

AACACTCTAT AACTCATTTT AGTAATTGTC TGATTGCGCA CTTTCATGTG 109

(2) INFORMATION FOR SEQ ID NO: 2044:

55

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2044:

10 TTTTATGGAG GTGATGAAGT GGGTGAAGCT GAAAGGAAGC AAAAGCTTGG 50

(2) INFORMATION FOR SEQ ID NO: 2045:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2045:

TTGGCCCCCT TCCAACCCCTT GGAAATTTTA AAAGGCCaNT TTTGGGGTAA AACCCCTTGGT 60

25 TCCAAGGACC CCCAAAAGTT TTTTAACCTT CCAATTATTA T 101

(2) INFORMATION FOR SEQ ID NO: 2046:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2046:

ACCCTTTCCA AAAAGCCCAT TTTGAATTCC CCAAAGGGAG CCAAATTTAA GATGGCCGCh 60

40 AAAAAGGACC GGGGGGTCCA TGTTTAAATT TAAGCCGGAC 100

(2) INFORMATION FOR SEQ ID NO: 2047:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2047:

GTTAGTTATG AGCAACGTAT TAATGAAATT ATTGAGCAGT AATTnACCAG 50

(2) INFORMATION FOR SEQ ID NO: 2048:

55

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2048:

10 TACGTATTTT CAAATGACGT TGGTGGACGT CACACTCCAT TCTTCTCAAA CTATCG 56

(2) INFORMATION FOR SEQ ID NO: 2049:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 82 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2049:

TTTTCCCCC CCCCCCAAA TTGGGGGTTA AAATTTTAAA AAAAGGGGTT AAAGGGAAAC 60

25 CCCAATTCGG GTTAACCTTT TG 82

(2) INFORMATION FOR SEQ ID NO: 2050:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2050:

TCAGATGGAT GGCAGTTATT TGGTATTCCA TGGGTATAAA GATAGCATAT T 51

(2) INFORMATION FOR SEQ ID NO: 2051:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2051:

50 TGAACGGGAG AAAGATGTTG TTGCATGGTG TCTCGGAAAC GTTTGTGTCC ACGTA 55

(2) INFORMATION FOR SEQ ID NO: 2052:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 74 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2052:

ATACCTGGAT GCAAAGGCAA AGTCGCAATT TTCCCTGTTC TAATGTGTCT AACTTCTCTT 60

10

CTAAAGTTCA GGT 74

(2) INFORMATION FOR SEQ ID NO: 2053:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2053:

AATCTTGTCT GATGTAATGT TCAGGTCCTCCT TGACCCTCAT ATGCATGAGG T 51

25

(2) INFORMATION FOR SEQ ID NO: 2054:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2054:

35

CATCGACTTA TAGCTTAATT ATTATAAAAA ATTTCTCCAG ATTAACTTT CT 52

(2) INFORMATION FOR SEQ ID NO: 2055:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2055:

ACTGACACAT TATATTAGTG AATTATTA AAAATGATGAG AAAATTAAAA TCATCATGAA 60

50

TGAATTCGGT ACTTTTGATA TTGATAGCAA TAGTATTTCA AATGAAATTG AAGTCCATTC 120

ATTGATTAAT GGTGTGTTT GTTGCGATCT TAAACAAGAA CTTGTCTATG AACTAAAAGC 180

CATTGCTTTA AAAGGGGACG TTAATCATGT CATCATAGAA GCGACAGGCA TTGCGCATCC 240

55

TTATTTATGG TGTATTAGAT GCGACTCGAT TTTTAGAACG TCATCAATAT ACCGAAAAAT 360
 ACAGTTTCGC TGGATGGGGA GGATCCAGTT GGAAACTAAn 400

5

(2) INFORMATION FOR SEQ ID NO: 2056:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2056:

15

TCAAAACTTT GAAGTTGTGC TTGCTTTGCA CCATTTTAA AATGTTTCAGC TGAGAGTATA 60
 TCCTCCGCTG TAAAATTTAC TTCTCCTGGA CTTAAAGATT CAATTAACAA CCAAGCCGAT 120
 AACGTATCAT TTAGCAATTG ACTCATGAAA TCCCACCTTG TTCCCTATTT GTTTTTTACT 180
 TAATGCTATT TTAACAAATA ATTTAATCAT ATTAGTGTTT TTTCAAAAAT ATTCATATAT 240
 TATCATTACC ATATTTATTC AACAAATGTT TGTAATAATCC TCACTAATAA AATTAATCGA 300
 TATGACCATA ATTCATTATC CAATAAATGA CTATAAAAAT TTCTnCTATG CCTTCATTTG 360
 CAACTAAATT TGGACATCAA AAAAGAGCAC TCCTGAATGA 400

20

25

30

(2) INFORMATION FOR SEQ ID NO: 2057:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2057:

40

TTGTTGTTGT GATTTCACAT TTTCAAAATT TTGTTGCATG TTGTTAACTT CATAAATTAG 60
 TGATTGCACT ACATCATTCA TGAGGACGCC TCCTACATTT TTTAATTTAT CACAATATAC 120
 TGTATTCGTC ATGTTTTAAC ACTCTATATA ATTTGATTTA ACTATTTTTT CAAATGTGTT 180
 ATCTGTAAAT TCAAGTAAAT CTAAAACTT CCTATATAAA TACAAAATTT TATCGTGTAT 240
 GTTGTATAC GATGAAAATA CTTTAAATCT AATAAAATCA TTTAAATCAA ATACACCTCT 300
 GCTGATTAAC AACACATACT TGTAATTGCC TCAAAAATAA AAATTACTAA TCATGATTTG 360
 ACTTTTATAA CAAAATTCAA AAATATTGTA ATGAGTATTC 400

45

50

(2) INFORMATION FOR SEQ ID NO: 2058:

55

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2058:

10 TCTTTTACT CGCAATTTTA GGAAAAATGG TTGGATCAAT TGATAAAACC GGAAAATTAT 60
 TAACAATAAT CAATAAAATA TCAAGCATAA TAATTATTAT TGTGCTCTG ATGATATTAC 120
 AAAAAGTTAT TCAATTATTA TTCTAAAGCG TTATGTAGTT GTATTTTAAA AGCGTTATAC 180
 15 AAAAGACATA CTTGTGTCTA TGTATAACGC TTTATTTATT ATAAATTTGG ATCAATTAAC 240
 TCAACAAATT TAAATGTTCC ATTGTCATAT TCAAATTTCA GGATATTACA ATTACCGATA 300
 TTATGCTTTA ATGCTTCATC TAGTTTAAGG CAATATCTTA AAAATACCnC CCTTAnTGGT 360
 20 CCATGACTCA CGACTAATGC ATTATTCTTT GGTTTGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 2059:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2059:

AAAACAACAC AATCAAAAAT ATTGGATACA ACTGAAAAGT TATCAAAGCT A 51

35

(2) INFORMATION FOR SEQ ID NO: 2060:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2060:

TTATCATGTT TAGTAGATTT TAAGAAGCTA GAACATTGTA GATATGATGA 50

(2) INFORMATION FOR SEQ ID NO: 2061:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2061:

5 AACGTCGTnA TATCAnCTTG CCAAACAAAG ATATTGTCAC CTTTTATCGG 50

(2) INFORMATION FOR SEQ ID NO: 2062:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2062:

ACCATGGTGn ATATGGTCAT GATGATCGTT TGTGCCGGGA GCTTGAGCTG 50

(2) INFORMATION FOR SEQ ID NO: 2063:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2063:

30 TTTCCCTTGG TTTTGAATT TAACCAAATT TGGGAGGGAT TTGGGACCAC CCCCAGGATT 60
 TTAAAAA AAAATCCCG G 81

(2) INFORMATION FOR SEQ ID NO: 2064:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2064:

45 TTTTGGGGAC CTAACTGGG TGGGTCTGGA ACTGTTTCCC TTTCAAACAC A 51

(2) INFORMATION FOR SEQ ID NO: 2065:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

ATGATGTATT CAAAAGGTAT CTATAAAATA GCTTTAGTTG GAAAAGATGA GA

52

(2) INFORMATION FOR SEQ ID NO: 2066:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2066:

15

TTTCATCACT GGCATCTTGT AATTTCTTGG TCTCATATCT GGAATTAATA GGT

53

(2) INFORMATION FOR SEQ ID NO: 2067:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2067:

AACCATTAAG AAATTGGATA CACAGAGCAA ATATGGTTAT GATTAGGAAC CATGGCATT

60

30

ACC

63

(2) INFORMATION FOR SEQ ID NO: 2068:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2068:

AAAGGCAGCG ATGTTACTCA TACCGAACCT GGTTATATAT GAGCGATGAT GCAATGTA

58

45

(2) INFORMATION FOR SEQ ID NO: 2069:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2069:

55

AACAGGA

67

(2) INFORMATION FOR SEQ ID NO: 2070:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 86 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2070:

15

CATTTAACCC ATCTTCTTTT TTTAATTCTT CTATACTACG GTTTAAAAAC TCTACAATAA
 CTGCCATTTC ATCATCATCA AAGACT

60

86

(2) INFORMATION FOR SEQ ID NO: 2071:

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2071:

30

GTTTCTTCAA AATATGTGTA TTACCTTTTT GTATGGTTAA ATCTTTTAAT TCTATCATT
 TTGTCTTACC TCTTTTGGTG TATCCTCTTT TTCAACATAT GTGATCGATA TGACATATTG
 CCCTTTATGC TTTATTTTGA CACACGTTCT ACTAGGTGAA AATCCATTAA ATGTTAATTT
 ATAATCAAGC TTTTCCCCTC TTCACTATA AGCCGTAATA TTAACATATT GTTGCCTACC
 TTTTGGCACT TTGGCATAAC TATACTCCGT TTTTAAGAAA GGATTAAAAAC GATCAAGTAT
 AGGATGATGT ATGANTGTAA AAGCAATAGT AATGGATAAT ATTAATCCTA ATAATATTGC
 AATGATAAAT TTCATAGTTA A

60

120

180

35

240

300

360

40

381

(2) INFORMATION FOR SEQ ID NO: 2072:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2072:

ATCCCCGAAT TGCTTCGCAA ATGTATCATC TTCGAGGCTA CGTTACTTAA AT

52

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2073:

CCAAAAACAG CATCACTGTG ATTATGGTTT TCATCTTCTA TAACTAAGAA TACATGTTTT 60
 TTTGTAAAAA TTTTTTTGAT CA 82

(2) INFORMATION FOR SEQ ID NO: 2074:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2074:

TTTATCGCAA TGAGGGAAGA TAAAGGATCC CGAAAGCGCC GTATGGGTTG GCAAACATTG 60
 GGGACCAAGA CCGTTCCCCA TA 82

(2) INFORMATION FOR SEQ ID NO: 2075:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2075:

CTTGTTGCT CTTTATTTAT TTAATTGAGA CCTAGAAATA AGTTATTAAG CACAATCATT 60
 CACTTT 66

(2) INFORMATION FOR SEQ ID NO: 2076:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2076:

(2) INFORMATION FOR SEQ ID NO: 2077:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2077:

TACGTTCTAT CATAGAGCCT GGAGATGAAA TTATAATACC GGGACCAATT TATGCAGGCT 60
 ACATACCACT CATCGAAGTA CTAGGTGGTA AACCAATTTA TATTGATACA ACAGCAACAC 120
 AATTTANAAT TACACCTGAT GCATTAGAAA GTCATATTTT TCCAAAGACA AGAGCTGTCT 180
 TGTTAAATTA TCCGACTAAT CCAACTGGCG TAGTTTTTAA AAGAAAtGAA GTTyTArATA 240
 TCGTAAATGT ATTAAAAAAA TATCCGTTAT TTATTATTAG CGATGAGATT TATGCTGAAA 300
 ATACATTTAG TGGTAAACAT GTATCC 326

(2) INFORMATION FOR SEQ ID NO: 2078:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2078:

ACCCCTTAAT TTAATTGATG TTTTGTATT TTTAAATGA ATAGTTGAAG AAAAAT 56

(2) INFORMATION FOR SEQ ID NO: 2079:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2079:

CACGTACTGC CATGTATGCA CAAGCCGGCA TTCATAAAGC CTTCCATGGC AGTCGTTATC 60
 A 61

(2) INFORMATION FOR SEQ ID NO: 2080:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2080:

TGGGACAGGG CGTACCATT CAAAATGATA GTTCTGAGCT GCTAATTAAT ATGCCTTCGA 60

10 AAAAGATGAG TTAAATTGA GATGATGAGA CTGA 94

(2) INFORMATION FOR SEQ ID NO: 2081:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2081:

AAGACGACAT GCAAGACATT GCCTTATCTA ATGACAATGT TAAAGCGAGT 50

25 (2) INFORMATION FOR SEQ ID NO: 2082:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2082:

35 TTGTTCCGGCT AAAAATAAAG TGGCATTGAC GTGACCGCAA GTTGACGTAC 50

(2) INFORMATION FOR SEQ ID NO: 2083:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2083:

CTTCCCAACA TTGCGCACTG AATGGCGATG GCGCTGATGC GTATTTCTCC TACGCTCTnG 60

50 CGTATTCAAC CGCTATGGGC ATCTCATACA TCTGTGATG CGCTATTAAG CAGCCCGAAC 120

CGCACACCGT GAG 133

(2) INFORMATION FOR SEQ ID NO: 2084:

55

- (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2084:

10 GGTAGGGGCA CTATTTTGTA TGTAGAGGTT TTGTCGGGCA GTGTGAAATC AACGACT 57

(2) INFORMATION FOR SEQ ID NO: 2085:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2085:

CCCCCCCCAA AAACCGCCCC CCCCAATTTG GCCTTTTTC AAGGGGGGTG TTTTAA 56

(2) INFORMATION FOR SEQ ID NO: 2086:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2086:

35 AATAGCGAGA GCCCGACCAT CGCCTCCAGA TTGCGACTGA ATGGCAATGC GCTGATGCGT 60

ATTTCTCCTA CCATCGTGGT ATTCAACGAT ATGGGCACTC TCATACAATn GCTC 114

(2) INFORMATION FOR SEQ ID NO: 2087:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2087:

50 AAGGGGGAAA AGGAACCCAA GGCCCCCTTC CCAAGGAAAT TGGGGGGTTG GAAAAAACCA 60

AAAATTTTTT AAAAACCCGG 80

(2) INFORMATION FOR SEQ ID NO: 2088:

55

(A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2088:

10 GGGGTAAGTG GTTGAGACAG GAACTTTACA AGAGGTGTTT CGTCATCCTA GAACGACGCT 60
 TGCTCA 66

(2) INFORMATION FOR SEQ ID NO: 2089:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2089:

25 ATCAATGTAT TACGTATCGA AGGTGAATTA TATCATACTG CTAAATATGA CGGTTTCACA 60
 TC 62

(2) INFORMATION FOR SEQ ID NO: 2090:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2090:

40 GAATTCGCTA TCCTGAAATC CTGAGTCGCT GTCCTGAAAT CTGAAATCGC 50

(2) INFORMATION FOR SEQ ID NO: 2091:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2091:

CGGGGTCCCC CCGTTCAATT CCCTTTGAGT TTTC AACCTT GCGGGTCGTA ATTCCCCAGG 60
 CCGGAATTGC TTAA 74

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2092:

ATTGTTGGGT ACGGTGGTGG GTTAATAATC CAAACACGTT AAACACCCG TTTTAGATAT 60
ACCTATACAA 70

(2) INFORMATION FOR SEQ ID NO: 2093:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2093:

GTTTTGGGTC TTGGGTATTA GTTTAATCTC CATCATGGTT AATTGGTATG GTATTGGTAT 60
TAGTAATCAT GTATGATGGG CTGGGCGG 88

(2) INFORMATION FOR SEQ ID NO: 2094:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2094:

TGGCCATTGA GGCGCATTAC GTACTACGGC TTGTCGTAGG GACAATTATT AT 52

(2) INFORMATION FOR SEQ ID NO: 2095:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2095:

AGTTGATGCA ATGAGTGATG CAAGGCGACT GAAAAGTTGG TATGAATGAC AAAACTTTAA 60

(2) INFORMATION FOR SEQ ID NO: 2096:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2096:

ACTTAAAATC TAATACGGTA TTTTCAAAAA CGAATAAAAG TTACCTCTTG TCT 53

(2) INFORMATION FOR SEQ ID NO: 2097:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2097:

AACTTAATAT TGCTACGATA TGAACGGCAT nAACATACTT AGCGnTGnTC 50

(2) INFORMATION FOR SEQ ID NO: 2098:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2098:

CAAAATAAGA AATTAATTAA GAAAATGCCA AGATGCCAGA TGCCATCGGC GGAAAGGAAA 60
 TTGCACGTAC GG 72

(2) INFORMATION FOR SEQ ID NO: 2099:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2099:

CCACCCAAAC CCAAAAATA AAGCCCAAAA AATTGCCAAG GAAGGAAAAG GAAAATTGTT 60

(2) INFORMATION FOR SEQ ID NO: 2100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2100:

CACCAATTTTCTGGnGCT GGATCTCGAC CTAAGTCCTG TAATAATTGA CGTTGAACAC 60
 GAATTAATTT ATTAATTGTT TCTACCATAT GCACAGGGAT ACGAATCGTA CGTGCTTGGT 120
 CAGCAATTGC ACGAGTGATT GCTTGTCTAA TCCACCATGT TGCATATGTT GAAAACTTAA 180
 ATCCTTTGTT AAAGTCAAAT TTTTCAAC 208

(2) INFORMATION FOR SEQ ID NO: 2101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2101:

TAATGAAATT AAGTAAATA AAAATTATTT CATGGATTGC TTCTATCTAT ATCGAAATAT 60
 TAAGAGGAAC ACCAATGTTA GTTCAAGTAT TTATCGTATT CTTTGGTATA ACTGCTGCAT 120
 TAGGACTAGA CATTTAGCT CTTGTTTGTG GAACAATTGC ATTAGTTATT AATTCCTCAG 180
 CTTACATTGC TGAAATTATT CGTGCAGGTA TAAATGCTGT TGATAAAGGC CAAATGGAAG 240
 CCGCACGTAG TCTAGGTTTG AATTATAGAC AAACGATGAA AAGTGTAATT ATGCCACAAG 300
 CAATTAAAAA TATTTTACCA GCTTTAGGTA ATGAATTTGT CACTTTAATT AAAGAATCAT 360
 CTATTGTGTC AACAAATTGGA GTTGGCGAAA TTATGTTTAA 400

(2) INFORMATION FOR SEQ ID NO: 2102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2102:

(2) INFORMATION FOR SEQ ID NO: 2103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2103:

TTTAAGGAGA AAGGTCATTG GTATAATCTT GAGAAAGAGT GGCAAGAGTT CTTAAACTCT 60
 GGGAAAGAGG TGAAAAATAT TAAAATGGAA GTAAAATATA GCGGTAATAG TCAAAGACCG 120
 ACTATATTTA AAGTTGAATA TGAAATTAAT GGTGAAAGAA ATATTAGAAG AATATTAAAT 180
 AAGTAGAGGT GCCAACATGA CATTTGAAGA GAAGCTTAGC AAAATATACA ATGAAATTGC 240
 GAATGAGATT AGCAGTATGA TACCGGTAGA GTGGGAAAAA GTATATACAA TGGCTTATAT 300
 AGATGATGGA GGAGGTGAAG TATTCTnTAA TTATACTAAA CCAGGnAGTG ATGACTTGAA 360
 TTATTACACC AATATACCTA AGGGTATAAC ATTCCGGTGC 400

(2) INFORMATION FOR SEQ ID NO: 2104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2104:

AACCATCATA AAATGTTATT AAACCGTCAT GGACCGCGTC ACCATTTAGT CCT 53

(2) INFORMATION FOR SEQ ID NO: 2105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2105:

AAGCACAAAT TAGCAGAGTG TTTTAATTTA AATGAACAAG TACCTTTACA ATTTTTGGAT 60
 AATGTAAAAG TTGGTAAAAA TAATATTTAT GnTGCTTTGG AAGAGTTTGC CAACAA 116

(2) INFORMATION FOR SEQ ID NO: 2106:

(A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2106:

10 AATTGCAAA AGAATCATGG ACAATTGAAA GCAAAAAGGA TCATCATTAA AATTGAACTG 60
 C 61

(2) INFORMATION FOR SEQ ID NO: 2107:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2107:

25 GAACCAATGT TAAGCTAATT AATGGAATCC TAACAGCGTT AATCTATTTA AAAA ACTTAA 60

(2) INFORMATION FOR SEQ ID NO: 2108:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2108:

ATTTGAAAT GAATCTGTGG AACATTTTGC TAATCATGAG GATAAAATCA TATGATGTTG 60
 40 AAAGCGAGAA TGGGATTACG TTAAACGTGG GCGCTGCTAA TTTAAGCACC TTATTTAGTG 120
 GAAGAT 126

(2) INFORMATION FOR SEQ ID NO: 2109:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2109:

55 ATAATGTTAA AAAACGGCA ACTAATCTTT TCATACTAAC AATGATTATA TGTACAATAA 60

CGTTAATAAT GCTAGATAAT TTAAAAA TGAAAAACCG TGAATATCAA AAAGAAATAG 180
 5 CAGAAAAAAA TAGACATATT AATACATTAA TTGCTGAACA AGAGCGACAT AGAATTGGTC 240
 AAGACTTACA TGATACGTTA GGGCATGTGT TTGCAAGTTT ATCATTAAAA TCAGAATTAG 300
 CTTATAAACT AATAGATGCT GATGTAGAnA AAGTAAAAGC TGAATTATTA GCAATTAATA 360
 10 AATTATCTCG TGAATCATTG nACAAAAGTC GAGAAATTAn 400

(2) INFORMATION FOR SEQ ID NO: 2110:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2110:

AAGATTTAAT ATCGGGGGTA ATGTTGATTT TCAAATATCG CGATGTGCTT GTACCACCAT 60
 25 T 61

(2) INFORMATION FOR SEQ ID NO: 2111:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2111:

TATACTAAAT TATGGCAACT TGGCTCATAT AGGTCGAGTT ACCAGACATA TTCGG 55

(2) INFORMATION FOR SEQ ID NO: 2112:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2112:

50 CGAATAAGTT CTGGGCCTTT TGTTGTTTCAT TAGCTTGTTT CTGTTTTGAT TGTTCTGCCA 60
 TTTGAACTAC ACCAACCTTT TAAATTTATT CTAGTGACAG GATAACTAAA ATATATTTCT 120
 55 TATGCAATAA TTTCCTATTG ATAAGCATTT TCAGATTTTA GTTGTAATT TTGCCCTAAT 180

AATTTATAAA GAATAAATTC GTCTCCTCTT TGACCTATAA TATATTGAnC ATTATAAGCC 300
 ATGCGATTCA TTCCAGACAC AGCCATAAAC TCTTGTTTAT CTATCATTTT AAATACCATT 360
 5 TTTAATTTGG CTTAATGGGA CATTCCGTAT TAAATCATTT 400

(2) INFORMATION FOR SEQ ID NO: 2113:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2113:

TGTTTTCAAA GCATGGTATA AATGCTTTGT AACATAGGTT TTGCCTACAT CAGTATTCGT 60
 20 ACTTGTAATA AAAATCCTCA TAAAAAT 87

(2) INFORMATION FOR SEQ ID NO: 2114:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2114:

TTTACAAGTT AAATATAnCA CTAAAAATTT TTAAGTCAAT AAGAATATAT 50

35 (2) INFORMATION FOR SEQ ID NO: 2115:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2115:

TGTGCATAAA ATCCTTTTAC TTTTGTAAAT TGATTGTTAT CTTTAACAAT TA 52

(2) INFORMATION FOR SEQ ID NO: 2116:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2116:

ATTTAⁿAACC CAATTCCCCA TTATTTTTTA AAACGGATTC CATGGGTGGA CCATTGGA^A 60
 5 TTTTAAAAAA ACCATGGCCC CATTCCAAAA AGTTAGGATG GCCAAAAAGC CTT 113

(2) INFORMATION FOR SEQ ID NO: 2117:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2117:

GATTTATCAA CTATTTCCGT ATTTTGATTA TCTCCATACA ATTTCCAATC CTCTGGCTTA 60
 20 TCAATAAATA ATGATAATGG CTTATCTTTC GAT 93

(2) INFORMATION FOR SEQ ID NO: 2118:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2118:

TGATTACCTT GAnACATGAC TTnCTGAn TGGTAAATAT TTACAGTTGT 50

(2) INFORMATION FOR SEQ ID NO: 2119:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 217 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2119:

AGATATAAAA TATAAAAAAT TATTAAAAGC TATATCCAAT CAAGACTTTA AAGGGTTAGT 60
 TCCAAATATC AATCAGAATG ATAATTATn TGAAATATAT ATAATTAACA ATACTAAAAA 120
 50 CTTAATATAT CATTTATATG ATGATAGAGG TCTATGGCTA GCTTTTAATA ATAATGAAGA 180
 TTATGCAAGA TATnCTGAAA AATATAATGA TTTAATA 217

(2) INFORMATION FOR SEQ ID NO: 2120:

(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2120:

10 AGACTTAGTA AAGTTAGATC ATCTAAAGAT GACCGTAAAA TTTATATTTA TTAAATAAT 60
GGATGATATA TCTAA 75

(2) INFORMATION FOR SEQ ID NO: 2121:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2121:

25 CACCACCTAC ATTTACTATA TAAAATGTAG GAATGGTAGA TTGATTTAGA TAACTGGAC 60
GTATCACTTT AAGTGCTTTT TCAAAGA 87

(2) INFORMATION FOR SEQ ID NO: 2122:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2122:

40 TGTTCCTTTAG CTAAAGCTTT AGCTTCTTCA TCACTTTTAA CTTCATAAAA ATCTACACCA 60
GTAGCTTCTT 70

(2) INFORMATION FOR SEQ ID NO: 2123:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2123:

55 TAAATCTAAA AGGAGAAATG CTGAAGATGA GAGAGGTATT TTTGAAATGT 50

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2124:
 TTAAAGGTA ATTGTTTTAA AAAAAGATT AACCAGGAC TTTTAATTGT TAAACCATC 60
 CCT 63

15 (2) INFORMATION FOR SEQ ID NO: 2125:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2125:
 TGTAACGAC TATTACATGA TCACAATCCA TTCAGCGCCA TTATATAAAG GTACTTAATA 60
 TAGGACATCA TTCGCAGC 78

30 (2) INFORMATION FOR SEQ ID NO: 2126:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2126:
 TTTGGTCGTG TGCAAGACAG AAGTCGACAT ACTCCAATGA AACATCATGT 50

45 (2) INFORMATION FOR SEQ ID NO: 2127:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2127:
 TTTGTGTCGA TCGCTTTTT CACTTCTTCT GAATGCTCGA AATCATTCGT 50

55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2128:
TGTCTGAAAT GATCATTAGG ATTGCTCCAG CTCAATGTCA GTnGnAATGA

(2) INFORMATION FOR SEQ ID NO: 2129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2129:
TCCAATTACC TACAAAGTGA GTGCTTTCTT GACCAAGTCA AAACGAACTT TTATATTTGT
CCAAC

(2) INFORMATION FOR SEQ ID NO: 2130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2130:
TTCCAAGGTG TCGCTGACTT TCAACACACT GAATATATAC CTGCCAGTCG GCTGGTCATG
C

(2) INFORMATION FOR SEQ ID NO: 2131:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2131:
AGTTCTTCAG TCCAAATGCG GCATGTTGAC CCACCATAGG CGAGGGCATT TTCACCACGG

(2) INFORMATION FOR SEQ ID NO: 2132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2132:

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CCCCCTCGAGT TTTTTTTTTT TTTTTTTTCTA CTGGAGCAAA ATGAATTTT TTTATTGTAC      60
TTCAGGGCAA CAAGTCAACA GCTGCAGGAA AACAAAACCA GGTCCAATCT ATGATCTAAG      120
AGGAAGTCAG GAAAGGCTTG GAAGAGAGAT CCAAAGGCCA TCCTGGCAAG GGAATCCCA      180
CATGAGAATT CCTGGGAGAG AGCAGGCCCC AGGCAGCAAG GTCATCTTGC CTGCTTCTCT      240
GTAAGTTAAT CCTTCACAGG GAGCCAAGGC TTCTCTTGAC TGCTTGACA AGAGGGTAAG      300
GGCCCTGGTT GCAGGATTTG CCAGTGAAGT CATCCATGTC AATAGACCAG ATCATGGCTC      360
CTCCCAGGTT AAATTCCTTA AGAACTGAAC CTTGnCTCCA      400

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(2) INFORMATION FOR SEQ ID NO: 2133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2133:

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TTCATCATAC AACATTACAC TTTGTATGAC TAAACCCAAA TTAACGATAT      50

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(2) INFORMATION FOR SEQ ID NO: 2134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2134:

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GTGGCAAGCT TTTTAAAGGT CTGACTGCCA TCGACGGATC TATGTTAACA GGTGGATCT      59

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(2) INFORMATION FOR SEQ ID NO: 2135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs

- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2135:

ATCAAAGTCA TCTnCATGGT CnATCACACC ACGCTTTATA TGGTAATTCT

50

10

(2) INFORMATION FOR SEQ ID NO: 2136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2136:

CGGGATCTGA GGTGCTATC TGCAATCTGC AATCGCTATC TGCAATCTGG AG

52

(2) INFORMATION FOR SEQ ID NO: 2137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2137:

nCTCAACCAC CCACACAACA ACACAACAAG CAGCACCCAC ACACCACACA

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(2) INFORMATION FOR SEQ ID NO: 2138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2138:

TGTATTGTCA TTGTAGACGT GTGTAGCCAA ATCATAAGGG CATGTGATTT ACGCATCCAC

60

CTTCTCGGTT TGTACCGCAG TACTTAG

87

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(2) INFORMATION FOR SEQ ID NO: 2139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2139:

5 TTCACCGTTG CGCAACGTTT AAGTTTGAAG TTCGTTTGGC ATGTTGAAAT AAGCACCAGT 60
TACACCAAAA CGCCAG 77

(2) INFORMATION FOR SEQ ID NO: 2140:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2140:

20 ATCTTCTAAC ATTCACCTAG TAGCGTnATT TTTCGCTTAT AATGAAATGT TAAGCATATG 60
CGGGATTTAT ATTTTAAAGA GACCTTTAGA TACCATATAT ACCTAGGTTA TTGAAAATAT 120
GGATACCTTA TATAAGTGAT TTGCAATA 148

25 (2) INFORMATION FOR SEQ ID NO: 2141:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2141:

35 GCTGGCACAT AGATGATCGT CAAGTCGATC TCGCCAGTCT GAAGTCAAGA 50

(2) INFORMATION FOR SEQ ID NO: 2142:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2142:

TTGTTGTAAA TACTATCACT GTACATGGGT GCTATCAAAA TATTGTCAGT TCGTAAAATA 60

50 (2) INFORMATION FOR SEQ ID NO: 2143:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2143:

GTAGTATATC TTATTAATTG TATCATGAAG CAATTTAAAT ATCATGACAA TTTAGTTTGA 60
10 AAAACACACT TTGTGTTGAC GTTGTGTTTT ATGGGATATA GnATAGTAAG GAATGTAAAA 120
TGAAGGAGTG AATGC 135

(2) INFORMATION FOR SEQ ID NO: 2144:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2144:

25 TTTTAAGGTT TGAAGAAAAA AAGTTTTAAA AATTCAAGGA AACATTAAAT TAATTTA 57

(2) INFORMATION FOR SEQ ID NO: 2145:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 148 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2145:

TTTCGAAAGT TTGATAGTCC ACCTTACATT CTCCTACTAT TTTCTGATGT CCCAATACTT 60
TATATTATTT AAAGTAATAT AAAAGCAATC TCTTTTGAAG ACATGTTAAC CTAAATATTT 120
40 TTATATATAA TATATATATA AAATATAn 148

(2) INFORMATION FOR SEQ ID NO: 2146:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2146:

GTTAATACAA TACGGTTAAC AGCACCTTTA CGnTAGTTGC TTTnCTGCAn 50
55

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2147:
 AATCCCCTCT TTTCTCTATT TCCTAAATCA TAGAACTTTT AACAGTAAAA TTCAATCATT 60
 AATACATG 68

(2) INFORMATION FOR SEQ ID NO: 2148:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 92 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2148:
 AGGTCCATTT GTAATTTATA ATGTTGACTA ATAACATCTA CAGAATTTAA CGTTCCCAT 60
 CCTCGCCACT GATTGTAAAT AAACAAACCA TA 92

(2) INFORMATION FOR SEQ ID NO: 2149:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2149:
 ACCATCCATT AAATCAGGAT CTTCACTAAT AAGTGCTAAA TTAGCAGCGC CACGTTTAAC 60
 GTAATCCAT 69

(2) INFORMATION FOR SEQ ID NO: 2150:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2150:

TCAAAATATA TACGATCACC TTTCTGTAAA ATCACACTAT TTTTATTGTC CGCTTCTGGA 120
 TGTGTTTTAA AAAATTGTTG GCCAACTTCA CCTTTTAACG TGGCAAATTG ATAATTTCTT 180
 5 GGTAGGTCAT GTTGAATTAA CCAAATGACA TAGTTATAAC AATATATACA GTTTCATCA 240
 TAATATACGA TTGGCATAAT TTATTCGCTC CTTTAATAGT ACTTATAGTC ATTTTTCCTA 300
 ATTTAAAAAC ATTTAAACAA GGTGTGCTACT TGATAAGTCC TCGCGACACG AAATTGCCAT 360
 10 AAAATTTATT TTTCAGnTTh ATAT 384

(2) INFORMATION FOR SEQ ID NO: 2151:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2151:

TGTGTTTAT CACTATATTT TAAAAATAGT CTATAAGGCT TATCAGATGA AGTAGCTGCT 60
 25 GCGTAACAC CACCAGTAAA TGT 83

(2) INFORMATION FOR SEQ ID NO: 2152:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2152:

GTATTCGTAC ATTTTTCAGC AATTAACCAA GATGGTTACA AATCATTAGA AGAAGGTCAA 60
 40 GCTGTTGAGT TTA 73

(2) INFORMATION FOR SEQ ID NO: 2153:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2153:

CCCCCCTCCC CCCTCCCCnC CCCCCCCCCC CCCCCCCCCC GCCCCCCCCC 50
 55

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2154:
 TATTTTAGGC TTAGCATTGA TGATGTTGCT CATTTTCAAT AATATAGGAA TTATT

(2) INFORMATION FOR SEQ ID NO: 2155:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2155:
 ATGCTTGCTG ATATAATGTA ATAGCGTCGT GATAACGTTG CTGGCTTATA ATATACATTT
 GCGAGATT

(2) INFORMATION FOR SEQ ID NO: 2156:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2156:
 TAATCTTTGT CGTCGAAATA CAACTAACT TTTGAGTTTA ATGATGAAGG TACGCATTGT
 GTATCACT

(2) INFORMATION FOR SEQ ID NO: 2157:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2157:
 TCATTCATTT TCCTCTTTTC TTTTATTTAA AATGTTTCATG GTTGTTTCTC TTAATTCTGT

AGATGCTAAA TGGTCAAATT GAATAATTGT TTCTAGACTC ATTTCATAAA TTTCGAAAAA 180
 TAATTCTTCG GGATTACGTT TTTGTATTTT TCCAAATGTT TCATAAAGCA AATCAATTTT 240
 5 ATCAGCAACT GAAAGTATTT GGCCTTCTAA TGAATCATCT TTACCTTCTT GCAGTCGTTG 300
 CTTATAAACA TCTCTATATT GTAATGGAAT TTCTTCTTCA ATAAAGGTCT CTACCATTTT 360
 10 TTCTTCAACT TGCGAAAATA ATTTTnnTAA TTCACTACTC 400

(2) INFORMATION FOR SEQ ID NO: 2158:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2158:

TATTTTTTTC TTCTAGGCAG TGTTAATACT GCTTCAATTT GTTTTTTACT AAATTGATAT 60
 TTCTCTATGA TTGAATTAAT CAATTGATTG TCCATTTACT TAACCCACAC TTTTCTTAA 120
 25 ATTTACTCAT TTATTTTAAC ATATTCTAAA ATACTTCTAT TAAGATATGA TACTTAATGT 180
 AATTTTCACT TCCAAAACAT TTAACGAA TGATTAGGnC ATACTATATT nT 232

30 (2) INFORMATION FOR SEQ ID NO: 2159:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2159:

40 CCGTTTTTCC AAAAATTGA TCATAAACCC GTCCTTTTT TCATCATAAC AAAATAAGAA 60

(2) INFORMATION FOR SEQ ID NO: 2160:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2160:

CGATTTACTG CACGACACAT TGCCACATCC TGGATGGGCA ATCTTTTCTC TTACCCGTCT 60

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2161:

ATTAGTTGAA GTTTTTGAGC AATTGAAAGA TATTCAGGGT CAAATAAAAA CGACAAAAAA 60
AGAATATCAA CAGACCAACA AAGAACTTTC TGCTGTAGAT AAAGAAATTA GAAATATAGA 120
AAAAGACCTC AATGATACAA AAAAAGCACA AAATGAATAC GAAGAGAAAT TGTATCAAGC 180
ATATCGATAT ACCGAAAAAA TGAAAACACG TATTGATAGT TTGGCAACGC AAGAGGAAGA 240
ATATACTTAT TTTTTCATG GCGTCAAACA TATTTTGAAA GCTAAAAATA AAGAATTAAA 300
GGGTATTTAT GGTGCAGTTG CGGAAATTAT TGATGTGCCA TCTAAATTAA CTCAGGCAAT 360
TGAAACAGCA TTAGGTGCTT CATTACnACA TGTCATTGnA 400

(2) INFORMATION FOR SEQ ID NO: 2162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2162:

GTGCGTACCA TTGTAATCTT CGTAAACTGG GTAATTATTT TGTCTTTCTT CATCATAAAG 60
TAATAA 66

(2) INFORMATION FOR SEQ ID NO: 2163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2163:

AGAATGGTAA CATGGTAATA ATAAAATATA AACAGAATAC TAGTTAATAC ACTTTATACT 60
AGAAAAAGAT AT 72

(2) INFORMATION FOR SEQ ID NO: 2164:

(A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2164:

10 CGATAATCTG TTTTTTTAAA TCTGTTGCTG TTAGATTTAG CACCGATTCTG TTAACTTCA 60
 AATAATTTTT ATTACCTTTG GAAGAAAGTG GAACTATTGT AACTGTTTCT TTTCTTTTAT 120
 TGCTTTTGTT ATCTAATATT ACACAAAAT GATTACCAGA AAACCTCACTT CCAATATTAC 180
 15 TCCCTAGTTT TACATATACC ACTGTTCTC TACnATATGA TTTATAATAT CTTTnTTTAT 240
 TGCTTGTAAC ATCGCTATGT ATAGCAATTG GAATAAACT CTAGCCAATG AGGCATGTnT 300
 ATAACCTTCA TGTTTTTACT GTCGG 325

20

(2) INFORMATION FOR SEQ ID NO: 2165:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2165:

30 TAAACCCCTT TTGGGTAAAA AAGTTTGGA AAATTTCCCC GGGGGGAAAG GCCCCCAAAA 60
 AATTGTGCCC CTCCnCGGGG GAAAATTAAA ATTTCCCCC TTTTAAAGG GTTTCCCTT 120
 35 T 121

(2) INFORMATION FOR SEQ ID NO: 2166:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2166:

CGGACAGTTA AATGAAGTGT TCAATGAGCC CAGGATGTTG TAAATGGTTC GG 52

50 (2) INFORMATION FOR SEQ ID NO: 2167:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2167:

ATTACAGTAA AAAATGGATT AACATTACAA GCGTGTCTTG CTAGAGCAGC CAA 53

(2) INFORMATION FOR SEQ ID NO: 2168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2168:

AAAGATTATT TATTTGCAGT CATTAAATTGT GATTTAATAC GGTCAGCTTT GTTTGAATGT 60

ATTAAATTAC nTTGAGCAGC TTTGTCTACT AACTTAACTG CTAAGCTTAC TAAT 114

(2) INFORMATION FOR SEQ ID NO: 2169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2169:

AAGGAACCCC CCCCCCTTAA AATTTTTGGT GGTTTTAAAA AATTCCTTTG GATTTATTAC 60

CTTTATTCTTCT ATnATTTTCC GTTTGGATTT TCCTGGATTA AATTTCCCCA TTAAGCCATT 120

TCCGCTTCCC TTATTTTATn ATTTTCCAAA ATTTCCAAAG GTTCCATTTG GGATTTTGGC 180

AATCCTTTTT TATTAAAATG GCCTAAAAAT TTTTT 215

(2) INFORMATION FOR SEQ ID NO: 2170:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2170:

TATCGTTTTT AGAAATGGAT GTTCTCTCCA AAGATGATGG TATCTAACAT TATCTTATTG 60

GTATCATTAT GCAACnTTA CAAAACATTT ACGCAAGATG ATACATTATC CAAC 114

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2171:

ATCACAGATG AGATAACAGA TCCACTGTAA CTTTACAATA AATAAATGGT ATCATAATTA 60
ACACGTAAAT GGTTC 76

(2) INFORMATION FOR SEQ ID NO: 2172:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2172:

ATTATCACAA AATGTTGACA CGCAAAAAGT TGGTCAGTTA TCAATATGGT ATATAAATCT 60
GAGA 64

(2) INFORMATION FOR SEQ ID NO: 2173:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2173:

AAAGGCCAAC CAACCAAGG CCAAAATTAA CCGGCCAATT CCAAGGGGTT AATTAAACCC 60
G 61

(2) INFORMATION FOR SEQ ID NO: 2174:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2174:

CACCCCGCAC TCTCCCATCT TTTACCTACT GGCTTCTTTG CATTGCCCTG GCACCTCCGT 120
 CCTCAGCCTC CCAGGCTGTA TTCATTCATT CCCTTACTGA GCACGCACCA TACACCAAGC 180
 5 ACCATTCAAG GTGAACCAAGT CAAATGAAGG CCTGGCTCAT TTTAATGGGG GACAATGAGC 240
 ATTTTGTGA CAATTTTCATG GAGTGATGAG TGCTGTGAAG AACTAAACAG GTCAGGTGTA 300
 10 AGTGGCTCAT GCCTGTAATC TCAGCACTTT GGGAnGCCGA AGCAAGTGGA TCATTTAAGC 360
 CCAAGAGTCA AGACCAGCCT GGGGnnACAT AGTGAGAnTC 400

(2) INFORMATION FOR SEQ ID NO: 2175:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2175:

ATATCGTTTA AACCATCAAC AAGATTTTAT AGATGCAACT TTTACTGCGC TGAAATCAGA 60
 25 TAGAGCACGT TTAAGAAG TGCCAGTTCA TGTTGAACTT ATAAGTTATA TTTCTAAATC 120
 AAAATAAACT GCTATCTAAA ACGCAAAGTT GATCAAAATA TCGATTTTGT GTTTTTTATT 180
 30 GAGAAATTAT ATAGGAGTGT CAATCGATGA TTTATTGTGA ACAGAGCGTT TAATATTAAG 240
 AGACTGGCAT GAAGATGATC TGTTACCTTT TCAAAAAATG AATGCGAATT ATGACGTACG 300
 TAAATATTTT CCAAGTTTAT TGAGTTAnCG nCGTTCAGAA TTAGATATGA GACCTATGGA 360
 35 TGCGGTTATn AAAGATTATG GCCATTGGGA TTATTGCCnG 400

(2) INFORMATION FOR SEQ ID NO: 2176:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2176:

TAAATCAAGG AAAGACATTT TAAGGTACGA AGGTTGATAA CAAAAACCA ACAGATTTAG 60
 GGGTATCAGA G 71

50

(2) INFORMATION FOR SEQ ID NO: 2177:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2177:

GTTGAATTAG GCAGCACGAT TATTGATGCT GAACTGTTAG AGTCAGATAA G

51

10

(2) INFORMATION FOR SEQ ID NO: 2178:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2178:

TTAATTAATG GTATTACAT ATTCATAACC AAAGGATAAA ATAATTGTGA AATTATTCAC

60

A

61

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(2) INFORMATION FOR SEQ ID NO: 2179:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2179:

CATTTTACCA TGCAGCAAAT AATACAGGTG GTGCCGTTAA CAAACGTGA

50

(2) INFORMATION FOR SEQ ID NO: 2180:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 73 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2180:

GCCGAACGAA TCAAATACCA TACCTAATTG ACTGCAGGCA TGTCCATATA GTGCAGTTAA

60

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CTGTCTACAA GGC

73

(2) INFORMATION FOR SEQ ID NO: 2181:

55

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2181:

TACTTTTGGC GATATTCGGT ATCGTTATTA CAGTTATTTT ATATGCAATT AAATTGCCGG 60
 10 GTTCTATCTT TATCGGTATG ATCATCACAG CAATCGTTGG TATGTTCACT GGATTGATTC 120
 AAATGCCATC TGGTATTGTG GGTAAGATTC CAAGTATTGA ACCAACGTTT GGTGCTGCAT 180
 TTGAAGCGTT TAAAGACCCA AGTCAATTAT TAACGATACA GTTCTTAATT GTTATTTTAA 240
 15 CGTTCTTATT TATTGATTC TTTGATACAG CTGGAACATT AGAAGCGGTT GCAnCnCAng 300
 C 301

20

(2) INFORMATION FOR SEQ ID NO: 2182:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2182:

30 TTGATTCGCC TTGGCCAGAA TTACTTTTGT TTTGGGCGTC ATTGCAAGTT TCTA 54

(2) INFORMATION FOR SEQ ID NO: 2183:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2183:

TTAGTnACAT TGGGACATTT AACTGATCCA CAGTACTTTT TGGCGATATT CGGTATCGTT 60
 45 ATTACGTTAT TATTGCATAA TGCGGTCAC TACGAGACACC GCACTGAGTC CGATATCA 118

(2) INFORMATION FOR SEQ ID NO: 2184:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

AGATAGTTAT ATAAAGATTT CATCTTCTGT ATTACATTGA TATTTT TAGG TCCCTGTATA 60
 TAAAAATCAT ATGCCTCATC AACACATCA CTTTATTTT TGATTGCAAT TTGATGTAAT 120
 5 ATCTTTTGAC TAAAAACACG ATTAATCATA TTTCTATTAT CCATAGCTAC GCACCTCCTT 180
 CAACATACAT TTAATGCTTA TCCTGTTAAT ATTATAAnCn ATTTTAAATG CCTATAGACA 240
 10 TTATTTCTAT ACACATACGA TTATnAAATT GTATTGAAAC CAAATGATGG TTGCCAAACA 300
 CAT 303

(2) INFORMATION FOR SEQ ID NO: 2185:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2185:

25 CCGGGGTTTT GGTAAACCC TCCCAAnATT TTTTnTAAGC CCAACCTTG GAAAAACCCA 60
 GGCCACCCGT TGGAATTTTT AAGCCTTGGA TTAATCCGGT TTGGTTAACC 110

(2) INFORMATION FOR SEQ ID NO: 2186:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 86 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2186:

40 CCTATATTGT CACCCAACCTT CATTACGGCA CCTTTACCGA AAGATTCTC CATATTTTnA 60
 ATTACTGTAT CTAAAGCTTT TTGACG 86

(2) INFORMATION FOR SEQ ID NO: 2187:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2187:

55 TTTGCTAGAA AACATACCAC ATTTGCCAAT TATATTATTT ATTCTGATGT TTATTTTCGG 60

TATTTAGAGG TGATAAAATT TGTCAACTAT TACAAAGACT AAAATAAAAA TCTTTATTAA 180
 TTATTTTATT GGTATATTAG CCTTGGCGTT TGCTGCTTAT ATATTATTTA AATAAAGGTT 240
 5 AGAGTGAAAC GTGTTTATGA ACTAGACGTT CTAGTATAGT TACTACAGCT TTAGTCAGAA 300
 GGTATCATTG ATAAGATCAT ATTAAATCAA AGAGGCATTG ATATACACTA AAAAGAGGCA 360
 AGATTACCTG CCTCTTTTTA GTnATTAAAT ATACGTGTTA 400

10 (2) INFORMATION FOR SEQ ID NO: 2188:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2188:

TTTTATAAAA TATCAGACAT TTTTGnTCAA CATACATCTC TTTCGATGTT TCTAATACTT 60
 TATCATTAAAC CATTACACCT TAAAGTTATG ATGTGGCATG TTTTCTTATA TTCATAACAT 120
 25 CAATTTTATC A 131

(2) INFORMATION FOR SEQ ID NO: 2189:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 85 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2189:

CGTAAATAT TTTGATTTAA AATGGAGGGT ATTAATATGA AAAGGTTTAT GTAAATCTA 60
 40 GGGGTATTCC AATATTATAA GGCAC 85

(2) INFORMATION FOR SEQ ID NO: 2190:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2190:

CCCGAGGAAT ACATGGCATT AAATACACGT TTAATATTTA TAAAGGTGAC TTAATTTTGT 60
 55

ATAATTGTTT ATCAGTGATA AAATATTTGC AATAAGAAGA GAATGACTAA ATAATCTTAA 180

TTTTCAGAnA AGTAATTGTA ACCTTACTGG TCTTATGGTA ATAn 224

5 (2) INFORMATION FOR SEQ ID NO: 2191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2191:

AGCTTTTGTA GTTTTCTTAA GCACACCGGC GATTTGATTA TTACATAAAG GATTCCCTTT 60

TTTTGTTGTG AATATGAACC CTCTGTCAAC ATAGCTCGAA TTCCATCTTT TCAACATTTT 120

20 GTTTTCCAGT ATTATCTTTT TAAAAATTTT TACGGTTCTA GAATTGATGC TGATACTTCT 180

TTTTGAACTT ATAGTCTTTG TAGTGTCTTT GTATCCGAAT CCTTTCTCGT ATTTAATGCG 240

GTGAATTGTA CCTGTTATAT TGATAGTnTT GTTTAATAAA TCTATATCTT TTTCCTGCAG 300

25 TGCTTGTAAGT TCTCCTATGC GCATACCACT TAAAGCCTGT ACTTCTAAGA TGCTGGCAAT 360

TAAAATGCGA TTTCGCTTTT GTAACCTATT ATCATTTAGT 400

(2) INFORMATION FOR SEQ ID NO: 2192:

30 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2192:

40 GACGACTGAG AGGCCGTTGA ATTTGACGTT GCCATATnTT CAAATTTAAC 50

(2) INFORMATION FOR SEQ ID NO: 2193:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2193:

GTGTGTTTCA TATCAAAACA CCGTAGAATA AACAATGAAT GGAATTACTT TTGCAATGAT 60

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2194:

10

CCAGTCACTG ACTACGTCTT CCTCGGTGCT GCGGGTGGAG CCATTCCCTT ATTACC

56

- (2) INFORMATION FOR SEQ ID NO: 2195:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2195:

GTAGGGAAAG GAAAACTGC TTCCATTGGG AAATGTTAAA CCTTGTCCT TGGTGATGCC

60

25

ATTGGATTT

69

- (2) INFORMATION FOR SEQ ID NO: 2196:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2196:

ATATGACACT ATATTTTATA AACATACATT TAATGATTCA TTATACAATT GCCAA

55

40

- (2) INFORMATION FOR SEQ ID NO: 2197:

45

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2197:

GCCCTAGTTC AATCATATAA CCATCTTTAC GATACGATTG AATCTTTCCC CCCGGACGAT

60

TCGATGCTTC A

71

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2198:

AGTAGCACAA CAGCCATGCG GAGACAGAGA ATCGTTAGAG ATTAATGGAG ATCA

54

(2) INFORMATION FOR SEQ ID NO: 2199:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2199:

GGCGGTTTTA TATTTATCGT TGCAGTTATG CAAATTGTAC TTGGTAGAAG TATAGATTCT 60
 CGTGATTCTGA AAAAAGTACT TTTAACGGGA TTGGGAATAG TAATCATATC TAGCTTTATT 120
 TGTGCAGTGA CACATAACTT TATATTATTT GCTATATCAA GGTTATTTCA AGCAATTGGT 180
 TGCGGAATTA TTCCTCTCGT GACTTTAACT TTATTAGCCA AACTAAGTAC AGATAATGGT 240
 AGAGCTCAAG CTATGGCGAA CTATCAAATA TTTTATCAT GTGCACCAGC TTTGGCACCA 300
 ATCTTAGGGA GTACTTTAGG TGGCAAGATG GGGATATATT GGTATTTTAG TTTTGTGGCT 360
 CGTTATATCT ATCGGTATTA TTTTGGATA nCnTnTTAA 400

(2) INFORMATION FOR SEQ ID NO: 2200:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2200:

GGATATGCGA TGGATGACGC ATTGCTATAT CGGCAATTGn GAAGCTGCTG

50

(2) INFORMATION FOR SEQ ID NO: 2201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2201:

ATCGAATATC ACTACTATCT CTnTTnAAGT ATCTACAATC TCTCCAATCT

50

5

(2) INFORMATION FOR SEQ ID NO: 2202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2202:

15

TCGACAATCC TAATGCAATT GCTTCATGTG GntGTGGTAG TTCATATTAG AACTGCAAAA 60

GTTGCAGGTG ATCCTGAAAA TTGCTAATAA AATAACTTTT TAATGGTTAA CCCAATTTTT 120

20

GGGATACAAA TTGATATCAA TAACGATTAA GGACATATTT GATTATGTCC TATTTTTGCG 180

TAAAGATATT TTGTTTTATT AAAAAGCTTA TTGAAAATTA AGAATCTGAC TATAAATAGT 240

ATTTTAAATG ATCGTGATAG CGGATACATT TTTAATCGAA ATCAGGCTAC GAAAAAATTA 300

25

ATTAATTTTT TCACAATCTG ACTGAATCTT GCTTGAAAAT ATAACATAAA AGCTATAGAA 360

TTAGTATTGG ATTAAAAATG TCTTTTTTGT GAACATCACA 400

30

(2) INFORMATION FOR SEQ ID NO: 2203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2203:

40

GCGTTGTCCT TTTCGTGACA TGAAACAATG TGGAAAACAT AATTAAATnn AGGGAAAGTG 60

TGAATAGTTA AAAAATTAGT ATTGTGTTAT AAAAAATAAT TAATACTGTT AGGATTTTCAT 120

TAACTAACTT AACGTTGGTT CAAAAATAGT TAAAAAGAGG TTAATTCATA GCGCAGTATC 180

45

TCACTTATAT AATGATAGTA GATTGTTTCG ATTACGTAAT TGAATTAATC ATATAAAAAT 240

ATATTAAGAC AAATTTATAA ATAGATTGGG AGAnTAGTAC TGTGAAATTA AAAACGTTAG 300

CTAAAGCAAC ATTGGCATTG GGCTTATTAA CTA CTGTTGTG GATTACATCA GAAGGCCAAG 360

50

CAGTTCAAGC AAAAGAAAAG CAAGAGGGnG TACCACCATT 400

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2204:

10

GTTATTTTGT ATGTTAGTC TTAAATAAT ATATAGATAT TAAATATTTA TTTTACGAAT 60
 TGTTAAGTAA AGAAAAATA TTAATCAATC CGGGTTACAT TTATGGCACT AAAGAAAAGA 120
 GTATAAGGCT ATCTTT 136

15

(2) INFORMATION FOR SEQ ID NO: 2205:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2205:

30

TTTTATTTTT TCGCAATGAA AAACAATCTT TCTGCATCTT CATTATGTTT ATCTATATTA 60
 AAATCAGTAA ATGTTTCAAC ATGTTTAAAA CCAACTTGAG CTAACCAAGA CAAATATGTC 120
 TTTTCATCAA ATGTTCTCTG AAAATGAGAC TCATCAAATC TTGAATATGT TTCATCTTCA 180
 TGTGCAATGA AAAATGTCAT ATCATGATAA ACACTTAAAG GTAAATCTCC TTGCACAGCA 240
 TCCCATGCTA AAAAAATGTC CCCTTTATCA TCAATATAAC TTTGATTATT AAACAAAGTC 300
 ATCATTTTAT AAACAGTATG TACATCAGAA ATAAATACAC CTGAATCAGT CAGATGATGA 360
 TAAACATTGA TGAATGTTTC AATCACTGCA GTTTCATCTT 400

35

40

(2) INFORMATION FOR SEQ ID NO: 2206:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2206:

50

TTGAATATCA TATAAAAACA TCAGGTCAA AGTTGACTAC TCTTAATAAT ATAAAAATAA 60
 GAATTAAAAA CATTAAACGA TACTGCTCTG AGAACTTGCT TTTAAACAAA CTTGATACAA 120

55

GTCAACTCGG AGATATGAAA GGAGCnATTA AATATGCAGT TAAATTTTAC AATTATCCAA 240
 ATGAATATTT GTTAACTAAT GTCAAAATTC CTAAAAGAAG AnAAACAATA GAGGATATCG 300
 5 AAAAAGATGA ATCTAAATG GTACCACTAT TTAGAAATGG AACCAAGTCC TACnGATACG 360
 TGATCATATA CTAATGGAT 379

(2) INFORMATION FOR SEQ ID NO: 2207:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2207:

20 CATCTTGGGA CGTTTTAAAA AGTAACGTAG CGAAGACTAT TGAACAACA ATGAGAACCA 60
 ATGCTAGAAG GATCAAAAAG TATTTTAAAA ATTTATTCAT GATTGATGCT CCTATATTAA 120
 ATTTnTGTTA AATCATA 137

25 (2) INFORMATION FOR SEQ ID NO: 2208:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2208:

35 GCGCCGCTCT GTTCATTTTA CCTAAATCCA ACGTTTCAGG AATAGATGTT TTCAAACCAC 60
 TTTGAAATGG AT 72

40 (2) INFORMATION FOR SEQ ID NO: 2209:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2209:

50 ATGTAGCAAC TAAAGATGAT AGTGGATAGC GACACGGTCA ATAACTGCC TA 52

(2) INFORMATION FOR SEQ ID NO: 2210:

55

(A) LENGTH: 206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2210:

10 TTTTTTATGT TCTTTTTTAA TAAGAGGGAA GTGAAGTTGT ATAAAAATGT ATTAAATATG 60
 CACTTTTTAT ACATTAAACGA TTCATATATG TCTATTATGT ACCAAATTTA TAATTTGTAT 120
 AATTTTCGAA CTGGTTAAAT TCGAAAAATA TCACTAATAT ATnTAGATCG ATGTGTAACA 180
 15 TTACGTTCTA nTAATTTAAT GTTGCA 206

(2) INFORMATION FOR SEQ ID NO: 2211:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2211:

ACGATGTATT TTGATATCGT TACCAAAGTC TTTTAATAAC TCATTTTCAT CTAAATAAAT 60

30 (2) INFORMATION FOR SEQ ID NO: 2212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2212:

40 TGATAAGGTT TGTCCCATCG CTATTTGAAA TGATGCATTG TAAAAAACTA TCATTTGTTG 60
 GTAATATCTT AGTTCGATGA CTTTCTTTCC AATCTTTCCG TGTCATAGAG ACAAGATTTT 120
 TTGTAGCTAT CTTAGTTGCT TCTTGAATGT TCATTTGTTA TTCCTCCTTT TAAGATGTTT 180
 45 GTnTTTCTTT AAATGCTAAA ATAATTGATT TCTTTTTATC ATTCGTGAAT ACGAAATTTT 240
 CGTATTCATT ACCTAAAAAA ATATCATCAT ATTTAACATT AAAAGCACTC ATATACTTAG 300
 50 AAAGTAAACT AACnTTAATG GnTGTAGAGT C 331

(2) INFORMATION FOR SEQ ID NO: 2213:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 61 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2213:

AGCATAAACC AAAAGATGCG GATATACTTG AACGCGTCAA AGATATACTT AATAAAAAAG 60

10

A 61

(2) INFORMATION FOR SEQ ID NO: 2214:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2214:

TCTATTTGAG TTTACATTTG ATTAAATGAA TGACAATTAT ATGAACCTGA CTTGGT 56

25

(2) INFORMATION FOR SEQ ID NO: 2215:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2215:

35

ATACCACTAC TATACAGTTA AATTAATATA CGTTAAACT TTAATCCGAT ACATTGGTTA 60

AAATGATGTT CCTCGCTGGT GGATCGAGAC ATACTTCGCT CTGACTTCTT TAGTCAGTTT 120

TTTTTCAGCT TTTTAGGTGT AATCACTGAC TTTGTTACAT CACGTCAAAT TTACAGTCGC 180

40

TATTATCTTA ACTTATCnAC GCTTATCACA CATCAATTCA GATATTATAT TGCATTGGCG 240

nCTATCACTT TGAACCTGCT GTGACTGGAA CTACTGGCTG TCAnGAGCGA GGGCTGATAA 300

TGAGCATAAA GCAACATATA AGTAATACGG CCGAATATGT AAATTCGGCA GCTTTAGGCA 360

45

ATGCTGCCCG GGCATGACTA GnACATTCA AAGAAGCTCA 400

(2) INFORMATION FOR SEQ ID NO: 2216:

(i) SEQUENCE CHARACTERISTICS:

50

(A) LENGTH: 133 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2216:

TTTTTAAAAA AGGGGTTAAC CAAAGTTTGT GAACCCCAA AAATTCCGGA GTTAAAAAAA 60
 5 CCCCCAAAAA TTAAATTAAC CGGTTATTCC GTTCCAGGAG CCAAATTTT ATGGTTCCAA 120
 TTnCCAAAGT GGG 133

(2) INFORMATION FOR SEQ ID NO: 2217:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2217:

TACTCGTACC ATTAACCACT CTGATTAAACC ACAATACTAA GGTATTCAAT ACATCACTGA 60
 20 CATC 64

(2) INFORMATION FOR SEQ ID NO: 2218:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2218:

TATTCTATAG AATATGGATA ACGTTTAAACA TGATGTAGAG TATTCATCAT TGTAACACGT 60
 35 CAATTTGATA TGTGAGATTA AC 82

(2) INFORMATION FOR SEQ ID NO: 2219:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2219:

TTTGACGCAA TGATTTAGCT GTAAATATGC AATCTAAAGG AAAGTACCAC TTATGAGATG 60
 50 TATTAAAACG 70

(2) INFORMATION FOR SEQ ID NO: 2220:

(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2220:

10 AAAAAATTACC CCAAAGAATT GAAAATTTGT TGTTTGGGTT ACCGGGTTTA AGATTAATCC 60
GGTTGA 66

(2) INFORMATION FOR SEQ ID NO: 2221:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2221:

GATCGCAACC AAAATAATGG TCTTCCTGGA TTATTACTTT ACCAGCTGGC ATAC 54

25

(2) INFORMATION FOR SEQ ID NO: 2222:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2222:

35 GTGTTGCTAC AGCTAnCATT TCATATTTAA CGnGTTGTGG TATTTCTAAA 50

(2) INFORMATION FOR SEQ ID NO: 2223:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2223:

AATGGGGGnA CCCAGCnTGA GTTATGTCAT CATATCGGTA TGTGATACAT 50

50

(2) INFORMATION FOR SEQ ID NO: 2224:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2224:

GTAGATGCGC CCTCATATGG ACAAAGATAA AGTATCAGCA GATTGGACGC TTTA

54

10

(2) INFORMATION FOR SEQ ID NO: 2225:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2225:

20

CGAGACTTCA CTTTGACTAA ACGCGTTAAG AATTTAGATT ATGCTTACGA TGAAGAAGAA

60

TTA

63

(2) INFORMATION FOR SEQ ID NO: 2226:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2226:

35

TGGCCATTTT TAATGGGGGG AAACCTTAAA AAGGGGTTTT TAATTTTAAA CCAAG

55

(2) INFORMATION FOR SEQ ID NO: 2227:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 131 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2227:

TCCATTTGGT TGCCTTCTTT AAATAAACCT TGGATTATGC CTTTCCTCCG GTTAATTAAT

60

GGGACCAGGG GCCAAAAATA CCCCTTTTA AATATAATT CCCAAAATCC ATAGTTAAAT

120

50

AATCCATTG C

131

(2) INFORMATION FOR SEQ ID NO: 2228:

55

(A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2228:

10 CCATCTGTGC TTCGTTAGGC GCTTTCGGCA TCACGGTGAT GGTTCGCGAC AGATCCGCCA 60
 TCCGGCTGAA TGGGAAGCCC GCGTTAⁿAAA GGCGCGTAGA TCCGGCATCG GGATGAAGTG 120
 GTAATACTTC GAGAAGTCGA TGGTGGAGTC GTCACCAATC ACCACATGAT TCTGCACCGG 180
 15 CTGGAAGGTA ATACAGTTAT CCACCGAACC GCCCGGCATC GGGTTCATAT ACTCAAAGTC 240
 GAAGCGCACT GGⁿTTTGGTC GCGCCCAGTT TCAGCGCCGG AATAGAGACA TCTGTTTTGC 300
 CATCCAGCAA ACCTTGTAAT ACCGGAnTCC GCAGCAGCAG GCGGTTTCGC 350

20

(2) INFORMATION FOR SEQ ID NO: 2229:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2229:

30

AACTAAAAAT ACTATATAAA AAAGGTTGTT ATAATTTAAT GGATATAAAT AAAAACGA 58

(2) INFORMATION FOR SEQ ID NO: 2230:

35

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2230:

45

GGGCGAAAGC TGGACGGAGC CAACGTCGCG TGAGTGGATG GAAGGTTCTT 50

(2) INFORMATION FOR SEQ ID NO: 2231:

50

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

AGCCATACGT GGTAAGCACA TGCTAAATTT GCCAGCCTGA AAATGTTTAG

50

(2) INFORMATION FOR SEQ ID NO: 2232:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2232:

15 TGTATCATTT TGGCAAAATC ATAATCTTTA TCGTCGAATA CAACTACTTT TAAGTTTAAT 60
 GATGAAGGTA CGCATTGTGT AATCACTTCA TCTAACTTTT TTAAATCAGG TGTTCATAGTT 120
 GAACTTGGnG GT 132

20 (2) INFORMATION FOR SEQ ID NO: 2233:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2233:

30 GATCTTGAAG CAGTTGAAAC ATATGTATCA GATGCATTAA GACAAGTACA CTTACAATCA 60
 GACATTTTTTG CTGTATCA 78

35 (2) INFORMATION FOR SEQ ID NO: 2234:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2234:

45 TTTAGGCACA GACGGTAATA AGCTACAATT TTCATAAAAT CATCTCCTTn 50

(2) INFORMATION FOR SEQ ID NO: 2235:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2235:

ATCCTGGAAA ATCTGGTAAG ATATCTTGGA AATAACTAAT ACCAATTCCT AAAA 54

5 (2) INFORMATION FOR SEQ ID NO: 2236:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2236:

15 GGGTGATGGT CATTGACAAA GTCAACTTGT GATAAGCCAT GGATATTTTT CGTT 54

(2) INFORMATION FOR SEQ ID NO: 2237:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2237:

TTATTTACTT TAAATTTCTC AATCTACAGT GTAATCTTAT TTCITTATTAT 50

30 (2) INFORMATION FOR SEQ ID NO: 2238:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

35 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2238:

40 CCTTAATGGG TTTTGGGGGG GGGCCCCCCC GGCCCAAAAC CTTGGCCCA ATTGGTTCCT 60

GGGTAAAGGA AAAA 74

45 (2) INFORMATION FOR SEQ ID NO: 2239:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 base pairs

(B) TYPE: nucleic acid

50 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

CCACCCATGG CGCTTGACAA AATATGGATG GAACATAACC ACACCGTCCA AGTTCACTGT 60
TAGCACCGTG T 71

5 (2) INFORMATION FOR SEQ ID NO: 2240:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2240:

CAGCTAGGTA GTTAGGGATT CGACTCGTAA AACGGATTAA TAGGTTTTAT AAGAAGGGGG 60
TTTG 64

20 (2) INFORMATION FOR SEQ ID NO: 2241:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2241:

30 CTTGACACGT ACATCTAATA CGACAGTCTG TCGGTTTAAA ACCTTTTGGG TCAAAC TG 58

(2) INFORMATION FOR SEQ ID NO: 2242:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2242:

GACTCATCAC CGnTTGTAA GAnATACAAT TTATTACCCA GCAntTAACA 50

45 (2) INFORMATION FOR SEQ ID NO: 2243:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

AAATTTGGAT TGGTTGGAAA TTTACAGTTA AAATTTAAAG GGTGGATGGA AAAATTTTAG 60
GAACTTCTAA G 71

5 (2) INFORMATION FOR SEQ ID NO: 2244:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2244:

GGGGGCCCCCT TGGGGGTTTG GGTTTTGGGG GGCCCCCCTT TTAAAAAnTT 50

(2) INFORMATION FOR SEQ ID NO: 2245:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2245:

TTATAATTTT TGAAATAGA AGAGGGAAGC CTAAATTAC CAAATGGATT TA 52

30

(2) INFORMATION FOR SEQ ID NO: 2246:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2246:

ATTAGTTGAA AAGTACAATA TTCCGCAAGT TACCAATCGA TACAGGTATT ACAAG 55

(2) INFORMATION FOR SEQ ID NO: 2247:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2247:

55

(2) INFORMATION FOR SEQ ID NO: 2248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2248:

GGGAAGGTAA AACTTCCTGC TTTTATTATA AGTATTCATA CTCTATTGCT ATATTAGTAG 60
 AAACCGTAAA ATCAGTCATT CACATACATT nTGAAACATC TAAATAG 107

(2) INFORMATION FOR SEQ ID NO: 2249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2249:

GTTGGATACC TGnAACTAAA TAACTATTCT TTAAAAGTTA AAAACCAACC ACTAGTGGCC 60
 ATTGGGGATT AAAATTCCAA CCTGGGCCGG TCCATCCCCA TGGTGGGTAA AATGGGGGAG 120
 GGAAAATCCT TATTAGCCAA AGGATTCCTT ACCTAATAAT AGGGGGAA 168

(2) INFORMATION FOR SEQ ID NO: 2250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2250:

TTTAGTTGTG ACATACTGAG AACTGTAGTA CTTAGTGCnA TACCAAAGGG 50

(2) INFORMATION FOR SEQ ID NO: 2251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GCAGAACATA CCACGTGTCG CTGATTACCA ATACAGTAGA TCAAGATGGA CTCGATTGC

59

(2) INFORMATION FOR SEQ ID NO: 2252:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2252:

15

GTTTGTGTTT TAATTTTAAG GGGAAGGGAT TTTTITACCA AATGGGAATT TT

52

(2) INFORMATION FOR SEQ ID NO: 2253:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2253:

AGTGTAATTA GAAAGGCAAG TACACCTGTT TAAAGTTTAT CTTCTAAGAT TTGTTTACTT

60

30

TAGAACTATA GCAGTTAATC

80

(2) INFORMATION FOR SEQ ID NO: 2254:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2254:

GTAAATGACA GAGGAAATAT AACAAATGATT AATAATGTTA CAGCATTTAC TGCAAATATC

60

45

TACTAT

66

(2) INFORMATION FOR SEQ ID NO: 2255:

50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

55

ACATGTGTTA ACTCTTTGGC AATATATCCT GTTCTTCTT CTAATTCACG

50

(2) INFORMATION FOR SEQ ID NO: 2256:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

10

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2256:

15

AATCTTTTAT AGGAAAGAAA GAAGAAGATG TTATCAGTTG CGATTATCGG CCCAGGCGCT

60

GTCGGTACA

69

(2) INFORMATION FOR SEQ ID NO: 2257:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2257:

30

TAGCGGGAGA TAGAAAAACC ATTCCGCATT AGCTTTGGTC AAGTTGGGAA TGGGTAAAAA

60

AATA

64

(2) INFORMATION FOR SEQ ID NO: 2258:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2258:

45

GGTTAAGGTA TGGCGAAATA TCTCCAACAA CACTTCAAAA GGTTCAGAA AATAGAAGTC

60

GACTGAACAA TGTCATTAC ATGTGTGCGT CATGCACACC nTATGT

106

(2) INFORMATION FOR SEQ ID NO: 2259:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

55

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2259:

CGGAATAACT GACTATGTAT CATTTGATGT TATTAACATC AATATTTTGT GTTAAATGAT 60
5 ATGCTAGAAA TAAAGCATA 79

(2) INFORMATION FOR SEQ ID NO: 2260:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2260:

GCTGGnTGTT AnTGGCAGAG CATGTGAGCT GGATAATCAG TTGGAGAGGC 50

(2) INFORMATION FOR SEQ ID NO: 2261:

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2261:

nCCATTAATG ACCGAGATTA GTGAGCATGC ACAAATTGTT ATGGTAGGAT 50

(2) INFORMATION FOR SEQ ID NO: 2262:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2262:

45 AATGAACCAC ATAATGACAA CTGAATGAC AATATGAATA TGATGTCAAC A 51

(2) INFORMATION FOR SEQ ID NO: 2263:

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

CATTAGGTGC TTATATAAAT TACTTTGTGG TGGCTCCAAA ACTTCGGGTT AAAAC

55

(2) INFORMATION FOR SEQ ID NO: 2264:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2264:

15

TTTCnTCCCC CCCCCGGGGT TTTTGGTCC CTTTTTTTTT TTAAATTTC

50

(2) INFORMATION FOR SEQ ID NO: 2265:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2265:

TCATTCATAG AGGTGTAAAG ACATAAGGGG AGCTTAACTG CGAGGACCTA CA

52

30

(2) INFORMATION FOR SEQ ID NO: 2266:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2266:

AGATGATGCA ATAATGGTGC AGTATAGAAG TACTGAGCAA TGCAAATTTT AGACG

55

(2) INFORMATION FOR SEQ ID NO: 2267:

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2267:

GTTTCATCACA TTTATTACAT TCAGCGTTGG AATCAGTACT GGGTTATCAT G

55

51

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2268:

CTGTTGACAA CAAATTAAAA ATGACAACAT GTCGTAGTTA TAGTTAATTG ATTG 54

(2) INFORMATION FOR SEQ ID NO: 2269:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2269:

AACCAAAAAG AAAGCAAGGT CAAGGAAATT TCAGCGnGAC GTATCTTTAG TTTTGAATAA 60
 GCATATTAAT ATGGTGATAA TATGCAAGAn AACCTGTTTA TTCGATTCAA TGAAATTATA 120
 TTATTAATAT ACTTAATCAG TATCATTGTC TATTTTTIATG ATTTTGTACA AAAAAGTCAT 180
 AAGATTAGAA GTTTAGGCAT ATATTTIATTG GGGATTGTTT GGGTTTTACA AACAACTCTCT 240
 TTATCTATTT TTATTATACA AACTAGACAT ATTCCATTAG GGnCTATTTC AGATGTATTC 300
 TATACTTTAA GT 312

(2) INFORMATION FOR SEQ ID NO: 2270:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2270:

GTTGATGGAT TCTCTTGTT TGGTGTAGTC ACAATTTCTG AACTGGCCCT TGTTTACG 58

(2) INFORMATION FOR SEQ ID NO: 2271:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2271:

CGTTCAGACG CTAAATCAGG CACCAGGTTG TACAATTGTC CTGGTTCTTC

50

(2) INFORMATION FOR SEQ ID NO: 2272:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2272:

CAGGTGTTGG TAAACATTT GAGATGCTTT CAAATGCCAT TGAATATTT CAAAGTAA

58

(2) INFORMATION FOR SEQ ID NO: 2273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2273:

TTATAAATTG GTGTAACAAT TTCATACACA TGATCATTCT TTGATTGAGG TAAAAATGAT

60

TCTACTAAAC GTACACGTTT ATGCTTCTTA TATTCTTTCA TCAATAAATA TCTATGATTA

120

GCTAATGATA AATTTAGTAG AAGCTTGTTA TCTCCATAAA CTAAATTCAC GATATTAGGT

180

ATATTGAATT GTTCTTGATA TTTCAAAAAT TGTGATCCC ATTCTTCATT TTTAGGTAAA

240

GGTAATACCA TCTCGTTAAT TTTCCAATAT GCTGGTTTAA GAATGACATT TTTATATCTG

300

ATTTCGTGGTG AATAACTAAA TGAATCAATA CTCACATCAT TCATAGGTTC AATGCATTTC

360

ACAGATTCCA TTGAAATTTT TCGTAACAAT CGATATnAAT

400

(2) INFORMATION FOR SEQ ID NO: 2274:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2274:

GGGTACAAAT TTGTnGATGA TAGAAAAGTT CGTATCGCTA GAAAGTCTGG

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2275:
TGATTTACCA GTTGATTACG ACAAAGAAGA ATTTTCAAGA ATTGTTGAAG CATCAAAACG
CATT
CATT

(2) INFORMATION FOR SEQ ID NO: 2276:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2276:
ATGGCGTTCC ACCAGCAGTC AATAATCCTG TTGGGATAAA TGCCAATACT GTCGA

(2) INFORMATION FOR SEQ ID NO: 2277:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2277:
TAATAAATCA CGTGCAATTA CGCTCACTAG CTTTCATCTC CTCATTTTTG CTTTTCAAAT
TTATTAAGTA TGAATA

(2) INFORMATION FOR SEQ ID NO: 2278:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2278:
GTGGCTTTGT CTGTGTTATT GTAGTTTTGT TTCGCTGCGT CCAGCTTTGC TGCTTTTCCC

(2) INFORMATION FOR SEQ ID NO: 2279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2279:

TTAAGTGCCA AAGTCCTTGG TAGCCAGAAT GAACCACCAA CCTCCATTTT TCCAAAAATG 60
 GTCTTACCT 69

(2) INFORMATION FOR SEQ ID NO: 2280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2280:

GGATGGAATT GGGTTAAGAA TAAAAAAGGT AATAATTGAG TTTATGATAA TAATAATAAT 60
 ATTGAGA 67

(2) INFORMATION FOR SEQ ID NO: 2281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2281:

TTGTTACTTC GGCACGGATA AATCCACGTT CAAAATCAGT ATGAATGATA CCAGCACATT 60
 GAGGTGCAGT CATACC 76

(2) INFORMATION FOR SEQ ID NO: 2282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AACCCAGAAG ACTTATTATT AGAATCTTAA TCCACAACAC AAAATAGTTT ACTATTCCTA 60
 AAAGCGGGAT TAAATCAATA ACAAACAGCA GTAAGATTAT TTCCTAGTCG AAATATCTTA 120
 5 CTGCTGTACT TTATTn 137

(2) INFORMATION FOR SEQ ID NO: 2283:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2283:

ACAAAGATTT ACTATTTAAC TAATTTATAT GAAGAATAGC TTTCCTAAT AA 52

(2) INFORMATION FOR SEQ ID NO: 2284:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2284:

ACTCCTGCAT ATCACAATA GATTAAATAT ACATCAAACA GATATAGTAA A 51

(2) INFORMATION FOR SEQ ID NO: 2285:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2285:

CTAACATGTG TGAACGATAT GCAAATTCAA TATCTCATTC ACGCTTTGCA CTTTATTACT 60
 ACAATCAACG TAACTAT 77

(2) INFORMATION FOR SEQ ID NO: 2286:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2286:

AAACCTGTAT TTTTAATAAA CAATCGCTTG GACCTATTCA CTGCAGCTCT TCTGGGAC 58

(2) INFORMATION FOR SEQ ID NO: 2287:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 204 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2287:

AATTCATAAA ACCAATAAAT AAGAATTTTA TAGTAAAAGG AAATGGAnTA GAGTTGGCAG 60

ACTTATACAA TATTAAAAAC AAAGAGCTTT TCACGATTAA AAGAGGAATT AATACATCTT 120

TATCTCTTTA TAGTCTAGAA CAGGAATATA ATAACAATTA ACGCCTTAAA ATATCCAGAA 180

TCATATAATT TTGAAGAATT AATA 204

(2) INFORMATION FOR SEQ ID NO: 2288:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2288:

GCTCGTAAGG CGTCAACTGT GGCCTTGGGT GCTACATGTA AAGGTTACTT 50

(2) INFORMATION FOR SEQ ID NO: 2289:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2289:

TCGCTTCGGT GGTAAAAATG TCGTGGAGGT CCCGTTGCAG ATGGTTTTAA ACG 53

(2) INFORMATION FOR SEQ ID NO: 2290:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2290:

TTGGAGGTCA ATGTTCCGGCG TAATCTTCAA TGTTCCGTA CACAATTGCT GCGGTTGACA 60

5

CACATACG 68

(2) INFORMATION FOR SEQ ID NO: 2291:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2291:

TTGACGAAT TAAACAAAT CCTTTATAT GTTGAAGTGT ATTCGAGATT AAA 53

20

(2) INFORMATION FOR SEQ ID NO: 2292:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 base pairs

(B) TYPE: nucleic acid

25

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2292:

ATCAATTGTC AACATCTAAT ATTCACTACC AATTATATCG CCACATGTTT TTTAGCAGTA 60

ACA 63

35

(2) INFORMATION FOR SEQ ID NO: 2293:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

40

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2293:

CGACTCAGGT CCATCAAGAG AGACACATTT CGACTACAGG TTATTACTTC TTGA 55

(2) INFORMATION FOR SEQ ID NO: 2294:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2294:

AAATTTTGGT TAATTTTAAA ACCAAAAAAC CTTGGAAGGA AATGGCCCTT TTCCAATTT 60
T 61

(2) INFORMATION FOR SEQ ID NO: 2295:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2295:

AATCTTAAAA CCTATGGCGT CTATTACATT CCCAAAACCT ATTTTCAGnA ATGTTACCAA 60
TTAAACTTGC CGGGGTATGG ACCAGGGTAC CAGGCTAAAA ACTGGAAGAA AGGAAGGAAT 120
TTTAGAAAAT AATTTATTAA CATGGACCAG GTAACATA 158

(2) INFORMATION FOR SEQ ID NO: 2296:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2296:

TGTTCCAACG ATGAATGTTT GCATGCTTTG TTGCACTGAA ATTGATGAGT TGCTACTTGC 60
AATCCTAG 68

(2) INFORMATION FOR SEQ ID NO: 2297:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2297:

GTAGGGATTT TTTTAAACCG GGATAGCCCA ACCAAAATTT AATTAATTTT GGGTTTTTGG 60
ATTGAAGGAA TT 72

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2298:

AAAAATTnTA CCAGGTGAAA AATTATTTTG GTAGGATTTA AATnTAATGG TTAAATGGT 60
 GGTTTATTAC CTAATTTAAA AATGGTTAAA AGGGCCTTTA CCATTTTTAA AATTTAATCC 120
 GCCTTTTGGG AGGGGGATTT TAGGGATGGT CCAGTTAGGA CCCCATTACC ACTGGAAACC 180
 AACTTAAAAT TTGACCAAAT TTCCTGGAAA AAA 213

(2) INFORMATION FOR SEQ ID NO: 2299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2299:

TATTTTAAAA GGAGGGTAAT AATCTTAATT TAAGTTCATT ATTTTACTT TCATTATAAA 60
 TATTTAATGT TACTTTCTTA TTTAGATAAC AATAAAAAAA TATAATCTCT nAAAACCCAA 120
 TGAAACAGCT GCTCCAAACA ATTAGTTCTT CTAATTGAA 159

(2) INFORMATION FOR SEQ ID NO: 2300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2300:

ACAAGGTCAT TCGGATTGA CTTTGTTC AATTGTAAAT TTTGCTCCAT CAATTGTCTA 60
 ATTCT 65

(2) INFORMATION FOR SEQ ID NO: 2301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2301:

5 TTTATTCTTA TTAAAAACC CANTGAAAGT ANTCTTTnCA TTANTAAAA 50

(2) INFORMATION FOR SEQ ID NO: 2302:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2302:

GAGATATATG CATGAGCTCT ACGACTTCTT TAGGTTTCAT GCGACTATC CTGGCAGGGA 60
20 TG 62

(2) INFORMATION FOR SEQ ID NO: 2303:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2303:

ACCAATCCCG TTGTTTTGGT TTTTAAAAA AAGGAAATTC CAAAAATCCC CCATT 56

35 (2) INFORMATION FOR SEQ ID NO: 2304:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2304:

45 TTAAAAACCC AACGGGTTTG GTTAAAATGG CCTGGGCTTT TCCAAACTT GGC 53

(2) INFORMATION FOR SEQ ID NO: 2305:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2305:

CGAACAGGTT GCCACTGTAA GATCTGGTGG CATTTAATGG CAATCGTATT TTATTTGGAG 60

(2) INFORMATION FOR SEQ ID NO: 2306:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2306:

CTTTATAATG GCGGCGCACT TGGCATCTCT GCATTCAGTT ACACGCGGTG GCAACACAAA 60

ATTTAGGGAA TTCT 74

(2) INFORMATION FOR SEQ ID NO: 2307:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2307:

TGTCCATGCA CAGCTTTATT GGAATTTACC TTTTACAGG CAACCGCTAA AGA 53

(2) INFORMATION FOR SEQ ID NO: 2308:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2308:

TAAATGATTA TGGGAATATC CAAAATTATC GAGATCTAAT ATGAAGTGAC TGCACACATA 60

TCAGCTCTGA ATGAAT 76

(2) INFORMATION FOR SEQ ID NO: 2309:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2309:

TCCTCAAAAT GTGAGTTAAT AGTCGAGTGG AAGCTGTGAC TTGAGCGACG ATACATCATC 60

5 AnACTATCAA TAATGTTTGC ACATCACTTT TACTACTATC ATTTGATGTA TAAATAC 117

(2) INFORMATION FOR SEQ ID NO: 2310:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2310:

AAACTCATAT CGCTTCCGAT AACCAACCCT GCTGCTGTTG GTACAAATTG TC 52

20 (2) INFORMATION FOR SEQ ID NO: 2311:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2311:

30 AACACTGGAG TCCTAATGTC ATCAAACATC TACCTATAAG ACCTTATATA ATCGTC 56

(2) INFORMATION FOR SEQ ID NO: 2312:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2312:

GATAACATCA TAGGCCATAA CTTCCATTTA GGCCATCACT TATAGCATGC GGACGACATA 60

45 CTGTGCCATA TG 72

(2) INFORMATION FOR SEQ ID NO: 2313:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2313:

CATCTAATGG GAACGTGTCG ATCCTAGTCA GTATAGTCAT CGGCAGGTAC GA

52

5

(2) INFORMATION FOR SEQ ID NO: 2314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2314:

15

TAAACTGAAA TTTAATTTTC GGATGGTATT GTTATTAAGA AATAGACATA ATTTGTGCTG

60

GATA

64

20

(2) INFORMATION FOR SEQ ID NO: 2315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2315:

30

CTAGTTTAAA TTTCTTAAAC TTCTACATCA GTAAAAGGCC GCTCTGGGAC CATACAATC

59

(2) INFORMATION FOR SEQ ID NO: 2316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2316:

GCATAGTAAC TTAATTGATA GGAGATGAAA ATCCGCAAAG TCATTGGAAG GATT

54

45

(2) INFORMATION FOR SEQ ID NO: 2317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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GTATATGCTG GAAAGATAAA GTATGGAAAA TGCATGGCGA ACATTTTGTA AGCAGAATGA 60
 GCTATAAGCG TTGAATGGGT TTGAACGTAA ACAATCGAAC AATGATATGT CAGACATACT 120
 5 TGCTTTAGAG CACATTTAGA GAGCGACATG 150

(2) INFORMATION FOR SEQ ID NO: 2318:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2318:

AAATCATCGA TGTTAAATAA TTTAATGACA AGGATTAATG AAAGACGGAT TG 52

20 (2) INFORMATION FOR SEQ ID NO: 2319:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2319:

30 TTAAGGAAAC CTGGCCAAG GTTAAGGAAA ACCGGGGGTT CCAAGGTTTT TA 52

(2) INFORMATION FOR SEQ ID NO: 2320:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2320:

ATGAAGTTGA TTTAGGATGA AAATTAATCT TGGGATATTT AATACTTTGT 50

45 (2) INFORMATION FOR SEQ ID NO: 2321:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

CTAACGCTAA GGGCGACGGA TGGTGGTnAT GTCAAAGAGA CAAATAGGAT

50

(2) INFORMATION FOR SEQ ID NO: 2322:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2322:

15

CGTGGTGATT AATTTTTCGT CGCGTTTTGT TTCCTTTCCC CAGTCATGTT TTATCATTGT

60

GGGCATCATT GCACCTGGGT TCCATATTAT GACGTCATT TTTAnAAT

108

(2) INFORMATION FOR SEQ ID NO: 2323:

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2323:

30

GTCACCGAAT TTCGATTTAT ATTATCACTC AATTTATTAT CTTGAAGCAC GCGTTAAATC

60

GTCTTTAAAT TGAACAGTT GCTACTTTAT TGTCTTTACC ATTGATCTGA ATTTGATCCG

120

CTTTAAGTCC ACTATCTTTT ACAACTTGCh CTACCTTTTG TTGAGTAATT GCTTGTTTAG

180

ATTGGAAATC TACGCGTGTA CCACTTGAAA AA

212

35

(2) INFORMATION FOR SEQ ID NO: 2324:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2324:

TCATTTGTTT TTAATACGTT GTCAAAATTA CCAACAAATG ACAAATTAAA TTTTGCAATA

60

CATATCAAGG TGTTATTTTT TTCCTATTTT AATTATGTAT AACGCATTAA AAGTGACGTh

120

AATATTCAAA GGA

133

50

(2) INFORMATION FOR SEQ ID NO: 2325:

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(A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2325:

10 ATGAACGACC GTGGACAGAC AATATTTAAA GCATTTAAAA ACAGCGTTCC CAGAAAGACA 60
 ATATATAACC AATATTAACA AAAGCAATGC ACATTACTTC ACAAATGAAA TCAAAGCAAC 120
 ACACATATAC AATGCAATAA GCGGGCAACA ACAAACAGAT TTCAACACGC CTGTCATACA 180
 15 GCAATATCGT TAACAAATGA CAnCCGCCnT TTAGGC 216

(2) INFORMATION FOR SEQ ID NO: 2326:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2326:

TGACCATATG ATTGAGGAAG GTTTTATTGA TCCTAAGTAT CGTGCTCTTG CACCGTTATG 60
 30 CGACACTAAG GAATCATTAA TTGAATCAAT ATTAAATTTn AAACCTCTGG GTACTCGTTC 120
 ATACGATTAA TCATTCTAAG G 141

(2) INFORMATION FOR SEQ ID NO: 2327:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2327:

TGAAACTGCA GCGTGGCCGA GTGGGGTTG TGCCAGGTGA CCCCAGATGG GCGTG 55

45

(2) INFORMATION FOR SEQ ID NO: 2328:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

GAAGCCAGCC TAATTGGATA CCACCGGAAG TAACTTTTGA CCAGGGCCGT CGCA

54

(2) INFORMATION FOR SEQ ID NO: 2329:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2329:

15 GTTCCCGGGT CCAGGCCGTT GTCTTG TGCC GGGGTGTTTG GTCCTTGGTT GTGT

54

(2) INFORMATION FOR SEQ ID NO: 2330:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 190 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2330:

TATATTATAT ATTTAACTGC TGTGATGTAT TCTGAAAAA TAGTAGTATT GCCTATAATC

60

ATCTATGCCA TTGTGTTTGT AATAATTGGT ATCACTTATA TCTTTATAGG CGACAGCTAT

120

30 GATCAATTAA CAAATTTC AA TGTGATTTTG TATATGGGGA GTTTGTnTTA TGCATGGATG

180

GCTATTAGAA

190

(2) INFORMATION FOR SEQ ID NO: 2331:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2331:

45 TTTTCACCTC GTGTTTTTAAA TTCAATTGAA TCTAAACTAA AAGTACCTTT AAGT

54

(2) INFORMATION FOR SEQ ID NO: 2332:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2332:

5 TTCTAAAAAT ATTAACGAAT TATACAACTT TAAGAGTTTT TAGTATGTAA ATATTCTTTT 60
 CATATTAATA CAATACACCC CTATATATGC TCACTTGTTT GAATTAATAA ACTTTAGCAT 120
 TCTGCAAATA ATATTTTAAA AATAACTATA CTTTTTATTT ACCTATTGAA AAATAGTGTT 180
 10 ATCATATTTA TTAAGAAGCT ATTTTATAC TAGTAGGTGT CAGTCATGAA TAACATTTTG 240
 TTAAAT 246

(2) INFORMATION FOR SEQ ID NO: 2333:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2333:

25 CCTTCTAACA TCTTTTACC ACTCATTGAA ACATGTGATC CTAATAACAT AA 52

(2) INFORMATION FOR SEQ ID NO: 2334:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2334:

AGAAAAGAGA CTGAAACAAC AAATTCAGGC AACTTTTGAA CAACAGAGAC ATCGATTAAT 60

(2) INFORMATION FOR SEQ ID NO: 2335:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2335:

50 CCTCAATCAG CTCCTAAAGA ACAAATAGC GACTCGATTG ATGAGGAAAC AGTAACGAAA 60
 AAAGAACGAA AAAGTAAAGT AACACAATTA AAGCCATTAA CACTTGAAGA AAAGCGGAAG 120
 TTAAGACGTA AGCGACAAAA GCGAATCCAA TACAGTGTTA TTACAATnTT GGTATTGTTG 180

55

(2) INFORMATION FOR SEQ ID NO: 2336:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2336:

CCTACAGTCC CAACACTGTC AGTACACTGC CGATACCCAA CCTCTGGCCG GTCCGGCA 58

(2) INFORMATION FOR SEQ ID NO: 2337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2337:

ATATTTTTnA TTTAATGGTT TTACTACTGC TACAACTATC ATAGGTGGCA 50

(2) INFORMATION FOR SEQ ID NO: 2338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2338:

CTCCTGTAGA TTAAAAATCT CCTAAATAAC AAACGAATAA TCGGCCATCT TTATGTATTT 60

TGATTGCTGC AGGATTCGCT TTGTGACTTA CAAAAGGTCG TTTGATTTC TCGTTTCAG 120

GATTGATTTT GAAAATATTG CCTTCGAATA CATCCAATAA AAAGAGTTGT CCCTGCCGAT 180

CAAAGTTCAA TCCTTCTAGT TGCAATCCTT TTTTGGAAAT TTCAAGCCAT GGTTCAGCTG 240

TAATTGTTTG TAATTCACCT TCAGATATAA TTGGAACAGC ACTATTGGAC TTCCCGCnAT 300

AAAATAATGG AGGGnAAAnC TGGTGGGGAC ATCCATGAGC CATTCCTTTC CATTCCATTC 360

GGTTTAACT AACCAATT 378

(2) INFORMATION FOR SEQ ID NO: 2339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2339:

ATGAAAATAA ACTGTGTCTC CnGATGTATA CGTCCCTTCA AGCAGACTTC 50

10

(2) INFORMATION FOR SEQ ID NO: 2340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2340:

20

TATCCATATG TGAAAAATGT CATATATGAG TCTAGTTTTG TATAAATGGA GACTCGAAC 59

(2) INFORMATION FOR SEQ ID NO: 2341:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2341:

ATTGATAAAA TATGATTAAG CGTTGTTGCA AATGACATTT TCTCAAAAAG CGCTTCACTA 60

35

TCAATTGGTA CTTGTGTGTh AATTTTCAGCC AGTCGCTTCG ATAAATATAG TTCATCTAAA 120

TTGTCATTAA TCTTATTACG TTGCCAGCT GATAATGCAT CAATGTTTTT AACCACATTT 180

TCAACGCTT 189

40

(2) INFORMATION FOR SEQ ID NO: 2342:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 165 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2342:

50

ATCAATTAAA ACAAAGCATA CAACAATTTG TTGATGTTGA ATCTAAATCA ATTTTAGAAC 60

AACAAATGAT TCATCAGCTT CAACAAATGG ATCGTTCTTA TGTAGAGATG ATTACAGAAT 120

55

(2) INFORMATION FOR SEQ ID NO: 2343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2343:

CTTAACCCCC CTTTTTCCC AATTTTAATG GGGAAAAATT GTAATTAACC TGGGC 55

(2) INFORMATION FOR SEQ ID NO: 2344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2344:

GACAAATAAA CATGACCTGG ACAAAGAAGA ACAATAAACA AGCCTGGCAA 50

(2) INFORMATION FOR SEQ ID NO: 2345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2345:

GTATTGCGAT GATGCATACG GGTATTGTTC TGATTAAATA ATATTTTATA TTAAATGTTG 60

ATAAATGTTG AATAACAAT CCGCAAAGnG CACTTGATGA TAGTGCTAAG A 111

(2) INFORMATION FOR SEQ ID NO: 2346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2346:

GCAAACAGTT TCCGTGTCCG TTTTCCAATT AAGTTAAGGA ACCCAAAGAG A 51

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2347:

TCGTAGGTGC CATAACACAC GTTACCTGGG ACTCATATGA AGTATTATGT CGAGACGACC 60

(2) INFORMATION FOR SEQ ID NO: 2348:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2348:

GTTTTAAATA GGCTCTTTAC GTATCTAAAA ATAATTGCAT TATTGGTGTG CCTTGATGTA 60

ATTGAATTAA AGTACCGTTT GGTTGTAACG TTTCAGGTAT ATCATTTTCA ACnATAAC 118

(2) INFORMATION FOR SEQ ID NO: 2349:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 176 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2349:

ATGACAGAAA GCAAAATCCC AATGTTGATA TACCGTTTTT GACACCACTT GATTATCATT 60

ATTTTTTCTT TAGCGATGGA TTTTATATTA CGATTTCAT TCTTACTATC GTTGCATTAT 120

TGTCATTCAA ACTGTATCGT TTTTACTnTT ATAGACTTTT CGCAATAGTA ACATGG 176

(2) INFORMATION FOR SEQ ID NO: 2350:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2350:

CTACGACTGA CATTAACTGT GCAGATGTAC CTGGATTCTA TTTTTC AAG AACAAATTGT 120
 AATAATTGAT AGTTATATGG TGCAATGTCA CCTTCATCCA TTGAGCGCTC AATAATTTCA 180
 5 GCTGCnAGAG CGGCnTGA CT G 201

(2) INFORMATION FOR SEQ ID NO: 2351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2351:

ATCGCTATAA CCTATCAGTG ATAATATTTG ATTGCATGGT GCACCATTTG AnATTTCACT 60
 20 TAGAATGGTG GTACCTAATT GCTTATTTTT ATATGTCATT TGAAGATTTA AAAATTAAAA 120
 ACTTTGATAC AGAGTGAAAC CATATTTCAA CAAATTAC 158

(2) INFORMATION FOR SEQ ID NO: 2352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2352:

TCGTAATCAA AACATTTTGA ACAGGATTAT AGTAAGGGAA TTTTGGATT TTAAC TTGTG 60
 TTTGTTTCATT TTTTAATAAG AGTCGAGCTA AGTCTTGCAA CATCA T TACT TGCTTGGCAT 120
 CTAAC TGTTG GTCATTAAAT TTTATGAAAC GATCACTCAT GTTTTATCCC TCTTTAAAAG 180
 40 TTTAGTTCTA CAGCATTATA TATTGCTTGT TGTTACGTT CATCTTCCAA TTTATCAATA 240
 ATTGTACGTT TAATTGCACG TTCAACTGGC ATTACAGTGA TTAAATCACA CAAGTCTAAT 300
 AATGCACGGG ATACTAGCGG CTTCTTCAGA AATTTGTCCC TGCTTAGACA TAGTACGTAA 360
 45 ATCTTCATTG AAAC TTnAAT AATTTGGTTC GATTTGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 2353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2353:

ATTAATGGGG TTAAATAACA TTTTGACTGC GAAAGATTTA TTCTTTTCAG GTAAATCATT 60
 5 GATAGATGTA TATAGTCAAT TTGCTGGATT AGCTGAAATG ATAAATGTnT TTGCGAATGC 120
 ACCATTT 127

(2) INFORMATION FOR SEQ ID NO: 2354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2354:

ATCTCGCTGT TTTTATGAAA GAAACTACA TTTTCGAGAG AATAAAAAGA TTTTCTGAA 60
 ATTTAATCTA TCAATTACAT TGATTTACTA ATATAATTAG AAAGTAAATT TTATTTGATC 120
 AAAGTAAATG GGGGAAGTAC TGTGATAGAA AATAAGAAAA CAGTTGAAGA TACATATTCA 180
 25 ACAGGCGCAA TTGTTGATT C AATATCATCT TCAGTnCAAA TGn 223

(2) INFORMATION FOR SEQ ID NO: 2355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2355:

ACACTTGTTT AAACACTCAC AATGATAAAG CATATTATCA GTATTGTAGT GTGTGGAAAA 60
 40 TGACAGCCAT CTAAGGAGAA AAATGATGAA AAGAATATTG GTAGTATTTT TAATGTTAGC 120
 AATTATATTG GCAGGTTGTT CTAATAAAGG TGAAAAGTAT CAAAAAGATA TTGATAAAGT 180
 45 GTACAAAGAA CAGAATCAAA TGAATAAAAT TGCCTCGAAA GTACAAAACA CTATTAAAC 240
 AGACATTAAA CAAGAAGACA GTAATACACA TGTTTATAAA GATGGTAAAG TCATTGTTAT 300
 TGGTATTCAA TTATATAAAG nTCGTGAAAA AATGTATTTA TTTCGCATAT GAAnTAAAG 360
 50 GTGGTTAAGG CCAGAGGATT TAATCAGnGG AAAnTAGACC 400

(2) INFORMATION FOR SEQ ID NO: 2356:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2356:

	AATTTACTTT GTGCCACAAG GTTATCAATG TCTTTTGAAC CACCAAACAT TCTAGCGATT	60
10	AAGTGACCTC CATCATCGTC TGGTAATCTA TCCTCTCCCC CCACAGTTCT TTGTGCATGG	120
	CTATTACGAT CCCCATCTTT TAGAGAGAGA TTGTCTACAT AAACCTTCTTT TATGCGACCT	180
	TTATGATCGG TTCGATATAT GTGACCAGTA GGTGTTGTGT ATTCAATATT CGCCTTTAGT	240
15	TTCTTAGGTh CTAAGTCTTG GCATAGTGTT CTCCGAATTC nAACCTTGGT GTTAGTTTGG	300
	TGATTCAACA TACTTTTGAT GGAATTCATT ThCATGGGCT ACTT	344

20

(2) INFORMATION FOR SEQ ID NO: 2357:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2357:

30	TATGCGCCCC TGCTTGATCT TTCATTTGCG TCCACTCAAT TAGTTGTTTG CGC	53
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(2) INFORMATION FOR SEQ ID NO: 2358:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2358:

	ATTTTTTCAC CTTCTGAAAT TGATAAATCT AGGTATCGA ATATAGTCTT ATCGGCATAA	60
45	GATTTATTTA AATGTTCAAT TTTATATGCT TCCATACCCA TCTTCCTTCT TCTGTTGAAA	120
	TCTCTACGTA CTTAAATCAG TTCTATACAT TATACACCTT TTTGAAATCA AAAGAAATCG	180
	ATACCGTTAA GTGTCATAAT TTAATATATT GTTGCTTCAA CTATAAATAA AACTTGTTAA	240
50	GGCTTTGATG ACTATGCTAA TGATCTTTAT AATATACCTT TTTATCAACA CATATAATGT	300
	AAAACATAAT ATAnAAGAAC ATAATAAAAA CCCGGATTGA TATTTTATCA ATCCGAGTTC	360
55	GTGTTTAGAT ATTATTTTTT AGAGTTTGCT TTAGGTCCTG	400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2359:

TTAATGTCGC CATTTTTTGT TAGGTAGACG TATAAATCTG GACCTTTTGA TGATTTGTAG 60
 TTAGTAAGCA TTAATTTACC ATTTTAAATC TCAGCTTTAC CTTCAACAGT TTCACCGTTT 120
 TTAGAACTGA nTGTACCTGT TAGGTGTTTT GTTT 154

(2) INFORMATION FOR SEQ ID NO: 2360:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2360:

ATATGTCTTG TGATTTTCA GGTGTAAGTT AGTATGCAAG TGATTATGAT TGATAGT 57

(2) INFORMATION FOR SEQ ID NO: 2361:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2361:

GGCATCAAAT TAGTAGCGAC TCACACGTGA TGCATCCTGT GTTTTGGATC TCATTTCT 58

(2) INFORMATION FOR SEQ ID NO: 2362:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2362:

TGTTATTATC GnAGAGGCTT TTCGCTTTGG AATAAGGTAT TACGTGAATG 50

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2363:
 CTCTTCTGGT CCCTGACATA CATAGGAGAA ATAGCnCCAT GTACAACGTG 50

(2) INFORMATION FOR SEQ ID NO: 2364:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2364:
 ATTGCCAATG TCGTTAGTTC GTGAGGCTGT TGGTGAAAGT TGTGTTTGAA 50

(2) INFORMATION FOR SEQ ID NO: 2365:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2365:
 CCATGATTTA AATCATTGAT TAATGGTGCT TGTCTACAT CTGTGTAAAA TTCATACAAT 60
 TCTTTAGCAT CGTCGAATAG TTCATCACGA CGTTGGnTAA ATTCTTCTTC T 111

(2) INFORMATION FOR SEQ ID NO: 2366:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2366:
 TAATGCTGAG CGTGTTACTT TAGTTGGATC AACGATACCT TCTTCTAACA TATTAACCCA 60
 CTCnTTTGTGTA GCAGCGTTAA AACCAACACC CGGCTCTGCG TTTTCAAAC GTTCTACAAT 120

(2) INFORMATION FOR SEQ ID NO: 2367:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2367:

CCTGATTGCA AAGTACAGCA AGCACTACAG ACGCCTAAnc ACTnACACTA 50

(2) INFORMATION FOR SEQ ID NO: 2368:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2368:

AAAATGGTAT TGCAATTAGT AATGTTACAA CAAGTGTGT AATAGCTGCA TAAAT 55

(2) INFORMATION FOR SEQ ID NO: 2369:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2369:

TATAGGATGA AAATCCTGCC AAAAGATTAA GGGGTGGCCT AATGAACCAT G 51

(2) INFORMATION FOR SEQ ID NO: 2370:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2370:

TTGCTCGAGG TGGTAAATAC GCAAAGTTTA TTTGGTTGTG CTAAGAGAGA AA 52

(2) INFORMATION FOR SEQ ID NO: 2371:

(A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2371:

10 TAATTTGAAT AAGGTGGAAG TGATAAACAG TGCTTTGCGA ATCTAGAGTC ATTAATCAAA 60
 ACCCTA 66

(2) INFORMATION FOR SEQ ID NO: 2372:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2372:

25 AGACAGGTAC TGTCCTACGG TATGGAGCAG AAGCGGGAAA GCTGCCCAGA GCCAACTGTA 60
 GACAA 65

(2) INFORMATION FOR SEQ ID NO: 2373:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2373:

40 TTGCAGTGAC GGCTTATAAT CATTCGAAGC GAACAATTAG ACATTCCATA TAAAATATAC 60
 AGATGGCTTT CAGTAGAGTA GTGGATTCGG ATTCACGAAC TATACTGGAA GCTTTTTTATT 120
 ATAAATGAAG AGAAGTTATA TTTTTCAGCAT GTATAGTTGA ATACTGGGTT AAAATACCAT 180
 45 ATTAATAATG AAGTAAAGGT ATGAGTGATT ATGAAAGTGT TTTGAATGAA ATATATTTAA 240
 TTGGTGATGC TTTTAATTGA AAAGATTAAC AGGATTCAAC TTGGTAAATT GTATTAAATG 300
 TGAGAAAATA AAAGTATATT CATTGAGAGA TATATGAGTC AATGATCGTT TTAAACAAGA 360
 50 TAAGTGTATT TTAATATGTA AAAGTTATGT AATAAATATT 400

(2) INFORMATION FOR SEQ ID NO: 2374:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2374:

CCTATCATGC CTCTCTCTCA CTGAATCCTT TAGATCCCCT TCCCTCCCTC TCCCCCTCT 60
TTTCCCCCTCC 70

10

(2) INFORMATION FOR SEQ ID NO: 2375:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2375:

CCAAGTCAGA GCAGCAGTTC AGTTCGTCAG CnGTTTCAGTT CAGAGCnGTC 50

25

(2) INFORMATION FOR SEQ ID NO: 2376:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2376:

35

GTTGGTGAAG CTGTTGCCGA nGGAGAAGCG GGTATGGATC CTGACGGTGn 50

(2) INFORMATION FOR SEQ ID NO: 2377:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2377:

AATTGCAGGA CAGGTCAAAG GCAAATGCAC GTATTCAGGT CATGCTCATG TGCATGTTG 59

50

(2) INFORMATION FOR SEQ ID NO: 2378:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2378:

5 TTTATCATCG TATAAATCTA TATCTAATTG ATTAACTTC GGGTGCTTAA CTAACCTCTCT 60
 CAATACACTT ACACCAGCAG TTCCCATGCC TATTATTGCT ACACGCATAT ATCATCCATC 120
 CTTTGTGAAT TCAAAATATT ATATTTAAAC TATTACCTAT AATTATAGCA ATTTGGTATT 180
 10 TCCAATAAAA TTTATnAAGG TAAGCnATTA TTTCACTTTC ACAACCATT 229

(2) INFORMATION FOR SEQ ID NO: 2379:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2379:

AGTTTTTTGT TTGACGTATT TAATTTACTA TTTGCTTGAT TGATATTTTT AGACATTAAA 60
 25 TAGTGTTCCTC CTAATCAATT TATTCTTCTT TATnTCAGCA TTATTCGCAC TGACAT 116

(2) INFORMATION FOR SEQ ID NO: 2380:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2380:

CAAATCTTAG CGGATGATTG GCATGTATAT TCTGCTGGTA TCGAAnCACG CGGTGTTAAT 60
 40 CCCAAAGCGA TAGAAGCTAT GAACAGAAGT CGGCGTTGAT ATGTCGAATC GTACGTCAGA 120
 TTTAATCGAT AATAAT 136

(2) INFORMATION FOR SEQ ID NO: 2381:

45 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2381:

55

TTAATTGATA GCTTTTATCT GTAGGAAAAG CTATTTTAAA GATTTCTAGT GTATCTATAA 120
 CTTTTTTGGG ACGATATTGA ATATTACAAT CTTTAAATGC CTTTTTAATA AAATTCAAAT 180
 5 CAAAATCTAC ATTATGAGCT ACAAAAATGC AATCTTTTAT CTTATCGTAG ATTTCTTGTTG 240
 CAACTTGATT AAAATATGGC GCTTGTTGTA GCATATTTTC TTCAATGGAT GTTAACGCTT 300
 GAATGAACGG CGGAATCTCT AAATTTGTTT TAATCATAGA ATGATATGTA TCAATAATTT 360
 10 GGTTATTGCG CACAAACGTT ATACCAATTT GAATGATATC 400

(2) INFORMATION FOR SEQ ID NO: 2382:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2382:

TATTTTGTTA ATAAAGTTAA TATATGTTTG TTGTACAGAT AGTTCAGGAT ACA 53

25

(2) INFORMATION FOR SEQ ID NO: 2383:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2383:

CCCGAGCTTG CCTCCTTCC CCCCTCTTCG CCTCCAGACG AAGTGCCCTT CTGTCCTTG 59

(2) INFORMATION FOR SEQ ID NO: 2384:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2384:

AGCCAACATC CCGATGGTA CTGCAATTA TGCATAACCT AGAGAGAAGA ATGATGCCAA 60

50

TAAACCAAAT TGTGGTTTTG TCATCCCTAA ATCATCCATC ATTTGCTTAG 110

(2) INFORMATION FOR SEQ ID NO: 2385:

55

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2385:

10 TGAAAGTTCT TTTAnGCATC AATTTTAAnA CTACGAGCGG AChCTAATAT

50

(2) INFORMATION FOR SEQ ID NO: 2386:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2386:

GGCAATTTAT TGACACAATG CTTGAGChAT TGATAGCAGG ACAAGAAAGA ATACTTGATG 60

25 AGTTAATACC AAAAATGGAT GCGACTGAAA AATTAACGCT TTATTTAACT AGTCATTATA 120

AACAGATAGA TTATGAATTT TTGTATCTCC TTTCAATGGA TAAATTGTTT GGAAATAAAA 180

GAAATAGATT AACATTAATT GATTTAGAAA ACATATTGGG AGTAGGAAGA GTAAAAATTA 240

30 GTnGT 245

(2) INFORMATION FOR SEQ ID NO: 2387:

(i) SEQUENCE CHARACTERISTICS:

35

- (A) LENGTH: 140 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2387:

CACAAAATTC GAAATCGTCA TCGGTGATAT GTTTAATACT TGGGAAAATA TAAAACGCGC 60

45 CTTCAGGTTG AGCGGTAATC TCAAAACCTA ATTTAGTTAA TTCAGATACT AAATAATTTTC 120

TTCGTTTChAC ATAAGCTTCG 140

(2) INFORMATION FOR SEQ ID NO: 2388:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2388:

ATATAACATT GTAGGGCCTA ATAATTTATT TTATGTCTCA GACTCATACA ATGGTTATTT 60

5 AACTTATTTA CCACAAATTG AGCACTAAGA CTCACTATTA TCGATTCTTC TATTGAACAn 120

(2) INFORMATION FOR SEQ ID NO: 2389:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2389:

TCTAAATCCA GCATGATCTA CATCAAAGCT GAATTCACCT TTTTCATCGA CTTGCAAATC 60

20 AGGGAATTCT TGACCTTCAC CTAGT 85

(2) INFORMATION FOR SEQ ID NO: 2390:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2390:

GGTGTTTATA AAGCAGGGGC TGAGCCTCGG TCAGGACTGG ATACACAGGC AGTACGGGTG 60

35 A 61

(2) INFORMATION FOR SEQ ID NO: 2391:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2391:

TAAAGTAACC ACTTTAGATG ACATTTTAGA AGTTATGGGC CGAATGCAAA C 51

50 (2) INFORMATION FOR SEQ ID NO: 2392:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2392:

5 GGTCGGAnTC CCGGGTCGAC CCACGCGTCC GCATCAACCT AGnAGAAGCn 50

(2) INFORMATION FOR SEQ ID NO: 2393:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2393:

ATTTCCAAAC GAATTGAAAA ACGGACGTAA ATTCTTAACT AAAGGCGATA AATGT 55

20 (2) INFORMATION FOR SEQ ID NO: 2394:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2394:

ATAGGTTGCT ACTATTTATA TCGACTCATT TTCACITACA AATATGACAT TGTCTCTAGA 60

ACACnAAAAT TAATTTGCGT CATATCTGCT ACAGTTTTGA GTGTGTTATC AAGTGTATTT 120

35 (2) INFORMATION FOR SEQ ID NO: 2395:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 261 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2395:

TGGACCATAG TAAAGCATTa CGGTCGGTTT ATTATTTTCT AAGGAAGTAT GTTTATATAA 60

ATCTATGCTC ATTTGTTTTT TAGCGTCTGT TTGACCTATT ATTTTAGAAC CAGCCATCTG 120

50 CTCTTTATAA AAATTTATTA CATCATCTTT TTTTAATGTT GTATATTCAT AGTTTATTC 180

TATTATnTCA GAATCGTGAA AACTATTTAG TGATTGAnAT ACTCTTTTTG GAGGATTCTG 240

AATATAGATT TTCTTAATAT T 261

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2396:

GTTTTGAATA TAGGGGCTTT TATCACTCTC CGAAGTCTnT TCTAAGTTAG ATTTGGAAAA 60
 TAACACTTTT TTAGTTTCAT TCAAGCGAGT CGAGTGACTC CAGA 104

(2) INFORMATION FOR SEQ ID NO: 2397:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2397:

GATTATCGAT CACAGTATGA TTACGTAGC AATTTCTGGT ACATATACGC CTAT 54

(2) INFORMATION FOR SEQ ID NO: 2398:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2398:

GCITCACCTT GAACTAGCAA ATAAGGATAA AACAAGCATT CTTTACATGT TTCTTTTAAA 60
 TACGTTTGAT ATTTAATAA TACTTTTTCG ATTTTACTCA TATAAGTTTG AAGTTCTAAT 120
 TTTTCATTCT CACTTATTTT GTATATATTA CATTCATTAT GTTCTGTCAG AAAAATATAA 180
 GGGTCAATAT TAATTCGTC TATCAATTCA TAAATTCAC TTAAGTATTT nTnCT 235

(2) INFORMATION FOR SEQ ID NO: 2399:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TTTGATGCAC TTATTTGTGT AATGACATCT TTACAGTCTT TTCCTTCCTC CATCATTTTA 60
 ATAATTCCAT TTAGTTGCCC TTGTATTCTA TTAATACGAT TAATCATTTT n 111

5 (2) INFORMATION FOR SEQ ID NO: 2400:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2400:

AAATGCTGGC TGAGTTTTGG GCCACCCGCA AAGGCACTGG ACCGGTGCGA AACC 54

(2) INFORMATION FOR SEQ ID NO: 2401:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2401:

30 AACCACATCAT CACTACTAAA ATGATACTTA AAAACAAAGT CTTAATACAC TTTTTCATAA 60
 TATCAACTTC TTTCTATATT TAATACATTA ATTATACATC TTTnTnAAAT AAAAATATGT 120
 GTAAAATTTT AAAACTTATT TAATTGATGT TTTAATAATG TATTATAGAA ATTATTGACA 180
 35 TATGATTAAA AACCCTTAGG ATAGT 205

(2) INFORMATION FOR SEQ ID NO: 2402:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2402:

AGATAATCAT AGAGAAAGTC CACAGTCGGT AGAGGTGGTA GCTGAAAACA ACATACTATT 60
 50 AATTATGAAG TGCTTTGTAA CTTGTCGAGA CGTTTGCCGC GAATCTATCA TGATGGTGAT 120
 CAACGTTTTG TnACAAATGA 140

(2) INFORMATION FOR SEQ ID NO: 2403:

55

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2403:

10 ATTTAACCAC TCCTCCAATG ATAAGATTGA AAGGCAAGAT GACCTTCCAA TCTTATTT 58

(2) INFORMATION FOR SEQ ID NO: 2404:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2404:

20 CAGCTTCTAC AATACGGCGT GCTATAGCAA GCATTAATGT AAATCCTAAT TCTGCAGTTG 60
25 T 61

(2) INFORMATION FOR SEQ ID NO: 2405:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 217 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2405:

35 AATAATCATT TTAATACGGT CTTCAGGAAT TGAAGTGTCT ACAGGTACAT ATCCACATCC 60
40 TGCTTTAATG GGCACCAATC ATCCAACAA TCATATATGG TGACATGTGA CCGAATAAAA 120
TCATCGGGTT TCTTACTACC TTGTAATCGA TGTGGCTAAT TTACTAGACT CATCCATTAA 180
CTGTTGATAA GTTAATTCCA TCAGTTGTGT GTCTAAC 217

45 (2) INFORMATION FOR SEQ ID NO: 2406:

(i) SEQUENCE CHARACTERISTICS:

50

- (A) LENGTH: 228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2406:

55

GTAGTATCCA ACGTATTTTCG GATTGCATCG AGTTGATTTT TATTATTTTC TTCAATGCTA 120
TCAAGCGCAn CTGTATTACG TCTTACTTTA GGTTTTATTT GCTCTATTGC CTGATTGTT 180
5 TGATnTCTAA CATCAGTAAC AGCAGCATCT TGATTTGTAT TGTCTATT 228

(2) INFORMATION FOR SEQ ID NO: 2407:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 110 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2407:

CCTTTCGTCT CGCGCGTTTC GGTGATGACG GTGAAAACCT CTGACACATG CAGCTCCCGG 60
20 AGACGGTCAC AGCTTGTCTG TAAAGCGGAT GCCGGGnAGC AGACAGCGAT 110

(2) INFORMATION FOR SEQ ID NO: 2408:

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2408:

GGAGACCCCA AAAATTTTGT CGTTGAAGAT GCCTTTTTTTT AAGCGTTATT TGGCTATATC 60
35 AGTTTCTAAC TGT 73

(2) INFORMATION FOR SEQ ID NO: 2409:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2409:

AAATCATTAG AGAGGAATAG TTCCCTTTGT TACGCCAAAG ATTCGATATT GAC 53

(2) INFORMATION FOR SEQ ID NO: 2410:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2410:

CCATATGATT GTATAGGATC CATGACGTCT CCACTGACCC CTGACTCTAG TATC 54

5

(2) INFORMATION FOR SEQ ID NO: 2411:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2411:

15

GTCCTCTTC AATTGTTATA TGTATATCAC AAAAATTATT TCATTATTTT ACCATTATTA 60

TTTTACAAAT ATTATCCCAA GAATACAATT CAAGAAATGA TTAACCTTAC TTTAGAATTG 120

TACCTTATTA CATTATTTAT GAAAGTACTC TCTCAATTAT AACNAAAAAG AAGGTGTTCA 180

ATACATnCAT ATTTAGTCTT ATAT 204

(2) INFORMATION FOR SEQ ID NO: 2412:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2412:

35

CAGTGGCGCA GAAACATAAC GCTCAGGGAA GCACAGCACC TCATTATGCC AAAGCT 56

(2) INFORMATION FOR SEQ ID NO: 2413:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2413:

45

TCGCTGGCGG GTCCGCGCG CCTAGCGTGC TCATGTGCGG TGTTC TAGGT GTTGGGGTTG 60

CAGTCA 66

50

(2) INFORMATION FOR SEQ ID NO: 2414:

55

(A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2414:

10 GGATAGAAAT GGGAATCCAC CCATCGGTGG GGGTACCAGG CTCTTCATAT GGCCTTGTGG 60
 ACTTC 65

(2) INFORMATION FOR SEQ ID NO: 2415:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2415:

25 TTAAATAGAT AGAATAGAAT TAAAGAGACG ATGATAGGTG CTGCTATCGT CTTAAAAACG 60
 ATGATAAAAG GATCAAAAAC ATATGATACT TTTTCGAAAA TAAAAATAAC AATACCCAAC 120
 AATACTAGCG CTATTAATGA GAAGACTAAA TCATTCCCAC CAACAAACTT CATATACCGT 180
 30 GATTCGGTAA ATTTTnnAAA ATTCTTTCTT ATATTCTTTT CATTTTCATT CAATTATAGA 240
 TTCACCACCA CTTAAAATAT TCATAAG 267

(2) INFORMATION FOR SEQ ID NO: 2416:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2416:

45 TTAAACAAAT GAATATAGTA GTTCCATTAT CCTCACTTTT AATCGTTTAT 50

(2) INFORMATION FOR SEQ ID NO: 2417:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

TTTGCTGGGA GTTGCAATTA GAAAATATAC ACATTTACTT GACATTCAAC TTGATAAAAA 60
ATTAGTTATT GCCATATGTT GCATCACATT TATAGGGATT TTAATATTTT ATGTACGCCT 120
5 AATTAAAAAA TCATCTTTAA ATATTTATAA TACTAAAAAT AAAAGGTCAA AAATnTT 177

(2) INFORMATION FOR SEQ ID NO: 2418:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2418:

AAAATGAAGC GGTGCAAAA TATAATGACG TGAAAGCATT TTATACTCAT GGACATTTAT 60
20 ATCAAGTCAA TCGAACAAGA GATTTATTAG CTGAAAAGG ACTTGAATTA GGTGTTTGT 120
TTGCATTTTA TGGACATACA CATGTGGCAA AATATGAGTA TATTAATGGT GTTCATGTTA 180
TTAATCCTGG AAGTATATCT CAATCTAGAA GTTCAATGGA AGAAACATAT GCTGAAGTTA 240
25 TTATTGATGA TCAAACTTTA CATGGCACCA TCAATTTCAA AAATCGACAT CACGAAACAA 300
TCAGTCATAC TACTTTTTTA ATAGAAATAG CTATGGCTTT TTTTAGTTTA TAGACTGATT 360
TAACTAGGAG GTCGTGTCAT CCAATGTTTG TTTAAAAGTA 400

30

(2) INFORMATION FOR SEQ ID NO: 2419:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2419:

AGGGTGCCGA GTTAACCAAG AAAGGCCGTT GGTGCCCCG GGTATTTTCC CCC 53

(2) INFORMATION FOR SEQ ID NO: 2420:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2420:

55

(2) INFORMATION FOR SEQ ID NO: 2421:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2421:

ACCAGAAGAC AATAAGTGTA ATGATGCCTG TTCTAATACA GAATCTTTAC TTTTATTGTC 60
 CTTTCAAGT CGTTGTTCCA CTTTCTTAAT TTCATTGTTC ATGTTTAACT TTGCCAnGTT 120
 AATCACCTTT GGTATTATCT TTTCTTTAT AG 152

(2) INFORMATION FOR SEQ ID NO: 2422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2422:

GTACGTTTTC ATTAGTTGTT ATATTTCCAT CTGATAATT TTTTAAATCT TTAAATCAG 60
 CATACTGACT AAAAAATTTA AAATTTTCAA TTTTGTGT AAGTTTTTGT CTTCTACATT 120
 ATCCAAAAGA ACAATCTnAT TATTTTTTAG TTCAACACGA TATTTTTTCT CATTATGATT 180
 TTTGCTAATA TCATCATAAA CTTTATTTAC AAAATAATAA CCTGTTGCCT TTTTGGTATT 240
 TCTATTAAGA TATAACACCA TGCCTTCATC ATCTAATACT CCTGGTTTGT TACTTTTTGA 300
 AAAACCTn 307

(2) INFORMATION FOR SEQ ID NO: 2423:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2423:

ATTGTGTTGT ATTTTAGACA AGACCTTCAA TTTTGGAGAT TTCACGATTT ACCACC 56

(2) INFORMATION FOR SEQ ID NO: 2424:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2424:

10 AGTCCTTTGG ATCGTCAAGA TTTCACACAT TTACAnTTAT TAnCTCGTGA 50

(2) INFORMATION FOR SEQ ID NO: 2425:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2425:

ATGTAATATT ACAATTCAAT TAGnAAAGAA CTTTATCTTT AATTGCTTTT CGATTTTCATT 60

25 CATGTCATCT TCTGAAATTA TTATCGTTCC AGTAGGATCA GAATCATTTA TTTTGCTTAT 120

ACGTCTTTTG CTTATTGTTG TAATTGCTGA TATATTAAACG TATGTATCTT TCCCTTTGTG 180

CTTGGAATAA ACACCTATCA CTCTATACAG TTCATTAGCT TTTTGAnTTA AGTTAGACAA 240

30 AAGCTTTT 248

(2) INFORMATION FOR SEQ ID NO: 2426:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2426:

CCTTATTATA TGACAGGTTG CCTAAACAAG TGCCTAGAGA AAAAAGTAGC CCC 53

(2) INFORMATION FOR SEQ ID NO: 2427:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2427:

55

TATCCACTAA AATGATTGTC GCGTATTGTA ATATTAATCG TTCTACTTTT TATGATTATT 120
 ACAGGGAGCA ATTTGATTTA TTGGATACCA TCAACTCnAA GCATAGGTGG AGG 173

5 (2) INFORMATION FOR SEQ ID NO: 2428:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2428:

TACTTATGTT TATGTCGCAA TAATTAATGT TCGAnTTAGT GGAATTGAAC 50

(2) INFORMATION FOR SEQ ID NO: 2429:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2429:

AGTCATCATA TTATCAATAA TACGCCGCGT TAAATCTGAT AAATTCATAT AGTCTGTATC 60
 30 TAACTCTG 68

(2) INFORMATION FOR SEQ ID NO: 2430:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2430:

TGAATTGAAA ACGGTCGGTG AAGCGCTAAA AGGTAGACGT GAAAGGTTAG GAATGACTTT 60
 45 AACAGAATTA GAGCAACGTA CTGGAATTAA ACGTGAAATG CTAGTGCATA TTGAAAATAA 120
 TGAATTCGAT CAACTACCGA ATAAAAATTA CAGCGAAGGA TTTATTAGAA AATATGCAAG 180
 CGTAGTAAAT ATTGAACCTA ACCAATTAAT TCAAGCTCAT CAAGATGAAA TTCCATCGAA 240
 50 CCAAGCCGAA TGGGACGAAG TAATTACAGT TTTChATAAT AATAAAGACT TAGATTATAA 300
 GAGTAAATCC AAAGAGCCAA TACnATTATT AGTAATCATG GGnATTACAG TTTTAATAAC 360

(2) INFORMATION FOR SEQ ID NO: 2431:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2431:

TGACTTCGTC CAAGTACAAC TGCAGTCAGT ACCTACGAAA TCAAGATCAG CATGGAT 57

(2) INFORMATION FOR SEQ ID NO: 2432:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2432:

ATTCTTAATC GCATCATAAT TAATTAACGG ACGCATAACA AATCCGATAA TACTATTATC 60
 TTTCCAAGTC ACTGACACTC CAAATTGATT TGCTTCnTCT ATCCATATTT GCTCAATAGT 120
 ACCATCATTT TGAGTACACA CTTTAAATTC ATGTACATCA GACTGCCTTG TATAAGATTT 180
 GAAAAGTTTC CTAAACTGCC AATAACTGnA CTCTCGCTTC AAATT 225

(2) INFORMATION FOR SEQ ID NO: 2433:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2433:

CGGCCTGACG TTACATTCT TCAACTTCAC GTCAAAATTG CTTGCAATA ACCAGGA 57

(2) INFORMATION FOR SEQ ID NO: 2434:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TTAAACGTGT CTTTAATGTG GAAGTTGAAA TATTAGTCCG TAAAAAATG AACTTAAAA 60
 AAAAATAATA TTTATATTTG TCGTACAAAG ATGAAAGCGA nAGA 104

(2) INFORMATION FOR SEQ ID NO: 2435:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2435:

TTTGCTAATC GTTTCACGGA TTGTGGGGAT GGTAAAGAC TTGCTAGTG G 51

(2) INFORMATION FOR SEQ ID NO: 2436:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2436:

AAAnTTAATT TTTGGGGGGC CCTTTTTTAA CCGGAAAATC CAATCGGGGC TTTTAAGGAA 60
 TGGTTTTGGT TAACAGGCTT TGGAATTTGG TTTGGCAAAA CAATCCTTG TTTGGGGTTT 120
 CGGTCCGGAG GGTCTAATT 140

(2) INFORMATION FOR SEQ ID NO: 2437:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2437:

GAAGCGGAAC CACCGTTGTT TTTCTTTTCA GGTCCAATTG AATAAATGTT ATGAATAGAA 60
 TGGATAAAAA TATAATTATT TAAGTGTTAA AGTAAACCAA ATCATGATTT AAGATTATAA 120
 GAAAGAAAAA TTGACTAATG TTAAAACCAA CAATCATATG GGTGTAAACG TTTATACAAT 180
 CATCGTAAAA CTCAATATGC TTAATTTATT CAAAATGTTC GTCAATAAGT ACAATGAAAA 240
 GGAGATTGAT TTTTGAATAA AAAATATCTT ATGATTGTAA TTATAATTTT AATATGATTC 300

AAGATACGAT TTTGAGACCA TGTGAAGGGA TTAAATATAG

400

(2) INFORMATION FOR SEQ ID NO: 2438:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 59 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2438:

15

TCTGTTTTGA AAGTTGCAGT TTGGACAGCA CCCGATGATT AGGTGAGTCT TTTGGTTTA

59

(2) INFORMATION FOR SEQ ID NO: 2439:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2439:

TTGGTnAAAC CGTTACAGTT GCAAGTTTTG AAGTGAGTTA TTTTTTGGTT

50

(2) INFORMATION FOR SEQ ID NO: 2440:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2440:

40

ATTAAAAATA AATTAAAnGT TCCAGAACCA GTTAACCAGA ATATTTACGA

50

(2) INFORMATION FOR SEQ ID NO: 2441:

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2441:

TGCTGTTTTG GCGGTTTTTC TCCGTTTGGT TGAGTATGTG GTGTACCTTT TGTC

54

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2442:

GTTGTTGGGT GTGTGGTTTT GGGTGTGTG GGTTTGGGGT CTGGGTTTCGT TGGTGG 56

(2) INFORMATION FOR SEQ ID NO: 2443:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2443:

GAGACAACT AGTCGTCCAG AACGGAATTT AAGTAATCAT AATAATTACG GAAGTGCACT 60

TTTGTTTTTG ATTTATCATT GATGGAAATT AGAACAATTT ATCGAATGAT ATTAAAATTA 120

CATAACATCA TGTTGAATGT GAAATTAGGA TTGAACATTA CCTGTTTATT TGAAAAACCT 180

TCAGTTTTTA AATCACTAGT ATCACAATA AAGCGACTTA AATTCGATTC GTTAATAATA 240

GATAATGCAA ATTTAnGTAG CCCT 264

(2) INFORMATION FOR SEQ ID NO: 2444:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2444:

CCGTCTTTAG TACGTACGTT GTTTGCGGGG CTTGGGGTGC TTTCTGGGTG TTGGTCATTG 60

TATTGGG 67

(2) INFORMATION FOR SEQ ID NO: 2445:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2445:

AGCTGCATTT CTCGTGCAGG CTATCAGCAT CGATATCTGT ACCATTTAGT GATCATGC 58

5 (2) INFORMATION FOR SEQ ID NO: 2446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2446:

15 AACCAAAACA AACATTTGTT CGTTAAAATA TTGACACAGA ACATAAGTTC TGA 53

(2) INFORMATION FOR SEQ ID NO: 2447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2447:

CACAAATTAC ACCCATTTGTT AnTACTAATA CTnCCnTT CATTGTTTA 50

30 (2) INFORMATION FOR SEQ ID NO: 2448:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2448:

40 GCACAAACCA AACGCACCTT AACTGCTTTA AATGGCTGGA CGGGGGGTCA ACTGGCCTTA 60

ATGACACTTG AATCG 75

45 (2) INFORMATION FOR SEQ ID NO: 2449:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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GCAGCCTTCA AGTGTGTTGCT ATTTGCTTTG GTGTCACAAG CCATTATCTA CGGTCCCGCA 60
 ATTTAGCCCG C 71

(2) INFORMATION FOR SEQ ID NO: 2450:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2450:

TGGCGTGAGG AAAAATATCA TGTATTGTTA CACAGTCAAC AGTCTTACCA AATGATAAGG 60
 AATGCTTTTAA AAACGGATTT ATCACTTCAT CAAGTTCAAC AAATGATTGA TGTGCTTTG 120
 TTAATTGAAC CGGTATAGG AAGTGTATGT AATGCTTTTG ATCATATGTG GGGATATTTA 180
 AAAAAATGTG CGAATGAAGA AGGAAAGACA ACAATCAAAA CTACTTAAAA GCTGATTTTA 240
 TTTAATGGnA AAAATCGACA CCCCAACTTT ATTAGATTTT TTAGCAGAAC TTGCCTAATA 300
 AATATGGAnG TCAATATTTA CTACAAAGCC GnGTTTTTTAA ACCCCAAAAA G 351

(2) INFORMATION FOR SEQ ID NO: 2451:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2451:

GTGTACCGCC TCGGCTGGCG TTCGCGGTGG GTGGTGCGGT CGGTGCGTGT CTGG 54

(2) INFORMATION FOR SEQ ID NO: 2452:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2452:

TGCCATTCCA ATGTTACCAT CGTCTTGGA CTACTATATA CTGCGGCTAT 50

(2) INFORMATION FOR SEQ ID NO: 2453:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2453:

10 AGACGTGTTT CCACGGTATG GGATAAATGA AGCACCGACT GATAAATCAA TATAGCCTCG 60
 TGTTTTTAGT TTACCCGAAC TATCCCTTGA TAATGATTGT GACATCTGCG GATAATATTT 120
 CATTTTCTTA GATATCGTCG AAATATCACC GATTACTTGA AGTCCATCTG TCGTAAACAA 180
 15 TTCAATTCTG CTTTGTGTTGT TTTTACTTGG GCGGTATGTC ACTTCGGCAA TATATCGTCT 240
 AACTTCAGGT GTCATTTTCA ATAACGCCTT AATCATATCA TCTTCTTTTG TACCTTTGAA 300
 ACCATCCATG ACAGGTGCAT CATTAAATTTT GACATCATTT GAACCTTTAA GCAATTTACC 360
 20 ATTTTCTAAT AAAGGTAAAT ATTTACCTTT ATATTTCACT 400

(2) INFORMATION FOR SEQ ID NO: 2454:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2454:

AGAAAGAAAT ACCATTTGGA GATAGAGACT CGTGTATATT CTTAGCGATG GGAGATTTTT 60
 35 ATAATAAAGA AGATAGnAAG AAAATTATCA AAGGTTATGA AAATAATTAT GGTAGAGGTA 120
 TTAATATTCC TCGAGCACAT AGTATATATT TATATG 156

(2) INFORMATION FOR SEQ ID NO: 2455:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2455:

ACTTAGGTGA TATGAAATGT GGTCCGCGAC GATCGTCAGT AACAAAATAA CAGGCAGTCA 60
 50 TTGGATTATG TTAAACG 77

(2) INFORMATION FOR SEQ ID NO: 2456:

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(A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2456:

10 AGTGAAATCG CTAAAGAAAA AGATGGAACC TCGGTATCTA ATACACAACT TCTTGAACGT 60
 TTTTA 65

(2) INFORMATION FOR SEQ ID NO: 2457:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2457:

25 TATCAATAAT TGCCACTTGC AATGACTGAT TAATTGAGG TGCACATAAG CCAG 54

(2) INFORMATION FOR SEQ ID NO: 2458:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2458:

AATTTTATTT CGAGATTCTT CAATATAGAT GTTCTTCAT TAATTGATT CTCTAACTCT 60
 TGCTTACTAC CTAATAGTTT ATCTAATTCA GCTTTAGCTT TTTCATTTTC TTAAATTATA 120
 TTAATTTTTCAT TATTTATGTT CGTnATCGTA TTATTTAGTT CGATAA 166

40

(2) INFORMATION FOR SEQ ID NO: 2459:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2459:

CCAATGATTA AGCAATACAA TCGTCACTAA AATTACACCG ATAATCTGAA TCATCGTCAT 60

55

(2) INFORMATION FOR SEQ ID NO: 2460:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2460:

AAATCAAAAA AATGTATAAT GAAAAGAAAA AGAAATTGG AAAAAATTGG GAAGACGCTC 60
AAAAAGCTGG AAAAGCTGTA GGTGAAGATT TGAGTGThAA TGG 103

(2) INFORMATION FOR SEQ ID NO: 2461:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2461:

TTTATATCAG AATAGAATAG TAAACTAAGG CATTTGGAGA ACTTATTCCA TG 52

(2) INFORMATION FOR SEQ ID NO: 2462:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2462:

CAGCAGCGAA TTTTGTACGT CCAGTGTAGA ATGGATGTGA ATCAGATGAA ATATCTAAAC 60
GAATAACTGG GTATTCTTTT CCATCTTCCC ACTCCATCAT TTCTGAAGAn GTT 113

(2) INFORMATION FOR SEQ ID NO: 2463:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2463:

CTAACATAAT TGTTAACT AAAATATTTA CTACTTTTAG AACTGTGCGA TTAAATACAA 120
 TTGTCAGTAT TGTTATGACT AGGCTAACGA TACATAAAAT AAAGAAACCG TTAAAGACTA 180
 5 AAATTAAGCG ATCGATTCTT TGTGTGTAAT CATTGATATT ACCCAAATTA ATAnTTAATT 240
 GGATGCATTT nCCAA 255

(2) INFORMATION FOR SEQ ID NO: 2464:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2464:

20 TATGCGACAA TTCGAAACAT TTTATATGCA AAAGGTTATA CAACAGAGAA TGTGATT 58

(2) INFORMATION FOR SEQ ID NO: 2465:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2465:

TGAATTTTCAT TACCACATAT CGGACATTGA TCTCCAATAT TTACAGCAGA TTTAATTTCA 60
 35 CTTAT 65

(2) INFORMATION FOR SEQ ID NO: 2466:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2466:

CGTGACCTTC AAAGACCGAA CGAGAGAGTT GAAGAGCATT TGCGAAGGCC A 51

(2) INFORMATION FOR SEQ ID NO: 2467:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2467:

AGTTTGTAA GTTTTAGTTT ACTAATTTT CCATTAGATA TTATTAATGA AAAAC

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(2) INFORMATION FOR SEQ ID NO: 2468:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2468:

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TTGTTGGTAA GGCACCTCTT AAATATCAAC AACGCGATGA TATTTTCATT GGTACAAAAG

60

TAGGCAATCG TTAAAC

76

20

(2) INFORMATION FOR SEQ ID NO: 2469:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2469:

30

CTTCTATAAT AAAACCATCT GCAATTAAGT CTTCAATAGA CGATGGATTT CTATTATGTA

60

TCAATGCATA C

71

35

(2) INFORMATION FOR SEQ ID NO: 2470:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2470:

45

CTTCGTCATT GTATTCGAGC GCCTGTATAG CTTGCTCAAA TGATGCATAA AT

52

(2) INFORMATION FOR SEQ ID NO: 2471:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2471:

5 AGAGGTTATG TTGATGTGCT TTATTTTCAT CAATGTCATT AACACAATCA TATTTCTTCT 60
 GTTAATGCAC TGTATTATAT TCAAACGCGC TATCGACAAT TAATTTGn 108

(2) INFORMATION FOR SEQ ID NO: 2472:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2472:

GTCCCCAGTT GATATAGGAT CACAGTTTAA TATACTTGGT GAGATAGTAA TACTATTATT 60
 20 AATCAAATA GGTGGTCTGG GTATCGTGAC CGTAACCCTA TTGACACTAG TATTTTAAAA 120
 TAGAAAGATA TCAATGAAAA ATAGATTCTT GATTATGGTT ACATGGAATA TTGACGAACC 180
 TGGTGGTGTT ATTAAGCTAA TTAAACACTT GGCTATTTAT AGTTTAGTCA CTGAATTAAT 240
 25 TGGTATGATT TGTTTGTGTT TATCTTTTAT ACCAAAATTT GGTATAGGCA AAGGTTTATT 300
 TTTAAGCTTA TTCACATCAG TATCAGCTTT TAATAATGCT GGGATTGACC CTTTTTAAGA 360
 30 ATAACTTAAT AGATTATTCT AGTGATCCAA TTGTCATTAT 400

(2) INFORMATION FOR SEQ ID NO: 2473:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 147 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2473:

40 CTTCAAATAC TAAATCAGCG TGCTAAACA TACCGTATAC ATTTGATGGC GTTGATAACG 60
 CGTCCTGCGC TTCTGTTAAT AACTTTTCAG TTTCAGCATC TAAATATGA GGACGTTTTT 120
 45 CATTAATCAA CTTCAAATCA AATGCGA 147

(2) INFORMATION FOR SEQ ID NO: 2474:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2474:

CTTTAGGTGC TTGTGGTAAT TCTAATTCAC AAGATCAAGG TAACAAAAC T GAACAAAAA 60
CA 62

(2) INFORMATION FOR SEQ ID NO: 2475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2475:

CCTTTAAAT CATCTAGAAT ATCTCTGAG AAAAATTCGA AATCTACAGT 50

(2) INFORMATION FOR SEQ ID NO: 2476:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2476:

ATAGTGGTTA GTCAATGTAA TTAAATGAGA ATAGAATGGT GATTTTCATCT TAGCTTGATA 60
ATTAGCAGAA TCTTTAAAGA AAATTTTGTC TTnCAAGCCT AAGTTTACAA CGT 113

(2) INFORMATION FOR SEQ ID NO: 2477:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2477:

CGTAACTAAC TCAATTTACT GAAAAAATCG CTTGCGATGC AATAGCATTT G 51

(2) INFORMATION FOR SEQ ID NO: 2478:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2478:

TAGTTGCCGC TACGTTTATA CTCGTATTAA TGAAAAAAC TAGCAAAGAA TCTAAAAAAG 60

5

(2) INFORMATION FOR SEQ ID NO: 2479:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2479:

15

TCGGACATGA TGGTAAACC GTATTGGGTA TTCGCACTGA CACCTTAAGG GA 52

(2) INFORMATION FOR SEQ ID NO: 2480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2480:

30

TTCCTAATTA AGGATTAAAA AGGGTTTCCT AATTAGATTA TAATTCCGGG ACCTGGATGG 60

AAAAAAGTTT TTAACCTTTC CATCTGGTCC CGTTTTTTGA TTTTCGATAT AAAAAAAGCG 120

CAATTATCTC TAT 133

35

(2) INFORMATION FOR SEQ ID NO: 2481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2481:

45

AAATGTTTTG GAAGAACGTA AGAATAATCA ATCTGAAACA AATGCACGAT ATGAAGAAGA 60

ACAAGAAAAT TTAATGGAGC TTTTAGAAAA TATATCAAAT GAGATTCTG AAGCTCAAGA 120

TACTTATAAG TCTCTGAAAA GTAAACAAAA AGAACTCAAT GCTGTCATTC GTGAACTTGA 180

50

AGAACAACCTA TATGTTTCAG ACGAAGCACA TGATGAAAAA TTGGAAGAAA TTAATAACGA 240

55

TACTATAGAA GAGAATGAGG CTAAAAAATC CAGACAGGTT CTCGTTAGTT GGAGTTTTGA 360

GCCATTGAAA GTATTcGGG GGCCAATTAA AACCGCCAAA 400

5

(2) INFORMATION FOR SEQ ID NO: 2482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2482:

15

AAGGTGCATA GTCAACAACA TTTACAGCAT CATTGATTC TGAAC TAACC GAAACATTAT 60

ACTTACCG 68

20

(2) INFORMATION FOR SEQ ID NO: 2483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2483:

30

ATGAGCCnAC ACAGTGGTGA GGTAATCAAC GGTACAGTGG TTAGTGTGAT 50

(2) INFORMATION FOR SEQ ID NO: 2484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2484:

40

CGGAACTCGT CGAATAACTT TTTAGATTCT TCGTTAGCTT TTACATTAGC GAATGCTTCT 60

45

nTGATTGCTT TGTATTCTTC GCTTTCTCTT AAAGCTTGTT CTAATTGATT TGCATAATCA 120

TATAAATTTA CTGCCATGGT TATAGCACTC CTTGGTnGTG ATGTTTATTA AAACGTTCGA 180

TATTACTTTA CCACATCTCG CTTTTTTAGA CAA 213

50

(2) INFORMATION FOR SEQ ID NO: 2485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2485:

GACCAAAATT ATCTTTAGCA CTTATAGGTA TCTTTTAAAT ACTTTGTGAG TTTTCTATG 60
GCATTCCTTT TTTAGGTGCA ACGTTTATTT TAAGTTTGG ATGGCAGCCT TTACTCTTTA 120
ATGCATTACT TTATCTAATT CTTACTATTA TATTATTAGT GAATAGACAA AATGCGATTA 180
GACCTATAGC GATTATTCCA ATATTGGTA TAGTAGGTAG TTTTTTAGCT ATTATCCCCT 240
TCTTAGGAAT TTTGATTCAT TGGATTTTAT TTTTCCTAAT GATTCCAnTT GTCCTAGTTG 300
GATTATCAGC GCCAACCTAT ATACCCAATA AAAATGCTCG TGrCnTTTTA CACACAATAC 360
AAAGATGGAC CTAGAG 376

20

(2) INFORMATION FOR SEQ ID NO: 2486:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2486:

TTGACCTTGA CGGAAACTTT TTTCCAAGTT CTAAAAGTGG GCCAAAATCT T 51

(2) INFORMATION FOR SEQ ID NO: 2487:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 103 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2487:

GAATTTTGGC ATACACATAC ACTTTAAAAG ATATTATTGA AATTACAGGT GTAACATAAA 60
GAACTTTACA TTATTACGAT GAAATAGGAT TATTAGTTCC AGn 103

(2) INFORMATION FOR SEQ ID NO: 2488:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2488:

5 AATTACATTA GCACCAATCC ACACATCATT TTTAATTGTT GTACGGCTAG GTTGGTCATT 60
 AAAGTCTATA AACGTTTnCT TTAAGTTAAA TGGATTATTA TTTAGA 106

(2) INFORMATION FOR SEQ ID NO: 2489:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 61 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2489:

15 TGAATTGCT TGAGTCGTGC TGCTGATAAC AATAAAATTG CACATGGATA AAGAATGACG 60
 20 C 61

(2) INFORMATION FOR SEQ ID NO: 2490:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2490:

30 GCTCGTATGA TACAAATTCA TAATCTGAAA CTTCTGTCGT TTGTCGAACA TGTGGTAACC 60
 35 AATTCTTCAA GATGCTGTAT ATTTCTGCGT AATTTTCGTC ATTCCTGAAT AACCTCAACT 120
 TTAATAATGTC ACCTTGTTTG ATATAACGCA TTAATAAATA TTGATCTATA TCTCCCTTAT 180
 CTTTAAGATG TTTTACAAAT GGATACAAAT TGTCGATGAT AAATGTATCT TGCATGGCT 240
 40 TATCGATATG AATATGTAAT GCAAACCACT CTTTGTGATA TTCAATATCT GTATTTTAT 300
 ATTTTGAAT TTCGATTTTC GGTCTCGAT AAGATGATTT TTTATAAATT GGTGTAACAA 360
 TTTCATACAC ATGATCATT CTTGATTGAG GGAAAAATGA 400

(2) INFORMATION FOR SEQ ID NO: 2491:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

GACTGTTTTA TCGCAACTAT TTACACCTAT ATTATCGTTA GTAGGACATC TCGTCGG

57

(2) INFORMATION FOR SEQ ID NO: 2492:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2492:

15

CATTGAACTT GCTTTTGACG TACACCAGTA ATCAATGCCA TAATACGATC CGG

53

(2) INFORMATION FOR SEQ ID NO: 2493:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2493:

AATACAATA ACATACACTT ACCCATGTCC GAAGTCCnTG TTGAGGAATG

50

(2) INFORMATION FOR SEQ ID NO: 2494:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2494:

40

GCTGTTTAGC TTGCTCAAAT GATGCATAAA TATCTGATGC AACTATCATA TCAGCTAGTT

60

CATCA

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(2) INFORMATION FOR SEQ ID NO: 2495:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2495:

55

ATTAAGCTTT CTAAATCATT GATGTTAGGA GCTAATGTGC TCGATAAGCA GAGTAAAGAA 120
 GAATTGCTTA AACAAAGCTAA ACATATAACA GGTTTAGAAA ATCCTAATAG TCCTACACAG 180
 5 TTATnGGCTT GGTAAAGGA TGAACAAGGA TTAGATATAC CTAATTTACA AAAGAAAACG 240
 GTTCAGGAGT ACTTAAAGA AGCAACAGGA AAAGCTAnAA AAATGCTAGA AATTAGATnG 300
 CAAATGTCTA AAACCAGTGT GA 322
 10

(2) INFORMATION FOR SEQ ID NO: 2496:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2496:

ATCAGTGTTA ATTGCGACGG AATTTCCTTC CATTAAGCTA ATCCGATCAT ATAATGGAT 59

(2) INFORMATION FOR SEQ ID NO: 2497:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2497:

35 CTAATTAAGC CAAAAGGGGA AGGGTCCACC AACCCCTGGT TTCCCCCAT TGCCCGGAAA 60
 CCACCAGnAA GTTTAAAGCT TCCCTTTAAG CCGTCCGATG GGTAGTCCGA ACTTTACCGT 120
 TCCCGC 126

40 (2) INFORMATION FOR SEQ ID NO: 2498:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2498:

50 CACTTTGCGC CAGTTTTCAG TTGAGTGGCA TAGAGTCTGC TCATCAGTTC CTTGCTCC 58

(2) INFORMATION FOR SEQ ID NO: 2499:

55

- (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2499:

10 TCATGATGCA GACGCAACAG CATTTGGTTA TGAATATGGA CAAATACCAC AGATGCCGGT 60
 AGCATTTCAA TCAAGTAAAC CTTTAATAGA 90

(2) INFORMATION FOR SEQ ID NO: 2500:

15

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2500:

25 TGCTCAAAGT CGTGTAGACA GCCAACTAAT GCATTTTCAA GATCAGTGAC ATCTCCGACA 60
 CCAAAGAAAT CACCGAATAT TTTTGCATGT TCGATTTTAC CTCGTTTAAAC ATCAAACCTTA 120
 ATTTGTACAA ATCCTTTTTTC AAATTTTTTCC TCGCGTTCAA AGTTATATTT AGGGTTTCTA 180
 30 CCATAATTCC ATTCCCAAGT TCTATATTG TCGTTACTTA ACTTTTCAAT ATTnTCCCAA 240
 TCTTCATCCG TTAATTGATA TTCTTChACT TCAGTTTCGC CAAAGATAGT TT 292

(2) INFORMATION FOR SEQ ID NO: 2501:

35

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2501:

45 GGTGTGTGTA GAGGTCGAGA GTTGGGGGGG GAGTAACGTG GAAGTTGCCC GGACAGCA 58

(2) INFORMATION FOR SEQ ID NO: 2502:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

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ATACGGGAGG TATCAGCACG TACGTGCAGT CGGTAATGGA TCnAAATACG

50

(2) INFORMATION FOR SEQ ID NO: 2503:

5

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2503:

15	ATCCCCACTC TTTTAAAT GATTTAACCA TATTTTATTT TTAAATATAA TATCCATCAA	60
	AGTGTATCAA TAAATTTATC ACATGTCAGA AAGTATGCTT CATCTGAATA CACCAATACT	120
	CTCATGAAAC TTATTAAAAA TTACTCTCTC AACGTAAAAA ACCATTCAAA TTCATGAATG	180
20	GTTTGGAAGA ATGATTCATT GTTACGCTAT TTAATCACTA CATCTTAATT ATTGTTGCTC	240
	TAAACGATTA CGCTTACCAT TTAAGAAAGC ATAAACGAGA CCTACAAAAA TACCGCCACC	300
	GACAAAGTTA CCTAAGAAAG CAAAAACGAT ATTTTTTAAA ACGTGTAACC ATGAAACTGC	360
25	ATCAAGGGTA AAGAATACCA TACCTGCATA TAGACCTGCA	400

(2) INFORMATION FOR SEQ ID NO: 2504:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 355 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2504:

	ATTATCTATG AATAAAATTT ATAATAACA TATATTGAGA AATTCTCTAA TACCTATTAT	60
40	TACATTTTTA GGTGCTGATA TTGTAAGTAT TTTAGGTGGA GCCGTGATTA CGGAGACTAT	120
	CTTTTCATAT AACGGTATCG GTAAATTATT TTTAGAATCG GTAATAGGCC AAGACTATCC	180
	ATTAATGATG GCATTAACGT TATTTTCTC ATTTTATAGGT TTACTGGGTA ATTTGATTTT	240
45	TGATATTACT TATGGATTTA TAGATCCAAG AATTAGAAGT AACTAGGGGG GATTAGAATG	300
	CAAAATAAGT CAAATCGCC TTnAAAAATT GCATTTTCTA AATTnATTCA TAnTA	355

(2) INFORMATION FOR SEQ ID NO: 2505:

50

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 254 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2505:

5 CCGTTAGTTC CATACCATAT TTTTCTCTAT AAAATAATTT AACATCTAAT TGCCTTTCTA 60
 ATTTTCAAT AGGGGTAGAT ACAGTTGACT GTGAATAGTT AAGTAACTCT GATGCTTTAG 120
 TAAGGTTCTT TGTTTCACTA GTTACTAAAA ATGATTTTAA AATGTTTAAG TTCAAAGTAG 180
 10 TACCTCCTTT AGGGTTCCTT TTTATCGAAT CCTGAATTCT AAGAATTCTG ATTTAATAAT 240
 AATATATnAn ATAT 254

(2) INFORMATION FOR SEQ ID NO: 2506:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 268 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2506:

AACTCCACCG TGTAATTGCG CTTTCATCGCC TTGAGGATGC GATTGGCGCC GTGCTGCGCG 60
 25 GCACGTGCAG ATAGTGCAG CACTTGGGCA GATCGCGCAC CGCCTCCAGC AGGTCGTCGG 120
 TCATATCCTT GGGATAGTTC GTTACGAnTT GGATCCGGTC GATGCCGTCG ACATCCGAGA 180
 TGCGGCACAG CAGGTCGGAC AGTCGCGTTG nCCGCTGGCA GTGTCGTAGT GGTAATGTTT 240
 30 CACGGTTTTG ACCTAGCAGC GTTCACCT 268

(2) INFORMATION FOR SEQ ID NO: 2507:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2507:

AAAAGTGGCT AATATCATCA GCAGAATGTA TAACATAATC GAATTGCAAC CAGCGATTAT 60
 45 ACCTTT 66

(2) INFORMATION FOR SEQ ID NO: 2508:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2508:

ACCTCCGCTT CAAATGTCAT TGATAGACAT TTAAAGCGGA GGCATGTACA TGT

53

5

(2) INFORMATION FOR SEQ ID NO: 2509:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2509:

15

ACCCTATGAn AGATGAAGTn ATTAACCAAA AACCACGTGT TGTAATATTA

50

(2) INFORMATION FOR SEQ ID NO: 2510:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

20

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2510:

TTAACCTATT ATATTAATTT TAGTATCAAT TCTTTCTCCA GTTCCTGCGT CATTTTT

57

30

(2) INFORMATION FOR SEQ ID NO: 2511:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

35

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2511:

40

ACGTGTTTCAT AACCCATAAA GGCGAATATG GTAACACCGA ACATCATGAC A

51

(2) INFORMATION FOR SEQ ID NO: 2512:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 base pairs

(B) TYPE: nucleic acid

45

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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GTAAAGCGGT CCGCGCTTAA AGCGCTTGCT AACTTCGAAC AATGAATCTG CGGAACATCT 60
 TGCGAATCCA CGAGATGATC TCATATGACG GGCAGCGAGG T 101

5 (2) INFORMATION FOR SEQ ID NO: 2513:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2513:

15 GGGTAATGTA ATAGTATTCA TCTACATCAT CTTGATCATC GTAATGCTGA TTGTACCCTT 60
 CTAAATC 67

20 (2) INFORMATION FOR SEQ ID NO: 2514:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2514:

30 CCCGTCGTTT TCGTGnTTTT CGCGGCGTGT CTCCTGTTG CGCCTCTACT 50

(2) INFORMATION FOR SEQ ID NO: 2515:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2515:

AAGAAAATAT CTCTGAATA CTGATCGATT GCCATCGAAA AACACTGTTA AATCAAGTTG 60
 45 CCCAGTCCAT TGTGTTCAT CCATTATGAT AATCCTTTGA GTAAAGTGTC GCGTTCAATC 120
 CAATCGATAA CTTTCATCCAA ACCTTCGTCG GTTTTTAAGT TAGTAAAAGT AAATGGACGT 180
 TTACCACGAA ATACTTTAGT ATCTTCAGCC ATTTGTTCTA ATGATGCACC TACATAnGGA 240
 50 GCTAAATCAG TnTTGTTAAT TACAAAGACA ATCTG 275

(2) INFORMATION FOR SEQ ID NO: 2516:

55

(A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2516:

10 CTGCACCACC AATAACGTAA ATACTGTATA TACTAGTAAT CGCTAATACA CCGATATTA 59

(2) INFORMATION FOR SEQ ID NO: 2517:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2517:

TCTGCTACTA CGTATACGAT AGAATGGATT TCTTTTGGAA CCTAAACGTG TTAAACGAAT 60

TTTAACTGCC ATTTATAAAA TCTCCTTTAA GTCATGTTTT AATTTTTATT TTCTACAnG 119

25

(2) INFORMATION FOR SEQ ID NO: 2518:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2518:

ATTTCTTTT AAGTTTTTAA AAATCCAAAA TCCTTGTTGGT AGGGCCATGA AAGGGTTGGG 60

(2) INFORMATION FOR SEQ ID NO: 2519:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2519:

50 ATAGAAGTGA AGCACGTAGA TTGAAACGAT GGTAAATAA CGAGAGACAT TTAGAAAACA 60

ATAAAAAATGA GGAATAATCA ATGATACATG GAATTGGTGT AGATTTAATC GAAATCGATC 120

GAATACAAGC GTTATATAGT AAGCAACCAA AATTGGTTGA GCGGATTTTA ACTAAAAATG 180

55

GGTTTGCTAC AAAAGAAGCG TCAGTAAAGC ATTAGGCCCC GGCCTnnGGA AACA

294

(2) INFORMATION FOR SEQ ID NO: 2520:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 145 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2520:

TTTTAGGCCG AAGAnGTAGT AATTTCGGT CCTTTAAGGG GCGGGTGGTT AACCATGGCA 60

ATTAATCCCA GGGATGACCT TACCTAATAA CCACCTAATA ATTACCCGGA CCAAAGGTGG 120

AAATAATCCC TCCGGTCCTT CCCGG 145

(2) INFORMATION FOR SEQ ID NO: 2521:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 169 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2521:

TTTTAGTCAC CAAAATTCTC GCATTTAACT GATACGAATG TGCAATAACT AAAAATCGAT 60

CTAATAATTG CGTTGAAAAA TTTGGCTCGA CAGCACTCAT TACAATTACn AGTGTATCTA 120

TATTACTTAC AGGTGGTCTT TTCAACTCAT TTTCCCGCTC AAACACTTG 169

(2) INFORMATION FOR SEQ ID NO: 2522:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 88 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2522:

ATCCAGCCTT TCAACAAATA AATCTGAAAT TCGATGTTCT AAAATTCTTG CTTCTTGATG 60

TACTTCTTCC CAATTATATT TCAATATT 88

(2) INFORMATION FOR SEQ ID NO: 2523:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 228 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2523:

CAGTAACATC AATCTGTCCT GTAAGCTTGT GGTACTCCGA TACAACCATA AGTCAACGCA 60
 CCACCAAAAA CGCCTTGGAG CCGTTCTACT TATTAGTCCA AGTTTAGACA TTGAAATACC 120
 AACAACTTTG CAnTCCATAG TATCTGAAAA TGTAGACATT GCCTGCAATA AATTTAACnC 180
 ATCATTTTTTA TTATGTGGCA TTAGTGCTAA TTAAACGTAT TCTGGGTT 228

(2) INFORMATION FOR SEQ ID NO: 2524:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2524:

CTCATCCATA GCGCTGGTAT TAGTATAGGT GTCAAACCAT TAGCGTATAT CATATCTTCT 60
 GGATGTnCTC ACATATTCAT AGATGCACAT TTTACTTCTC TCGTACCTTA GTACTGGGA 119

(2) INFORMATION FOR SEQ ID NO: 2525:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2525:

TACCAATATT AAATTTGAAC ATTATAGTTT GACCATCATA ATCTATCTTC TCTATTTTCAT 60
 TATAACTAAT ACTTCTATAA TAAAATTGGC CATTTCATATC TACATTCATA ATTAATCTTT 120
 CATTTGTTGC TATAAATGCC CCTTCAAATT CATTCTCACC TTGAACTTGA TACTCAATTA 180
 TTCCTAGCAC TGACGGACCC TTTTTCAG TGGAATAA ATCATTGGA TTCACATTAT 240
 CTAAAATCAT AATATCCCTC CCACTTAAAA CTATAAACTA TTCTTCATAG GTATATGAAA 300
 TACAAGTGAT TAACTATTnA TnATnAAGCT TAACTTGAT TCCCTTTTCA AGATAAT 357

(2) INFORMATION FOR SEQ ID NO: 2526:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2526:

	CACGCGTCCG GCCACCTGGA CATGGCCGAC CTAGAAGCCA AGCTGCAnGA GGCCCAGAAG	60
10	CATCGGCTGC GCCTGGGTGG CCACTGATGG GGCCTTTTCC ATGGATGGCG ACATCGCACC	120
	CCTGCAGGAG ATCTGCTGCC TCGCCTCTAG ATATGGTGCC CTGGTCTTCA TGGATGAATG	180
	CCATGCCACT GGCTTCCTGG GGCCACAGn ACGGGGCACA GATGAGCTGC TGGGTGTGAT	240
15	GGACCAGGTC ACCATCATCA A	261

(2) INFORMATION FOR SEQ ID NO: 2527:

20	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 108 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2527:

	CTnTAGAGGA TATGAGTTCC TCATCATAAG AATTTCTGGA TCCTTAATAG ATCTCTTGCT	60
30	ATATATAATG TAATAGAAAC ATCTTTTAAG GATCCAGAAA TTCTTAGA	108

(2) INFORMATION FOR SEQ ID NO: 2528:

35	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 109 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2528:

	TTTTAAATA CTTGGTAGAA GTTGGAATGG ATTAATCATT AATTATCTCT CAAGATGTAA	60
45	TGACTGTTCA GCACACTTTT CCGATATGAA AAGAGATTG AAnACAATA	109

(2) INFORMATION FOR SEQ ID NO: 2529:

50	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 150 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

55

GATTAAATTT GTTATACCTG GCTTGTTGTC ACGATCAAAT TTAATAATAC CATCTGAATC 60
 AGTTACTGCG CTTTAAATTT TTTTAGCTGC AACATTGGC TCGTCTAATA ATGAAATnGA 120
 5 GTTTTtagCA TTATCATCAC TCTTACTCAT 150

(2) INFORMATION FOR SEQ ID NO: 2530:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2530:

TTCTTTTGG CCAGTGGCAG GAAGTACGGT CTTATTGGT GTTATGTTAA GAAGGTATTC 60
 20 CCATTTATTT ATCGTTAAAT ATGnATATAG TATAGTAATT TTAATTGTT GCATCATAAT 120
 ACTAGGT 127

(2) INFORMATION FOR SEQ ID NO: 2531:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2531:

CACATAATGA TTCGAATTAT TGTTTTAATT AAACCTTTTT CACATATGTA TAAATTTTAn 60
 35 AGAGCGCATG CGTGAATATT TTCATTTGAT TCAAAGGCAA AAGATAGCCT TATACTCTTT 120
 TC 122

40 (2) INFORMATION FOR SEQ ID NO: 2532:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2532:

50 AAATAATAGA GCAATTGGCA CATGTAAGAA TGCAAAATTGA CTATGGCATC CAGTATTTTG 60
 GTCACAAATG GGTGTATAT GAGCATGTTG AAAAATAAGT CTTATGnTAA ACACTTAGTA 120

55

(2) INFORMATION FOR SEQ ID NO: 2533:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2533:

GAGAGCGGCC GCGTGTAAGG AGAGCGGCGT TCGTTCGCGT GACGCGAGTG TGGTTCGCGA 60
GAAGnGGACC AGAGTTCCCG ATCGAGGCTG TTCGGGTAAA T 101

(2) INFORMATION FOR SEQ ID NO: 2534:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2534:

TTGCTCATT AAGATTATCC CAATCAATAT CATCTATATT TGTTGTACCA CTATTATCTT 60
TTTCTCTTTC TCTTACTTTG TnCATTTGTAC CAGTAGATTC AAGATATATT GT 112

(2) INFORMATION FOR SEQ ID NO: 2535:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2535:

ATAACGAATC CAAAAATATA GAGAATGACA GTGAAACTTA AATAGGACTC T 51

(2) INFORMATION FOR SEQ ID NO: 2536:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2536:

(2) INFORMATION FOR SEQ ID NO: 2537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2537:

GGATGTACCA CCAGCATAAT AAACAAC TTC AAATGGATTG ATAAAGAAGA nACCAGCAGA 60
 GATAGGTAAT TCATTACCAT GTTCTTCTTG TAGACGTTTA CCTTCTTCAA TCTTTTGCTC 120
 ATTTGCATCA AGTTGTTGTT GTAAGTTATC TCGCTTGT 158

(2) INFORMATION FOR SEQ ID NO: 2538:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2538:

TATATTCATT AAATCCACAA AGCGGTCCCG TATAAACATG GGTTCATT 50

(2) INFORMATION FOR SEQ ID NO: 2539:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2539:

AAAGTATACA TATCACTCAA CTAATCAATA ATCATACTTA CCTTCAACAA ATTCTTTAAC 60
 ATGCAGTGTT ATCCCTTGAT AATATGGATA TTTnGTTAAT CTA 103

(2) INFORMATION FOR SEQ ID NO: 2540:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

CAATCAATTT GTCTATCTGT TGAGTGGCAA CCTCTAATAA GCCTTTTATA TTGTCA

56

(2) INFORMATION FOR SEQ ID NO: 2541:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2541:

15 TGGAAATAAC GAAAGTATTA TTAATTTAAA GCATCTTTCT CCCAATACTT TAATGAGTGA 60
 TATTGTTTAT ATACCGTATA AACACCTAT TTTnGAGGAA GCAGAGCGCA AGGGAAACCA 120
 TATTTA 126

20 (2) INFORMATION FOR SEQ ID NO: 2542:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2542:

30 ATCAGTTTCT TCAAAAATAA CTGAAGTATC TGATGCTGAA AATTGGAATA GTTGATGGGT 60
 CGGGnTATTG ATTTTATCT GATGTAAAAA TCCATAAGTG CCATAAGATG TATATAGTTT 120
 CTTCATATGA AAGGTCCCCC TTATGThTTT ATTTATTATA CGATGATAAA CTAGTCATTA 180
 35 CCACTATTAA TAATTGATTA A 201

(2) INFORMATION FOR SEQ ID NO: 2543:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2543:

GAACTTTATT ACAGGAATAG ATAAGCACAG TCGTGTTACA CAGACGCTAA ATGCGCGTTC 60
 50 GTATG 65

(2) INFORMATION FOR SEQ ID NO: 2544:

55

(A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2544:

10 AGCTATTAAT GGCGCTATAA TTGATACAAT AGTTATGATT AATAAAAAAA TAACCGATAA 60
 CATTGCAATT TTATnATGAA TAAATTTAGG AAATGCAATT TT 102

(2) INFORMATION FOR SEQ ID NO: 2545:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2545:

25 AATCTACATC CAGCATGATC nACATCnAG CnGGATTCAC CCTTACTTCA 50

(2) INFORMATION FOR SEQ ID NO: 2546:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2546:

AACCATTCAA CACACGACAC TAAAGTGCAG TACAATCCTA CAAAACGATT GTTTTTATCG 60
 GGTGGTCTAA CCATTGAATA AATAATGAAT AATGGTAAnA 100

40

(2) INFORMATION FOR SEQ ID NO: 2547:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2547:

ATTGAAAATC TTTTATCATT TCATACGTGT GCATAATTAA AAAGGTGAAA CCTCTTATTT 60
 TGAGATTTCA CCTTTTTTAT TGTTAATTTA AATTTAATTT TAATGATTAT TTTGTTTCAC 120

55

(2) INFORMATION FOR SEQ ID NO: 2548:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 142 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2548:

AAAGTGAAAA TTGGAGGTGT AATTTTGA CT AGAACTTATA ATATTATTGG TATCCTTTCT 60
 TGTCTTATAT CTTTATTAT TATGGCGTTA CCAATnATTT GGTACACAGC TTCAGCATT A 120
 TGGTTCTTCC CAGGTGCAAT CA 142

(2) INFORMATION FOR SEQ ID NO: 2549:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2549:

CCCAACCCTA CnAACGACAT TACACAATCA GTAACAGATC GGTATTAAGA CTGGATATCG 60
 TGGCATCTGT TGAGTTAATA TCAACAGTCG TCCAGAATC G 101

(2) INFORMATION FOR SEQ ID NO: 2550:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2550:

TGTAACCATG ATTTAGATGA CTAAACGTGC TTGCCAACAT GCTTCATCCA ATGCCGAATC 60
 CTTTAGCTAC AT 72

(2) INFORMATION FOR SEQ ID NO: 2551:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2551:

5 CAGTAAGAGG ACAAGGCTAT AAGGTGGAGA ATCATGTTTA AAACACTCTA TGCTAGAATT 60
 GCGATTTATT CCATTACGGT TATTTTATTT AGTGCATTAA TAAGTTTTGT ATTAACAAAT 120
 GTTTACTATC ATTATAATTT AAAAGCATCT AATGACGCGA AAATCATGAA GACGCTTAAA 180
 GAAGCAAGAC AATATGAACA ATCAGCTAAA CCAACGCACA TTCAACAATA TTTCCAnACA 240
 10 TTTAGGGTCA AATGGAATTA CCAAATAATG ACCATGGATC CATAAAGGTC nTnAGACCTT 300
 TTT 303

(2) INFORMATION FOR SEQ ID NO: 2552:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2552:

25 TTACTTTTAG CCTTTATTGC ATTTGTAATT TATAGAACTG CGAACAGGTG ACTACTGTnA 60
 ATTTATGTGA TTAAAGTTTC AATGATATTT GATTIATTAG ACCATTGCAA AAGCGCAAGG 120
 TTCTCATGTG CTGCTACAGT TTGCGGTCTT 150

30 (2) INFORMATION FOR SEQ ID NO: 2553:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2553:

40 GCACTCGTCA ATAAAGATGA AGCAGCATTT AATCAATATA CGGCAGAATA CAAAAATT 58

(2) INFORMATION FOR SEQ ID NO: 2554:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2554:

55

AAAATCGTTG AATAATCAAT CATAGCAGTA AGCTATGTnA TATATTTTnA AAAATTGA 118

(2) INFORMATION FOR SEQ ID NO: 2555:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2555:

15 ACAACTTCAA AGAAATCATG TCACAAAAAA AGTATTTGAT TTTAATCATA nGTGGCGACA 60

ATCCGCATAC CAAAGCACAA CCTTTAGTCA ACCAATTCAG AT 102

(2) INFORMATION FOR SEQ ID NO: 2556:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2556:

AGATGCATTA GCAGCATTAG ACGTTAAACC AGTTGGTATT GCTGATGATG GTAAGAAAAA 60

30 ACGTATCATT AAACCAGTTA GAGAAAAAAT TGGGGATTAT ACTTCTGTAG GTACACGTAA 120

ACAGCCAAAC TTAGAAGAAA TTAGTAAATT AAAACCGGAT TTAATTATCG CTGATAGCAG 180

35 TAGACATAnA GGTATTAATA AAGAATTAAAn CAAAATTGCA CCAACATTAT CATTAAAGAG 240

TT 242

(2) INFORMATION FOR SEQ ID NO: 2557:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2557:

TGCACTCATA ATCATCGGAA TATGTATAGA ATCAACTATC ACTTTGCCGT GTTTATCTGT 60

50 GTTAAATGTG TAACCATAAC AGTGTGTCCC ATTTGGATTA TGAATCTCAG AATAATCATC 120

AAAAATATCC TGAATTTnCA AATTAATTTT ATTATAGCGG nAGCAATGTC TATAAAATTT 180

55

TATTTCAA

248

(2) INFORMATION FOR SEQ ID NO: 2558:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2558:

15 TTTGGGTCGT GATTGAAAAA ATCTAAGGCT AATAAACCAT GTTGTTCTGC GCTTAATAAT 60
 TGTTTGAGTA TACGGTTAAT AATTAAGTCT GTATCATGAG GGTGACGCG AAAGTCAGAG 120
 CGCATATAAG TCATATAATT CTCGAAGATT TCTCTATCAG TATTGCTTAA TCTTAATGAT 180
 20 TTAACATTAT TTTCTTTTGT TAATTGCGCA GTACTTTTCA TTGTTACTTA AGCGCTCCTT 240
 TAAAAATGTT TAATTCCAAA TTAAATGGA AATGATTTTA TAGTATTAAT AAGGTCAATC 300
 ATATCATATT AAACGCATAA ATATAACGAT TAATATTGGA GAGGAAAATG AGGACACTTA 360
 25 ATAAAGATGA ACATAATTAT ATCAAGCAA TAGCTAATAT 400

(2) INFORMATION FOR SEQ ID NO: 2559:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2559:

AAGGGAAATT TAAAAGTATC ATTTGATTAT ATAGATTGGA TTAAATTAGG TTTTGGCCCA 60
 TCAGGAAAGG AAAACTACTA TATGTACAAA AAATTTGGTA TTTTACCAGA TATGGAATAT 120
 40 GAAATGGAAG AAATTCGAGC AGTAGAGAAG TATGTTAAAG AGCAAGAGTA GCAGACATGT 180
 TATAAAAGAC TGTGCAAAAT CACCCTCGTT TTACATTTGA TTCAAAGAAG AAGGTAAAAG 240
 45 ATAAGAnTAT TTGCAACTTA AAAAGTCAAT nAGCTTATCG GTATCCATAC ATCATGGATA 300
 AATGAGTnCA ACTAATTAAC AAATCAGCAT ATA 333

(2) INFORMATION FOR SEQ ID NO: 2560:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2560:

GTAAGACATT CACATTTATC ATTTACCAC AATGGGTTTA CCAACCATGG TTAAACGAAT 60
 5 CCAAAACTTT GATGCTCGTA TGTCTCA 87

(2) INFORMATION FOR SEQ ID NO: 2561:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2561:

TTGCATTTTG ACGTAAATGA TTAAACAAAT CGTGATTATC TCTTAATTTT CTAACCGCCT 60
 20 TTTCAATTTT TAACGGCGTA ACTTCCTTTA GAACAATGCC AAATTTATAT TTnTCAT 117

(2) INFORMATION FOR SEQ ID NO: 2562:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2562:

AAGTCAAACA AAATAAGCAA ACAGACTGGT CAGAAGATAA GTTGAATAAT ATAGCTTTGA 60

(2) INFORMATION FOR SEQ ID NO: 2563:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2563:

AAGTGTATT ATTGTGATCA TAAAGTGAAG TATTACCTTT TTTATTCGTA ACCCGATTCC 60
 ATGCGCCTTC AACATAAACT 80

(2) INFORMATION FOR SEQ ID NO: 2564:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 64 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2564:

AGACATGGGC TTATCAGATA AAGTAAAAGC ATTACCTAAA GGGGGAGGCG GTAAGTCATT 60

10

ACCG 64

(2) INFORMATION FOR SEQ ID NO: 2565:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2565:

GTTTGTTTAT AGTACCCTGG ATTTTCTTTA TTCCATCAT GTGAAACTGT GTCAGTGAAC 60

25

GCTGAT 66

(2) INFORMATION FOR SEQ ID NO: 2566:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2566:

TTAATTATTT GTGACGTATT ACACGCATTA CTTTAGAAAG TGATTCCCAA AGCGAATTAT 60

CTTTACGATA AACTA 75

40

(2) INFORMATION FOR SEQ ID NO: 2567:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2567:

ATATTATTAT ATTGCTTTTT TTCAGTTTGC CGTTGTTACT TTCATAACTT 50

(2) INFORMATION FOR SEQ ID NO: 2568:

55

(A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2568:

10 TTTTAGGATT TGTAGTAGGT GAGCGACGTA TTnnGGATGC AATCCAGAGA ACAATAAATA 60
 TTGAGAGAGA GCAATTCATA ACGCAGTTGA AATACATGTG TTACGAATTG CTTTTATGTT 120
 AGTTTTTATC ACACAAGTTT TTTGATGCAA CCCCCTGATA GCGAAACTCA TATGTAGATA 180
 15 ATACAGCTTT TTCAGCATCA TCTACATGAA TTCCAAAACA TCA 223

(2) INFORMATION FOR SEQ ID NO: 2569:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2569:

AATAATGCCA TACAGTGAAG ACCATGCGCA TCAATCGATG TCTAGTGTGT ACTACGTC 58

(2) INFORMATION FOR SEQ ID NO: 2570:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2570:

40 CGTTTCATTA GTTTTAAATG ATCCCCAATA CTTTTGTAC CTTACCAAC TATCGTTCCA 60
 ACACTATCTA CAGCTTTTTTC TGTGGTATTT TTAACAGCG TCTATTTAAT GTCTTATCCA 120
 ATTAGTTTTA TCTCTTAATC CAAATTATT AGTATGAAAA GTCCAATTTT TAAGAATTGT 180
 45 CTAAACAGAT TCCGCAACAA AACCAGCTAn AAACCGTCCA TACTATTGGA ATnAAAACGC 240
 CAATGTTATA 250

(2) INFORMATION FOR SEQ ID NO: 2571:

50

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2571:

AGCTCCTTTC TTCTAGTTA ATATCATThA ATCTTGTTTT TCAGTGTCAA AATTACCTGT 60
 5 AAAACAACA TTTTATCTT TTAAATAGG GATTACACTT TCCACTTCTA TTTTATTAAT 120
 CTCAGATATT TTCATATGAA TTTTTTGAAA TCCTGAATCG AAAAGTTTAG TTGG 174

(2) INFORMATION FOR SEQ ID NO: 2572:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2572:

CATGCGGTAG GTATTTCTAA TCTATGGACA AATGGCGGAT TTATGCCAAA TGGTATTGTT 60
 20 GGTTCCTTCT TTGCATTATC AATTGTAATT GGTTCATACC AAGGTGTGGA ACTGATAGGT 120
 ATTACGGCAG GTGAAACTAA AGATCCTCAG AAAAATATCG TTAAAGCAGT GAATGGTGTT 180
 25 ATCTGGAGAA TTTTAATTTT CTATTAGGC GCTATTTTTC TTATTGTTTC AGTGATCCT 240
 TGAATCAAT TAGGAGACAT TGGAAGTCCG TTTGTTGCAA CATTTGCTAA AATCGGTATT 300
 ACATTTGCAG CTGGATTAAT TAACTTTGTT GTAnTAACTG CAGCAATGTC AGGATGnAAC 360
 30 TCAGGGnATT TGCAGTGCGA GTCGTAATGA 390

(2) INFORMATION FOR SEQ ID NO: 2573:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2573:

TAGAGTACAG AACATACGCA AGGAACTCGG AGTTTACTCA CGGGACTTnT 50

(2) INFORMATION FOR SEQ ID NO: 2574:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2574:

TACAATTACA AACGCATCGT GAGATGTTTT AAGCATCAAT GAGAATCTAA CTCTCCAAG 59

5

(2) INFORMATION FOR SEQ ID NO: 2575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2575:

GACACAACGT ATGACGCATG AAGAGTTGCG TGTTGACAAT CAAGATGATC ATAGCCAAGT 60

TAGTCTAAAT GGTTACACAA AGGGGTCTGA GAAAGATCAA GAAGCATTCA CTAATAATAA 120

20

GGATGAGGAA GCAGTTGCTG CTAAAAATCC TGAATCAGAA GAATATAAAG TGAATGAAAA 180

AATAAAAAAA GAACATAAAA ACTTTATTTT TGGTGAAGGT GTTTCAnGCG GTAAAATATT 240

AGCGGCATTA TTATTCGGTA TGTTTATTGC GATTTTAAAC CAAACATTAT TAAATGTTGn 300

25

TTTACCAAAA ATTAATACGG AATTTAATAT TTCTGCGTCA AnAGGGCAAG GTTGATGACG 360

GGATTCATGT TAGTAAACGG TATTTTAATA CCAATTACGG 400

30

(2) INFORMATION FOR SEQ ID NO: 2576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs

(B) TYPE: nucleic acid

35

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2576:

40

TTTAAATCGT ACCTTAAATT TGAAAGTAAT AAGACACACC AATTACCTTC TAACTCTATC 60

GATAGTTTCA AACAAGAAAT CGnTAGTACA TTCAGTTATT TAGAACGCGT TGATTACCAG 120

45

CT 122

(2) INFORMATION FOR SEQ ID NO: 2577:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

50

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

CACATTGAGG TGCAGTCATA CCTTGTTTAA ATGTCCAAGC ACGTACTTCT T 51

(2) INFORMATION FOR SEQ ID NO: 2578:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2578:

15 AATTATGACT ACAGGTCTGA CTCCCCCTTG TTCAGATCCC TGTACTGGTG ATAAATCTGC 60
 TAAATAAACA TCTCCTCGTC TAATCATTCA TTCGTTGAAT TAGAAGATAA ATATGTTTCG 120
 TTGCAATCGC ATGCTTCACA CTCTATCGGA AAAGCTTCGT TCGCTAGGGA GAGATTTAAA 180
 20 TCAGCCATTT GTGAATATCC TTCTTTTAAA GATTGTTCTA AGCTATGACT TCTATTTTGA 240
 CTAAAAGATA ACATATGAGA ACCTCCAATT GATTCCAAAA GTTATTAAAT GACCTTTAAT 300
 TACTCTAATG ATAACAAATT TTATATGCAC TGACCATATT ATTTTAACAA TTCATTGTGT 360
 25 ACAAACGGT GGATCACCCA TCATGGATAG AGTCGCGGGn 400

(2) INFORMATION FOR SEQ ID NO: 2579:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2579:

ATAAAAACCT AATTGACTCA TAATCTTCTA ACGGTATATC ATCCACAATC ACAGTATGAT 60
 40 TAGGATTATC GTTAGATACA TCTnTCACTG CCTTATCTAA CCCCTCATCA CC 112

(2) INFORMATION FOR SEQ ID NO: 2580:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 231 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2580:

CATGAnTnTA ACGGATTCAT TCCATATATC AATTGCGTTT GTTATTTTAA TAATGCTATT 60

55

ACTACAAC TT CGATTTAAGC TATATTTATA AAAAAATGCG CCTACTCATA ACATTCTTTG 180

GCTATTTAAC TTTAATAAGC TAGGGCCAAG TTTGTCATAA GATAAGCGCA C 231

5

(2) INFORMATION FOR SEQ ID NO: 2581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2581:

ACTTCGTAAA ATTTATCTTG AGTGGTTGTT TCTATATTAA GATTCATTTT ATTACACTCC 60

(2) INFORMATION FOR SEQ ID NO: 2582:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2582:

GTCAAATGCT GAGTTCTAAT AATGATGTTG GCCACCATGC ATACAAAAAT GCTAAAAGAG 60

AATTACGCAA GATTTTAGAT AGCTATCTCG AAAATGGTAA ATTAAAAATAT TACGATATTA 120

TCGTTACAAG CAATTTAGCT ACTAAACATC CGTTTTTCGA GTATGCACGT TCATTTGATT 180

TTATCATTGT TTCAGATATC GGTTTAATAA ACGTTGATGT AAAAAGCTGG GGTGAAAAAA 240

CATTTTATCA CTTTGATGTA CCTGATGAGC ATGATACAGA nAnA 284

(2) INFORMATION FOR SEQ ID NO: 2583:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2583:

GAGTCAGTCG AAGTTTGTCG TTCGACCCGT AGAAGTGTA AACC GCATTG TGAATG 56

(2) INFORMATION FOR SEQ ID NO: 2584:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2584:

TCGACTAATG TAATGTAGGC ATTGGACGTC AAATGTAATG TGGGGCAATC CGACGAGATG 60

10

ATGGTGTC 67

(2) INFORMATION FOR SEQ ID NO: 2585:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2585:

CGTAACCGCC CCTTGTCGG GCCCTCCAAG CCTTTAAGG GGACCCCCCG GA 52

25

(2) INFORMATION FOR SEQ ID NO: 2586:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2586:

35 ATTAGCAACA ATGTCAGATA ATCGATACCA ACTAATTAGG CGAGAAGCGG TTTCTCATGG 60

TCTTAGTGGC CTAGAAATTG ATGTATTTGA TTTGCATTCA AATAAGTCTA GACATATTAG 120

CTCGTTATCA GGTGGAGAAA CTTTCCAATC GTCGCTTGCA nTAGCTTTAG GGTTAAGCGA 180

40

AATTGTACAG CAGCAATCAG GAGGTATTTT ACTAnAATCA ATATTTATTG ATGAAGGA 238

(2) INFORMATION FOR SEQ ID NO: 2587:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2587:

ACTGGAAAAA ACCGCnAACA CGACATTGTC AAAACGACGG CCAGTGCCAA 50

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2588:

GnGCAATTAT ACCACTATAT TTATTTCTTA TACTCCATTT GATTTATAGT TGTATTAATA 60
 CATTGACTCA AAAACTAATT AATCAAATAT GTTTTTTAGA TT 102

(2) INFORMATION FOR SEQ ID NO: 2589:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2589:

GCATAATATC GGATATGCGn GTGTGTCAGT CnCATAGTCG nTGGATTGCG 50

(2) INFORMATION FOR SEQ ID NO: 2590:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2590:

TTAnAAATTG CCTnTCCAAT TnTAAGAATC CTTTTTCCAA GGTAACAAAAA 50

(2) INFORMATION FOR SEQ ID NO: 2591:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2591:

CTTCATCCCT TACTTTTAAT TGTCACGTCA AATAATATTT GTCTTTAACT AGTAATAACT 60
 CCAAATATAT TTAGTTTGTG GTGCTAGCTA TAAACACAAA TGAnTCATAA CACTATATTT 120

TGATTTTnAA TTATTTATAT

200

(2) INFORMATION FOR SEQ ID NO: 2592:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2592:

15

TGCATTAATC ATCTTGGATA CTCTTTCTAC CAAAGTAATG ATTGCACTAC CATGACGACG

60

ACCAGCAATA GTAT

74

(2) INFORMATION FOR SEQ ID NO: 2593:

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 244 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2593:

30

CACCTGCTCA CCTCTATTTT CAAACAATTA TGATTGAATT GAATCATTCT AATTTTTGTA

60

AAGTTACTTG TTAAATTAT TATATTTATT AACTCTATGA TAACAAAAAT ACTGTTTGTG

120

TATAACAATA AATTGAGATA CTCAATAATT TGATAATGTG AAATTGATAC TTTTCAAAT

180

35

AGTTGAATAT GACAATTAAT GATTAGTTTT GCAATGGTGC TATAAnCAAT ATTTAGCAGT

240

TATC

244

(2) INFORMATION FOR SEQ ID NO: 2594:

40

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2594:

50

ATATGGTATG GAACTAACGG AAGAAGGCTT AGCATACGTT AAATATGCTA AAGTGATTTT

60

AGATAGTAAT AGCGAATACG AGAGAGAnAT AAAAGGACTT TACAATAAGA AGGTAAATAT

120

AAGTATTAAC ATGCAAGAnA GTCAGTATTT GTATCGCTAC TATAATAAGA TTAGTGAATG

180

55

(2) INFORMATION FOR SEQ ID NO: 2595:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2595:

AAAAAGTATT AAAAATTGCA ATTCTTAAAC TGTTATTCAT ATTAATATTT CTAGCAAATA 60
 ACATTGTAAA ATAAAGAAAA ATAATTAnAG TATTGCACTT TATTGAAATT TATATTACGA 120
 TAGTAATGCA GAAATTTATA TATGCAAAAT ATTATA 156

(2) INFORMATION FOR SEQ ID NO: 2596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2596:

TGATCCGCAA ATCGCTGAAC ACGTTCTTCT ATTGGAATCC CTCCATTCAC TTTTAGCTAG 60
 AC 62

(2) INFORMATION FOR SEQ ID NO: 2597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2597:

TTACCTTTAG nTTTTAAAAC CTGACCCTCC AACCAGCCTA ATTGGTTAAA TGGGGATCCA 60
 TTTATATAAT CCCAGGCCTA ACCTTCCAAG GACCAACCTA AGGGATTAAT CCCCCCAATG 120
 GCCAAAGTGG GATGGGTAAT 140

(2) INFORMATION FOR SEQ ID NO: 2598:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2598:

5 ATTAATTGGG GAGTTAAATT AAAAAAAGG GGTTCCTTCC AACCGGAnCC ATTCCCATT 60
TGGATTAAAA ATTCCCGCCT TTGAAAAAAT TGTTCGCCGA ACCGCCCTTA AG 112

(2) INFORMATION FOR SEQ ID NO: 2599:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2599:

ATACCGCCCC CAGTTCAATA AGAAGCCCTG GATCAGACCT GACCCTGGTA TGGGGGAAT 60
20 CCC 63

(2) INFORMATION FOR SEQ ID NO: 2600:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2600:

ATACTATGGA ATGCCTTAAT GGTGGATAAT TTCACCAAT TAATTTTAA AAC 53
35 (2) INFORMATION FOR SEQ ID NO: 2601:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2601:

AACTAAAGGT TCTAAAGATA CAGTAAAAAT TGAAAATAAC TATAAAATGC GTGGCGAGAA 60
AAAAGATGGT AGT 73

50

(2) INFORMATION FOR SEQ ID NO: 2602:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2602:

CGGTTGCCAG CCAAACTTG GCAnCCAAGG CAATTATAGC AAGGCACCCA CCTAAATTG 60

10 CGGACCACCC GGAATGCGGC CACCAAAGTT GGTGGGAGGC CATTTTAA 108

(2) INFORMATION FOR SEQ ID NO: 2603:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2603:

AAGCTTATAA CTATTTGTGT TTGTGATCGA GATAGGTTTG CCTGTAAAAA TGGCCATCA 59

25 (2) INFORMATION FOR SEQ ID NO: 2604:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2604:

35

ACGTCCAAAG GGCCGTTTCG CCCAGAnGTG CTGGCAAGGT TCCACAACGn 50

(2) INFORMATION FOR SEQ ID NO: 2605:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2605:

GTCCAATGTC ACATTAATTG ATTGGTATAA GCGATCACAA GGnCATAGTG AATATTTTGC 60

50 ACCAGACGGT GTACATTTAG AGTACAAAGG AGTCCTAGCT TTAAAAG 107

(2) INFORMATION FOR SEQ ID NO: 2606:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 54 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2606:

GTTTAAAGCA ATTTGGAAGG ACATTGGTTA AAGGATGGGA GTGGCAAAAT CTGG 54

10

(2) INFORMATION FOR SEQ ID NO: 2607:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2607:

20

GTTTTAGCTG AAGTTAATGA TGAAGATATC GGAGCTATGG TAATTAAACT AGTTAACTT 60

ATTTTCATGC TTGATTATGT TTTATTTTCAT TCAATTCAAA AAAGCTATAC AACACATATG 120

25

AATGAGCTTA AAAATTGTTT CGATTACATA GCTGAATTAG ATAATCATTa TGCATTAGCA 180

ATGTATCGTA GAACGCTAGA ATGTTATACT GAACCACAAA TTGATGATTC AAATGATGGC 240

ATAGTATTCT CTGAGTTAAC ACATCCACTC ATAGCAGATG GCAGTAGCCA ATGATTTCTn 300

30

ACTATCACAn AATATACTGT TAACTGGGGT CGAATGCTTC GGGnTAAATC AACATTTTAT 360

GGAAAT 366

(2) INFORMATION FOR SEQ ID NO: 2608:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 142 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2608:

45

TTCTTAGACG TCAGGTGGCA CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT 60

TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA TAACCCTGTA TAAATGCTTC 120

AATAATATTn GAAAAAGGAA GA 142

50

(2) INFORMATION FOR SEQ ID NO: 2609:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2609:

GGGTCGTCAA TTGAnGGCAG GTAGAGCATT AAGTCAGAAT TG TAGTAAAT

50

(2) INFORMATION FOR SEQ ID NO: 2610:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2610:

ATTGGGTGAT GAATTTTGAC GGTATTGTCA AGTCCAGTGG CTAAC TTCCG G

51

(2) INFORMATION FOR SEQ ID NO: 2611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2611:

ACAAACTTCG GACTGCCAAT TACATTTACC TTGGGGGGTC AGAAACAATG GGTGCATAAA

60

GGCCCGTGTT TCGAAACGGG AAAAAGCCCA GCA

93

(2) INFORMATION FOR SEQ ID NO: 2612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2612:

ATGATGTTTT TCGGCTAATT TTTATACTGA ATTTAGTTTA ATTAAC TTAT GATATTTT

58

(2) INFORMATION FOR SEQ ID NO: 2613:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 102 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2613:

TTCTCACCAT TAACTATGCA TACTCACTTT ACACATAAAT TTGCTTAACA TGCAGAACGG 60

5 AAATAAATCA TTACCACATA TAGATCCCAT CATATATTTA nA 102

(2) INFORMATION FOR SEQ ID NO: 2614:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2614:

TGAACTACAA GACGCTTATA TCATTGACGC ACATTTCTCG CAGTGAAAGA AACACTTGCG 60

20 TA 62

(2) INFORMATION FOR SEQ ID NO: 2615:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2615:

TGGAGCATTT CACATACATT GGCAACCTCA TGGAGCTTAT CATTCTACCT TGGGGnACAG 60

35 ATATAACAAC ACTAACGCAA CATGGATGGT GTCGTTGATA ACTTTCAATC TATAGAATTA 120

(2) INFORMATION FOR SEQ ID NO: 2616:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2616:

CTGTAGTAAA TTGCCAGAAT CCGTATCAAT ACCAGTCTGT GACTGCGTTG GCC 53

(2) INFORMATION FOR SEQ ID NO: 2617:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2617:

ACATATGATA TGAGTATATT AACGTTTAAA TTATGGATAC TCTAAAGACA GGCGATTTTG 60
 5 AAAAAATCAGC AAAAAGTTAT ATGATGTAAG TGGGACAGAC ATACTAGATG TAACACATTA 120
 ACCAAGTG 128

(2) INFORMATION FOR SEQ ID NO: 2618:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2618:

20 CCTAACCGTG TGTGTATGTA TACCTACAAA AAAATTTACA TTGTGACACT GCGTACGTG 59

(2) INFORMATION FOR SEQ ID NO: 2619:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2619:

30 GCCCATGGTC AATCAGACAC ACGGATTGAA CGTTAACAAT TTATGACTTT AACA 54

(2) INFORMATION FOR SEQ ID NO: 2620:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2620:

45 ATCATTGTCA CATTGAGTAG CCGTAAAATG GTCAGACGAT CAATGCCGAAC TGA 53

(2) INFORMATION FOR SEQ ID NO: 2621:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2621:

CTAAGTGTCTG CCCGAATAAC CGTCAATCCA CGGAGCACAT AGGATCTCCC ATG

53

5 (2) INFORMATION FOR SEQ ID NO: 2622:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2622:

TGGGACCGAT AATCATTCGC ATGAACACCT TCCACCGTCT CTTACTCACT ACCTACGGC

59

(2) INFORMATION FOR SEQ ID NO: 2623:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2623:

ATTAAATTGT TATTCGTCA TTAGGTGACA ACTTGATGT AGATATTTTA ACATATTTTA

60

30 TGCT

64

(2) INFORMATION FOR SEQ ID NO: 2624:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2624:

CCGTCCCAGA ATATCATATG ACAAATGTTA AGAGACTTGA ATGATCATAC ACGTG

55

45 (2) INFORMATION FOR SEQ ID NO: 2625:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2625:

GTGGTCACCA GGTACGGGGG ATACAGGGGG TTAATCCCAC CTTGGATAAG TGGAAAACGG 60
 5 ATTTCC 66

(2) INFORMATION FOR SEQ ID NO: 2626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2626:

CCACCAATGG GTGGGGGATG GAATAACCCCT TAATGCGGTG GTACCCGGGT AATGGTAGCC 60
 20 CC 62

(2) INFORMATION FOR SEQ ID NO: 2627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2627:

CATGTTTTTT CATTCTTGA TGACGACACT AGAGGTTCCC GTGTTCATTA TTAA 54

(2) INFORMATION FOR SEQ ID NO: 2628:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2628:

TTGGCCAATG GCGGATACAC CCTCTCAATT CGATACATAA CTCAAGGCTC AGTCAT 56

(2) INFORMATION FOR SEQ ID NO: 2629:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2629:

TGTCGCTAGG TAACCGTGCA TCGTTCACAG GTACnTATGA TTTCACCnGA 50

5 (2) INFORMATION FOR SEQ ID NO: 2630:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2630:

GAAGGnCCCA AACCAGGCGT TAAAGGCCGA TTGGGTTTAA ACCAAAGGTT 50

(2) INFORMATION FOR SEQ ID NO: 2631:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2631:

CGCGAGTGTA TCCGTCGATA TGTCGAGAGG AAAGATTGAA GTGTGGAAGA GTGTTGAGTA 60

30 ACCCT 65

(2) INFORMATION FOR SEQ ID NO: 2632:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2632:

TGAAAGAACT TTAGCTAGAC GTTCGTAAAG GTCTTTTGAC ATAAAGCTAG AGA 53

45 (2) INFORMATION FOR SEQ ID NO: 2633:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

AAAAGCCAAA AGGAATTAAT TAACCCCGGG GTTTAATTC TAATGGGAAT TTG

53

(2) INFORMATION FOR SEQ ID NO: 2634:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2634:

15

GGTGTTTACA TTCTGAAGGT TTAGAGAGTT AAGATTATAT ATATATAAGT TTTGGGGTGA

60

TAGATATG

68

(2) INFORMATION FOR SEQ ID NO: 2635:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2635:

30

CCAATTTTAC TTGGTGCTGC CATTTCCGTC TCTCGTGTAC TTGTGATTGA GGTGCCATTG

60

TTCCCGTAGA TGGTTCACAT

80

(2) INFORMATION FOR SEQ ID NO: 2636:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 144 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2636:

45

CTTACACCCA ACTTATTGAC TTATAATCTA TTAAAGTGCC ATTTTACAAT CTGAATCCCT

60

TAATATAGCA ATAATTACAA CTTCGACAA ATGACTTGTT TTATGTGCGT GATTCATCAA

120

TGAACATCGT AATGCGACnT AATA

144

(2) INFORMATION FOR SEQ ID NO: 2637:

50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2637:

5 TAATTCGGCA ACTAATATCA AGATCATGAT CAAATACTAC TGCCATTTTC TTATACCTCT 60
 TAATGTGAAA TCACTGnCAA CACATAACAT CTTAAAACTT TGAC 104

(2) INFORMATION FOR SEQ ID NO: 2638:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2638:

20 CATTTCATCCG TTTTTTTGGT TCATGTACAT ACCATTGTTT TGTACACAGC GAAGTCAGTT 60
 AACCTTATAT CCTTGATATA CAGTTGAAAT CGGCAATATT AAACAGTACT TTCCCAATTG 120
 CTTTCTTCCT CAATTGTGCG ACGGACTGTA n 151

25 (2) INFORMATION FOR SEQ ID NO: 2639:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2639:

35 AAGATCAACT GAAATTCATG TGTGCCCCTT TATTAAGATC ACATGGAAAT A 51

(2) INFORMATION FOR SEQ ID NO: 2640:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2640:

TTAGCTAGTT GGTAGGACGG CTACCAGGCA CGTCATAGCG CCTGGAGGGG TC 52

50 (2) INFORMATION FOR SEQ ID NO: 2641:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2641:

CAGGCTTAAA CCTGAGTTAG TGCCATTCAT AATTGCAATC CCAAGCGACG GAA 53

10

(2) INFORMATION FOR SEQ ID NO: 2642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2642:

20 ATGTTTGTCA TCTGGAGCnA TAGAACAGGG TTCATCATGA GTCATCAACT TACCTTCGCC 60

GACAGTGAAT TCAGCAGTAA GCGCCGTCAG ACCAGAAAAG AGATTTTCTT GTCCCGCATG 120

GAGCAGATTC TGCCATGGCA AAACATGGTG GAAGTCATCG AGCCGTTTTA CCCCAGGGCT 180

25

GGTAATGGCC GGCGACCTTA TCCGCTGGAA ACCATGnCTA CGCATTCACT GCATGCAGCA 240

TTGGTACAAC CTGAGCGATG GCGCGATGGA AGATGCTCTG TACGAAATCG CCTCCATGCG 300

30

TCTGTTTGCC CGGTTATCCC TGGATAAGCG CCTTGCCGGn CCGCA 345

(2) INFORMATION FOR SEQ ID NO: 2643:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2643:

40 CTTATACGGA TGTATAGGTC GGTCCAAACA TTTGATTTTA GTGGAGAGCA GCCTTTCACA 60

AATTATGTTT AATGT 75

45

(2) INFORMATION FOR SEQ ID NO: 2644:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

TACCGGTAA TTAACCAGGG CCCCGGTAAA AAAATCCCCG GTATTCCCCA TTCCAAC

57

(2) INFORMATION FOR SEQ ID NO: 2645:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2645:

15

AAAGCAATTC GCCCGATAAG AGTAGAGACG AATTGCTTTT AAGGTTAAAA CAAAGTGAGT

60

TCAATT

66

(2) INFORMATION FOR SEQ ID NO: 2646:

20

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2646:

30

CAGTATAACT TGTGACCTAT TTAGAGGGGC ACGGTTGGTA CAATGAGTCT GAAACCGTAT

60

CAA

63

(2) INFORMATION FOR SEQ ID NO: 2647:

35

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2647:

45

TAGAACATGG ACCGGTATTT TACATCCTGT ACGCCTAATC TGTTGTAAGT ATCTTTAGTG

60

AACCGTTGCT CTGGAATAAC CGCGATTCTG GGCAAACAGT GTGTAAACCG ACTnTATGGG

120

GATGTGTGAG TAATCATTGT GnACTGTTGA TTCTGTTCTG GAATCCCATT TCACAACACG

180

ATCTTGGAAG TGCTGTCATT TTAGATGC

208

50

(2) INFORMATION FOR SEQ ID NO: 2648:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2648:

TTTTAACCTA AAGAATACTA AACTAAAAG AGAATGATTC TGTACCGCTT TCCTTTTTCa 60
CTCAATAACT TTATATTTAG TTATCCTTAT AATTGTAATT TATGTTAGTT GGTAATnTT 120
TACATATATG TATTTGATAT GCTTGTAAT 150

(2) INFORMATION FOR SEQ ID NO: 2649:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2649:

AGTTTAACTG ACATCGAGTG GTACACAATA GCAATGGTTG TGTGTAAAGT CCTGGTGACA 60
ACATATGAGA GTAACATTTG TAGTGATTAT CTTGTACTGA GAGAATTGAC ATCTATGnAG 120
TTTATCACGT GCAAATAT 138

(2) INFORMATION FOR SEQ ID NO: 2650:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2650:

TCACAATTGC AAACCTTCTGG CACGCACTCA TCTGCGATTT CACAAGCTAC AT 52

(2) INFORMATION FOR SEQ ID NO: 2651:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2651:

GAGTCAAATT AAAATGCCTA TTGGCCATTG TGATGTATAA TCACTTAGTT CACATATACT 60

55

(2) INFORMATION FOR SEQ ID NO: 2652:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2652:

GGGCGGTAAT TGTCACCATC ACAAATTGCT ACGTTGAAAC ATCGAGGATT CAAGCTGGAC 60
 AGCAGAG 67

(2) INFORMATION FOR SEQ ID NO: 2653:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2653:

ACACATCTTA TATGTCTTAC TGATTTAAGG AAAGAATCAG TGGATCAAAC TG 52

(2) INFORMATION FOR SEQ ID NO: 2654:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2654:

CAAGCTGTAA ACCAAGAATT CCAGCATTAA ATATCTCTCn TGGTATCGGT TGAGATAAAT 60
 ATTCCGTGTG CTCATTAAAT GTAGTAATCT TTATTGTAGT TCCTCAACCT ATGACACGAA 120
 TATTGCACAA TATTAGTATA GACAAATATT TCCTTTATAA TCTCATTCAA TTTTCTCCTT 180
 TAATTATGTA TCATACATTG TATATTCTCA TATAGACGTT TTGnCATATT CATAGCTTCA 240
 ATATTAGTGC ATTTATGTAT T 261

(2) INFORMATION FOR SEQ ID NO: 2655:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2655:

AATCCTATTA GCACCTATAA TGATCATGAA AAGATGTCAT CGAGAATCAC CTAGTACACG 60

5

(2) INFORMATION FOR SEQ ID NO: 2656:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2656:

CGCCGAAAAC AATAAATTCT CGGAACATAG AATTTATCAC ATACCACGCT TGGATTATCA 60

CAATGGACTG AGTCG 75

15

20

(2) INFORMATION FOR SEQ ID NO: 2657:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 202 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2657:

TATTAAATAT GCGGTTGCAT ATATCTACGG CATGATTTAA CCGTGAACCA TGAATCATTT 60

TAATCGGGCA CGCGTAAAT GCTCATTGAT CCGCAnATAC CACTATATAT CTAATAGCAA 120

35

GCGTCCAGGA TTCTGTGTTT TATAAATTTA AACTAACTGA AACGTGTGTA TCAGTTCACT 180

CCGnTCGATT ACCACACTTC AA 202

40

(2) INFORMATION FOR SEQ ID NO: 2658:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2658:

CGTACATGTG CATCATGTAT CTACGTCAAT AAGATGATGG GGTCACATGA TTGGACCATT 60

50

(2) INFORMATION FOR SEQ ID NO: 2659:

55

(A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2659:

10 CTAATCATGT CATGTCTACA ATTATTTGGA GTATTGCTGA CGAAATGCGT TGTACAACTT 60
 TTTCAATTCTA GCACCTTGCG GGGGCCCAACA AAGAATTGG TCCATTCTCA nCATCAGTGG 120
 GGGGCGCGAA TAATTTTCGAA ATTATTCTGC CACTCCCACT TCATCGATTA AGTTGTAACT 180
 15 CTACATTACA TTTGTCTTAA ACCATTG 207

(2) INFORMATION FOR SEQ ID NO: 2660:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2660:

TTAATTATGT ATAATACTTA ACAAGATCAC CTGATAGATG TCTAAATATT ATCT 54

30 (2) INFORMATION FOR SEQ ID NO: 2661:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2661:

40 ATTAAAAA AATGGGGTAA TTTCCGCCAA ATCCCGTTTC CCCCTTGCCA AGGCCAAATT 60
 TAACCACCT TGCCAAATnA TTAAGCCAAA TTTCCGATA TTTGTTCCG TAATGTTTCT 120
 45 TTAATTAATA 130

(2) INFORMATION FOR SEQ ID NO: 2662:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

AAAGTAAAC CAGTCTATTC AAAAAGGTGA AAAATGGTGA CGCAGCGTAA ATAAnTGGTC 60
 TCTGGTAGGG TAAATCGCGT TGTGGGTTTG TCACATCAGG AACT 104

5 (2) INFORMATION FOR SEQ ID NO: 2663:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2663:

AAAAAGAATA AAAGGACTCG AAAAActCAA AACTTATTnT AGATAGTCAT CGTGACAAGA 60
 AACAAACATT TAACTAGACT AAGAAAAATG CTTCGATTAA AAGGCAGACT CATCA 115

20 (2) INFORMATION FOR SEQ ID NO: 2664:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2664:

GCATGCGCCA CGGTGTCTCA GCAGAGTGAC TGCCACCTTG TGTGCGCAGA GTCTGCGCCT 60
 AGTACAGTCA GGGTGAAACA CnCTATACGC ATTAGGTACA GTACTTCCTG TCTCCGACTT 120
 35 GAGTAGAACG TGACATATCT ATCAGCATTC ACTCGAAAAA GGGA 164

(2) INFORMATION FOR SEQ ID NO: 2665:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2665:

AATTACGCAA TnTCCCTGTC TTAnTGAAAG GAATTGACCT GTTAATTCGT 50

50 (2) INFORMATION FOR SEQ ID NO: 2666:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2666:

5 ACAATTCAAT AGAATTTACC CGTAACAGCG TTGCACTGCA CTCAAGACGG CTGACGTATA 60
GCAC 64

(2) INFORMATION FOR SEQ ID NO: 2667:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2667:

GTAGAACCAG CGACGGCGCG GCGGCTGAGC AACATCTGAC TACCTATCGG CCGCGC 56

20 (2) INFORMATION FOR SEQ ID NO: 2668:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2668:

GGATCGATTG ACTACATGAC GTGGnGACGC AATTATACGG ATAGTCCACT 50

(2) INFORMATION FOR SEQ ID NO: 2669:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2669:

45 GCAAGATCGA ATTACAATCA CGACGATCAA CGCACGTAAT CATCTCTGAT CACAGTAA 58

(2) INFORMATION FOR SEQ ID NO: 2670:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
50 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2670:

5 ATACCAGCCA GACTTCGATC AACAGTGTTT AACTGCATTG CCCAGTAAGT TGGATAGCTC 60
GCACATAGTG CTACAAGTTA ACATATACAn CGAGTTTGTG TCTCAAGCTT GAAGCTTGAC 120
TACC 124

10 (2) INFORMATION FOR SEQ ID NO: 2671:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2671:

20 CGCTTACTGC ATAAAAGCCC CTAACACCGG GGCCTACGC TCGTTCGCCG GCTT 54

(2) INFORMATION FOR SEQ ID NO: 2672:

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2672:

TCAGCGATTT AACACTAATT CTCTAGCTA TTCTCTGTAT TTGGACGACG A 51

35 (2) INFORMATION FOR SEQ ID NO: 2673:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2673:

45 GATAAGTTGT ACCATATTTT GATGCAATTC AATGGACAAT GAGGTCACCT GGCTTGT 57

(2) INFORMATION FOR SEQ ID NO: 2674:

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2674:

5 TCCTTTGGCC AATTTTTCCTA AGTTTAAACC CAAACGGCCC GGGTTGGGTC CCCAATTCCA 60
ATCCAAAATA ATTTTA 76

(2) INFORMATION FOR SEQ ID NO: 2675:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2675:

TCCGGGAACC TTACCCAGTG GCCCTACCCT ATGGGTAAAC CCAACCAGTG GGGCCA 56

20 (2) INFORMATION FOR SEQ ID NO: 2676:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2676:

TGCGGGGTCT CGTGCCGCCG TCTCGGTGG TTGTTGTCC GGTGGTGTGT CGGAGTCTTT 60
GCCAGCT 67

35 (2) INFORMATION FOR SEQ ID NO: 2677:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2677:

GGACAGAGGC CTTGACCCCC CCACAATCCT GATTCACCGT AAGTTGCTCT CCCCC 55

(2) INFORMATION FOR SEQ ID NO: 2678:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2678:

5 AAATTGGGGC TTCCATCCCC ATTCCAAATT ATTAAAACCG TTTAGGGGCC TTATTGGCAC 60
CATGG 65

(2) INFORMATION FOR SEQ ID NO: 2679:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 176 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2679:

ATTTTGGGAT TAAACCCTTA ATTAAAATTG GCCGGGAAAA GGAAAAGGCC GGTGCGGAAA 60
20 AGGCCAAGGA AAAGACCTTG GGAACATTA AAAACCTTGG GCCAAGGCCT TCCAAAAACC 120
GGTTGGTTTT TATTTTGGGA ACCAAATTGG GGGCCGGGA TTGGGCCAAA ACCTTG 176

(2) INFORMATION FOR SEQ ID NO: 2680:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2680:

35 GCCCCAAAGA ATTCAAATAA CnTTCGGAC CCGGTAATGG CCACnTAATT 50

(2) INFORMATION FOR SEQ ID NO: 2681:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2681:

TGTGCATTTA TTGCATAACC TATATATGTG TGACCGATAT TTAGTGCACA CTTCAATGGT 60
50 GCG 63

(2) INFORMATION FOR SEQ ID NO: 2682:

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2682:

TTATCCAAGC TTCCGGATAG TTTCAAGAGA AACCAATGAA ATCCGTTATG GGACCAATGG 60

10

GT 62

(2) INFORMATION FOR SEQ ID NO: 2683:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2683:

AACAGCATTG AAGTGAGTTA CTGGGGTTTA TGCACCATCA TTGGATATCT GCACAAGGAA 60

25

TTTCAACGTG 70

(2) INFORMATION FOR SEQ ID NO: 2684:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2684:

CTTAAAATTC CCCAGTTTCC TTCCTTTTAA ACCCCATGGA ATTATCCCGG CCAAAAATGG 60

40

ACCATTAT 68

(2) INFORMATION FOR SEQ ID NO: 2685:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2685:

TTTTAACAAA ACACCTAGAT ATGTTGCTG ATCAGAGATG CCTGGTGACC GGTGATCC 58

(2) INFORMATION FOR SEQ ID NO: 2686:

55

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2686:

10 ATCCATCCTT ATAGGCATTC ATCCTTTAAC ACCAACGATT TACATTATGG ATATAACGAC 60

TTGAGGGGGA ACGTGGGGTC CATCCTA 87

(2) INFORMATION FOR SEQ ID NO: 2687:

15

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2687:

25 ATGGCTGGGC GCTTTACGTG GCCACATTAG GATTATGGCA CTGAAGCGTA 50

(2) INFORMATION FOR SEQ ID NO: 2688:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2688:

AACGGTCGTA GGCAAGGGAC TCCCCCnGG nGCTAnATGA ACTGGTCGTA 50

(2) INFORMATION FOR SEQ ID NO: 2689:

40

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 60 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2689:

50 GCTAGCATCC ATGGCTCCTA TGCCGAAGCT GAGTAGACTT AGGTGACGGG TGCCTGACAA 60

(2) INFORMATION FOR SEQ ID NO: 2690:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2690:

ACTTAAAAAA GGAAGATTAG AAAATTCATA AAAAAATTTT GCTGGGGATT CTTGATCCCA 60
TGGGCCCCATn TCTGGATTTA GGTATTGGG TTGGCCAGCC AGGTTAGCGG GGCCCCCATT 120
CTTCCAGGCT CGGTTTCTCC CAGGAC 146

(2) INFORMATION FOR SEQ ID NO: 2691:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2691:

ATTGGTGTCT AGATCATTTA ATACTAAACA TACAACACGA CTAATTCCAT TCA 53

25

(2) INFORMATION FOR SEQ ID NO: 2692:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 113 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2692:

TATTGAATTC AAACATATGTA CTATTCCTA AATAATACAA TAAAAACGAC TACCATACTG 60
GCCAGAAATA TATTTTATTT GTTACACATT AATTTCAATC CTCCATAATT TGC 113

40

(2) INFORMATION FOR SEQ ID NO: 2693:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2693:

GACTTATGTC CGTGTTCGCG TGAAGGCACG TCACGTAAAC TACCCGGTAC AGCT 54

(2) INFORMATION FOR SEQ ID NO: 2694:

55

(A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2694:

10 CTTCAGCATG AAGAAGTCGC GTGATATACA TCATATCGAT ATATACCGAT TATATCATCA 60
 GAACATTCTC CTGGTATCAT TAGATAGATG ATAATTTGAC ACAGTCCACA ATTTGTnACA 120
 ACGCCGAGAC TCAATGGCAT CCTGTACnTG ATCTATGCCG GAAAACACTA GTCTATATGC 180
 15 CCGCAGACGT CCACTATATG CATC 204

(2) INFORMATION FOR SEQ ID NO: 2695:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2695:

ATAACTCTAA TTTGAATTAT CTCTCACTAT TAAAACGCGA GCTGTGTAAT AACGAACGCT 60
 30 GAACATAATCT TGTATTGTCG CATCATTCGC TGGTATTATC ATAnTGCGGT TA 112

(2) INFORMATION FOR SEQ ID NO: 2696:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2696:

TGGCAAAATT AGATGTCTGA ATAGTTTTAT TTACAAGTAC AAACCTTGTA CCATTTTAAC 60
 GTAAACACAA TTTACTTATT GAAAAGAAAA TAAATGTATT CATGAAnACA CACTTTCCAT 120
 45 AGCACTCATC TATAGTACTC AAATTTCAG 148

(2) INFORMATION FOR SEQ ID NO: 2697:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2697:

CCTATAATGC TAAACTTCAT ATATCTCTTT GGCAACTATC TCCCTTCTAT TACCAAAGTT 60
 5 ACGATAGCAA nACAATAAAG CAAGCATGTC ATGCTTACTT C 101

(2) INFORMATION FOR SEQ ID NO: 2698:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2698:

TTGATAACAT TTGAAAAGCT GCTCCGATAT CAGCAACCAT TTCATCGACC ACAATATACG 60
 20 ACATAGTCAC AAAACTGATT AGAAGACACC AATTGCTGAT TATCAAATCA CAAATTTAAG 120
 nTGAGATTCA A 131

(2) INFORMATION FOR SEQ ID NO: 2699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2699:

GATAGCGGTT GTTAATCAAA CGATGGTACA TGCTTACATG ATGCGCCATG TTTGATAACA 60
 35 GCTCTCTATG ATTACGATGG AAGAATGGTT TATTTTCATCT CAATTATTCC TATTAAATGn 120
 AACATGCCCT AGCAAACGGA TACAACACAA TCACAACATC ACTTTGAAAT TGTTAAACCT 180
 40 GAGAACCACA TACGCGnAAC AC 202

(2) INFORMATION FOR SEQ ID NO: 2700:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2700:

TTCGAATTTA ACAAACGTAT CACGCCATAA AGGTTGTATA TGTGTTTGT AAATTC 56

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2701:

TATTGCGGGC TTATTAGTAC ACGATCTATA TGATGGTCAA ACTTATGTCT TTCATATTCA 60
 AGTGTGACAT TGTGCGGTGA TTATATTTAC GCGTCGTTAT CTACGAACGC CACATTAAGA 120
 TTCGAAACTG ACAATCAACT CATAACGCCA TGGTCCTAGA AAn 163

(2) INFORMATION FOR SEQ ID NO: 2702:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2702:

TAnACAATCG TAATCGAGTC AATGATGTGA ATTGCCACG TGAGCGCTAA GAATGCGACA 60
 TTCCACACGA TAAGGCAGTG CGCATGCGCA CTGACCTAAT AACACTGAGG ATGAGTACTA 120

(2) INFORMATION FOR SEQ ID NO: 2703:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2703:

CTGCTTGATT AGGATCGTAT TTATATGAAG ACTGTGTTCC ATAATGATGT GCGTTTTGGC 60
 TGAAGTCCCT TAAATGTACn TGTGTATAAA TGCTATAATT TAG 103

(2) INFORMATION FOR SEQ ID NO: 2704:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TCTATAACGC CTCTCATCGT TTGGTCACAT ATTACCATTA TTCATTTTAT GTTCTCGATA 60
 ATTGTATGCG nTGTTTCTCA CTGTCATCAC ATTGATACAA CTCATTGTCA CTTTATACGA 120
 5 TTCACACACC TCGATACGAG TGATGATATA TGACAAAGCT 160

(2) INFORMATION FOR SEQ ID NO: 2705:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2705:

TTATTGTTTA AGATGGTTAA ATGTCATCAT ATAACAnTTA ATTTTtagCA ATTcGATATG 60
 20 CCTATAACCT ATAAATTTCA CGTCAACAGA AAGTGACAGG CATACGGATG TGTGAA 116

(2) INFORMATION FOR SEQ ID NO: 2706:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2706:

TTACACCTGC AGTGTATGGA CTATGGCTAG ATACAATAAT TTTAGTCATC AAnCTACATC 60
 35 ATACAAACTT ACGACTTACA CATATCTGCT TCTAnATCTT CTAActGATT AAAGCTCGAC 120
 ATCGGAAGCT ATTCTAAAT ATTATCATAT ATCTAACTAA CTGACCTAAT ATATACTACC 180
 ATAAATAACC CGCCTCAAGG TTCGCATCCG CATATAATGC TTAGAAGTC 229

(2) INFORMATION FOR SEQ ID NO: 2707:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2707:

TCCATATCAA TCCTGAAAGT ACACATATAT CGTACACCAT ATGGTACAAT TTCCTATAnT 60
 ACACATCAG CATCTTTCAA GACACATGTT AGGCGCTGGT CGGTGTATCT CAGAAATGCA 120

(2) INFORMATION FOR SEQ ID NO: 2708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2708:

GGAAC TTTTC TGATT AAGTG TTCAC AGCC AACCA TAACA TGTATT CATG CACACA ATTG 60
 TTGCT AAnCT CACTA ACAAC ATACG ACCAT TTTACT TTCA ATACAT ATGA TCCGT ATAAC 120
 TCGAATT CnC TGCTT ATAAA TGACC ATTTT GACGTT CACA ATGTT AAAACG ATTGG AAAATT 180
 TTAAAG TTAG CATGT CCACA TCCGAG CAGT AACTAT GCCG TACCATT TGT ATA 233

(2) INFORMATION FOR SEQ ID NO: 2709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2709:

TTGTAC CTAC CAACG AGGAT ACAAT GGATG TCACAC GAAA ATTGG GATAT AGATGT CCCA 60
 GT 62

(2) INFORMATION FOR SEQ ID NO: 2710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2710:

CTTTAAA AAG GATAA ATGAT TGAGAn AAAA ACCCAT TCGA AAATCAT GCT GCTCAT GCTG 60
 TAGACT TATC GTTTG GACAC TCGCG TAAGA GCGAG CAGTG AAAT 104

(2) INFORMATION FOR SEQ ID NO: 2711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2711:

GTCCAGAATA TTAATCTGAC ACAACCATTT TAGCnGGTGG ATTAAATATA TACGACCTCA 60
 CCGCAAGAAT CTCTATTAA CTTAACCTAT CATGAATAAA CTGGCGCTTG TGATATCATA 120
 TGAAGATTAG CGAAAGATAG C 141

(2) INFORMATION FOR SEQ ID NO: 2712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2712:

TGGTATTGAA TAGCAAAATT TTGACACTAT TTGCATACTC AATGATACAT CATATCGTTA 60
 TATGGATTTT TATGGTCATT AATGGTAAGA ATTGATACG GAATATTGGC AGGTTTGGAA 120
 ATCAAATAAT ATGAGAAATT GTATTAACnA TTAGTCAAGT TAACGCTCAT AAATAGACTC 180
 ATCnCGCGCT ATAACGCTTA CC 202

(2) INFORMATION FOR SEQ ID NO: 2713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2713:

TTGAACTGTC TAAGACTTGG ACGCTAAATG AATGCGTTGA TACAAACGGT GAATCC 56

(2) INFORMATION FOR SEQ ID NO: 2714:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2714:

CATGACCGAC ATCAGGTGCA AACTCCCTCA TTAATCTGGG AAAACTGTAT CCCGGTAGCT 60

(2) INFORMATION FOR SEQ ID NO: 2715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2715:

CCTATAACTA CTCAATATTG CAATTACACA TCCTCACTTT TGTCAATTGT TTGACAATCn 60
 AATACACGTT ATGCACAACCT CCATTTTAAAC GGAATGGAGA GCACATATGG ACAGTAAATT 120
 AAAT 124

(2) INFORMATION FOR SEQ ID NO: 2716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2716:

GGAATATGTA CTATTATCAT TTGATGTTAT TACTCATATT TTTTGTAATG AATGCTATCA 60
 CCTACAAAAA ATTTACTTGA AACAGTAATA ATAATTAATT ACCACAAACC ATGATAAATT 120
 TAATAnCTAA TCTAAAATAT CGCATGTTCA nAGCCACAAG ATATAACGCG TTCCGTAGAT 180
 GGAAGTAGAT AGTATAAGGC GCCGTGGAGC CTGGCCT 217

(2) INFORMATION FOR SEQ ID NO: 2717:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2717:

ATGACATACG CGCATATACA TGCTATCCCG AACTAATATT GATGCGTATT ATGTAATTGG 60
 AGCGAACACT CA 72

(2) INFORMATION FOR SEQ ID NO: 2718:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2718:

CATATCATCA CTATATCCAT TCGTAATAG TGATGATATT GATTGGCATA ATGGTATATG 60
GCAGATACGA TAACATAACn AACACCTCGG ATAATTGCTA TTAGCTGCGA AGTTATCGTG 120
CCTGATTTAA CGATGTAGA 139

(2) INFORMATION FOR SEQ ID NO: 2719:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2719:

CTCTATCATA TCTAGCCATA TGCATGAGAT TATCGTTTAT CTCGACACGC TCTTAAAAGG 60
CGACACCGGC ATATGATGT 79

(2) INFORMATION FOR SEQ ID NO: 2720:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2720:

CAATCACAAT TGAAATTACA CAAATACAGC CCATTGCATG ACACAGACCA ATC 53

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(2) INFORMATION FOR SEQ ID NO: 2721:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2721:

CGCCCAGGC TACCATTTTA CCATAAAGAC CGGTCTAAAT CCTTCGGTT TCCATGGGCC 60
ATTGG 66

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 169 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2722:

TnCTCGCCG AAAATGACCC AGAGCGCTGC CGGCACCTGT CCTACGAGTT GCATGATAAA 60
 GAAGACAGTC ATAAGTGCGG CGACGATATC ATGCCCCGCG CCCACCGGAA GGAGCTGACT 120
 GGGTTGAAGG CTCTCAAGGG CATCGGTCGA CGCTCTCCCT TATGCGACT 169

(2) INFORMATION FOR SEQ ID NO: 2723:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2723:

CCGGGCCAAG CTGGTGATCA CCGATGTGGA GCGCCAACAT CGCATCGAGG AAAT 54

(2) INFORMATION FOR SEQ ID NO: 2724:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2724:

ATCGGTGATC ACCAGCTTGG CCCGGGACAA CTGCAGAGCG TGCAGCAGGA ATTC 54

(2) INFORMATION FOR SEQ ID NO: 2725:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2725:

AAAACCATTG TCCACCTTTA GAAAGCTTTT GTTTTGGGAA TACCTAAACC GTGGTTAATG 60

(2) INFORMATION FOR SEQ ID NO: 2726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2726:

TTTAGGCCCT GTAACnGnTT GCCGnTTGn CCGTGTGTAT ATCGGGGGAA

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(2) INFORMATION FOR SEQ ID NO: 2727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2727:

GGATCATTAACGTGTATCA CCATCCAGTT TGCAAGACGG ATAACTGCT GCAACG

56

(2) INFORMATION FOR SEQ ID NO: 2728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2728:

ACCCATGGAG AATTAAATTT AAAAACCGTA TTCCGGGTGG ATGCTGGGTG GGTAAGTTGG

60

CCATACTGGG

70

(2) INFORMATION FOR SEQ ID NO: 2729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2729:

ACCACCTTCC CCAATAAGCT GGCCTAAAGC CCCATAATGG GCCATGGTGC GGCC

54

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2730:

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TGTTTGGGGA CCTTAAATGG TTCCAAATTC CAACCACCCA CCAAAAGAAT TCCAGTTTCC 60
AATTAAGCCA GCCA 74

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- (2) INFORMATION FOR SEQ ID NO: 2731:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2731:

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AAGTTGGGGA TTAAGGCCAG TTATGGAAAG GATGGATGGT CCATTGGGC TTATTAGAAG 60
AGCATT 66

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- (2) INFORMATION FOR SEQ ID NO: 2732:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2732:

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TTTGnAAAAG CCnGTAAGAG TATTTGATTT TGTTGGAGGC CAAACCAGAA 50

- (2) INFORMATION FOR SEQ ID NO: 2733:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2733:

AGTACCAGCG GACAATTCGG ACCCAACTTG GCAATTTGnG GTTTTGGACC AGGAAATAAA 60

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(2) INFORMATION FOR SEQ ID NO: 2734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2734:

CCAGGCTGGC AGTTTTTCTA AAATGGTGGT AGGAAAATTA nCCAAACCAT TTAGGATGGC 60
 ATGGTCTTCC ACGGATGGCG GCCGTTAACC CCAAAAAAGG CCATTCCATT T 111

(2) INFORMATION FOR SEQ ID NO: 2735:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2735:

CGTATGGGAT GGCCATTCTG ATGACACACA ACGGTTAGGT TAGCAACGTT GTCAAA 56

(2) INFORMATION FOR SEQ ID NO: 2736:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2736:

CAATCCGGGT GTGCGGGCGT GTGTACAAGA CCCGGGACGA TTACCGACAT 50

(2) INFORMATION FOR SEQ ID NO: 2737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2737:

TAACATTAT TGTGGAGAAA GTnAGGTATC GTGGTAGTGA GGATTGTGTT 50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2738:
TAAATTATAA CCCGTCCCGG TTTCCCAAAT TTGGAATTTT TTGGAACCCC TGT

(2) INFORMATION FOR SEQ ID NO: 2739:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 85 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2739:
ATACCCACCT TGGATTCTTA ATACCCCAAA AAGGCCGGGG CAACTTGGCT TAAAAAACTG
GCTTGTTTAA ATTGGATTTC CGGCT

(2) INFORMATION FOR SEQ ID NO: 2740:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2740:
GGAAAGTTTA GTAGTTTAGA GTCGAAAAAT TAGTTTTCTA GTGTAACGAA TCCGGACCCA
AATTTTTTTC

(2) INFORMATION FOR SEQ ID NO: 2741:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2741:
CGCGCCAATT TACCTGGCGC AGCAGACGCT CAACGAGGAG CACGGCAGCT GCG

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2742:

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TGAAGAAATC GCACACACTA TCGAACGCAG ATCGCACATC GAATGCATCA GAATCAGCTC 60

- (2) INFORMATION FOR SEQ ID NO: 2743:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2743:

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TATCACCTCT TTTGCATATT ATTAGAATAT ATAATGATCT TTATAGAAAG GAAAGAAGAA 60

GAGTTATCAT nGCGATATCG CCCAGCGCGT CGTACACTAT GCCATGAATT ACACAATCAT 120

GCCTC 125

- (2) INFORMATION FOR SEQ ID NO: 2744:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2744:

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GAATTTCCCC CGAAACCGGG AAAAATTTTT CCAACCGGT GGCCTTCCCC CGTTCCCGT 59

- (2) INFORMATION FOR SEQ ID NO: 2745:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2745:

TTTTCCTTAA GTTAGTTTTT TTATTGGGCC AAAACCGGCC CCAGGAATTG A 51

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2746:
TAATTTGGTC ATAATGTTGT TTCAGATGAA ATGCTAACAA TACTGATT ACAGT

(2) INFORMATION FOR SEQ ID NO: 2747:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2747:
ATGGTGAAT GGGATTTAGG TGGATGGCCC CCCCAACCAG CCGGTCCTTT TTAAGGAACT
TTGT.

(2) INFORMATION FOR SEQ ID NO: 2748:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2748:
AACAAGAGTT ACATTGGTTG TGGAAATCAT CGGTTTAAAT TAGTCCAAAA GGATGGATTC
AATCGGTAGG GGGGTAAG

(2) INFORMATION FOR SEQ ID NO: 2749:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2749:
GCAAGTGGCG GAGTCACACT TATAGACAAG AAGTACGACA TCTTGATGT GGTG

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2750:
TATTTAGATT CAAAGCATCA AATTGGTTTC GTACCCTTTT GCACATCGGT TGGGATAA 58

(2) INFORMATION FOR SEQ ID NO: 2751:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2751:
GGAAAACCCC CCAAATTTTC CCCCCCGTT GGGAAAAGAG TTCCCAAAGT TGAATTAGT 60
TCCCAAACCC GGGAGTTCC 79

(2) INFORMATION FOR SEQ ID NO: 2752:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2752:
AGAACCGAGA GATAGTGCCG AGAGAGCGAG AGGTTTTAAT AGAGATGTTT GGCCGTACTA 60
GTTAGCCG 68

(2) INFORMATION FOR SEQ ID NO: 2753:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2753:
ATAATCTATG GGGGGACCGT CTGGTAAGGA ACCTGGTTGC CCTGCCAATG AAGCCACCCT 60

(2) INFORMATION FOR SEQ ID NO: 2754:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2754:

ACAAAGGTTT TACGCCCAA TTGTTCACTG GCTAACTGGG CGATGGTTAG TATTGGCAGC 60
GCAAAAGTGG CAGGGG 76

(2) INFORMATION FOR SEQ ID NO: 2755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2755:

ACCTCAGGGA CAATTAAAAG TTTTCTTCG GAATGAATGA CAACAACAAA T 51

(2) INFORMATION FOR SEQ ID NO: 2756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2756:

ACGTATTCCC TCGTTCTTAG GTCTTCTAAA CATAGGTGAC TTTTGGTTCG 50

(2) INFORMATION FOR SEQ ID NO: 2757:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2757:

AAATGCTTCG TATTAACGCC TATTTTAGCT CCGTTATAGA CACAACCTAC ACA 53

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2758:

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ACACGGCAGC GAATACTCGT TTGGTGAGCC TGTACACATC TAACACGAGA A

51

- (2) INFORMATION FOR SEQ ID NO: 2759:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2759:

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GGGAAAACCA ATTAAGGATT TAAAGGTTnA TTAAAGGGG CCGCCACCGG GTTGGGGATG

60

CCCTTTGGGC ACCTTAAGAA AGCCCCGATG GAAAGGGACC GGTTACCTTA ACCGG

115

- (2) INFORMATION FOR SEQ ID NO: 2760:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2760:

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TTTGGCCAGG CCAATTAATT CCTGGTGGCC AATTAAATTT AAGGGGACCT TTGGGGGAAT

60

AAGGTTTAAA ATTGGAAAAT GGTCCAATTT GGACCTTTTG GCCAATTGGA TTCCCGGCTT

120

AAAAAGATTT GGACCGGTAA ATCCCTTTTT AAATTACCTC GGGCCAnGGC CCAACCAAGC

180

CAAACCAATT TAAATCCGCC TGGAAACCAA CCCATAnTTC CTTTACC

227

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- (2) INFORMATION FOR SEQ ID NO: 2761:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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ACACTATTGT GCCAGCGCAC CTTGAGGTA TCTTGCATCA CTCAGCTGTT TTTTACTGT 59

(2) INFORMATION FOR SEQ ID NO: 2762:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2762:

TTATCCTGTT CCTAAGCCCG ACGGCTCGGC CACACGATTA ACCTTTAACG CCATCTTGTC 60
 CAACCTGT 68

(2) INFORMATION FOR SEQ ID NO: 2763:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2763:

TGGAAAGTAC CATATAAGTA ATGGTAGTCG TTTCAGAAAG ATATAAATCG TTGGGAAAAG 60
 AAGAAATGAC AaATTAATGT AAATATTTGT TCATGTACAA ATAAATATAA TTTATA 116

(2) INFORMATION FOR SEQ ID NO: 2764:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2764:

TTGTTACAGT GGTGTAGCGG ATCGCACGGC CTTCAACTAA GTGGTTCAAT GCTTGATACC 60
 AGTTATGAGT GTTGGTGC 78

(2) INFORMATION FOR SEQ ID NO: 2765:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2765:

ATATATTCGT ATGCACCTTT TGTAAGGCTT TGTAATACGA AAATTATCAC TACAATGATT 60
 5 GCTGTAACGA GTAACGACAT ATATGGCACA CCGTTTTTAT TnGTTTTACC AA 112

(2) INFORMATION FOR SEQ ID NO: 2766:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2766:

TATTGAAGAT TTTTTCGAAG ATAAAGGTGA CACATATTCA TGTCATGTTT AATATCGTTA 60
 20 CCTTACGTAA CCATATAAGA CTGTAAGTGG TGTCATATCA TTCGTAGAAC nTTTGGAAAT 120
 GAT 123

(2) INFORMATION FOR SEQ ID NO: 2767:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2767:

GTCCGCGCCA CGGAATGGCC CACGGGACGA TAAGTGAGGG CACCGACGGC CGAACCCAAG 60

(2) INFORMATION FOR SEQ ID NO: 2768:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2768:

GTACGCGGAG CACGAATTCC GCGGATCTGG GAGCATCTCT AGGTAAⁿTTT 50

(2) INFORMATION FOR SEQ ID NO: 2769:

(i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2769:

5 CTTAGGTAGC TCAGTGTGTT ATTGAGAGGC CTGTTGGCAG GCCCCGGACG ATC 53

(2) INFORMATION FOR SEQ ID NO: 2770:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2770:

AAATTGATAG CGTGCACAAA CCAGGTCCAT CCACGAACAT GCCAATCCAG CCCAGGAAGT 60

AATTGCCCCG 69

20 (2) INFORMATION FOR SEQ ID NO: 2771:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2771:

ACGATCATCT GGATGGATAT ACAGAACAGT GTGATTGTAC GTGGTGGGGA AA 52

(2) INFORMATION FOR SEQ ID NO: 2772:

35 (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2772:

45 TTAACAGTAT GATATTATCA CACGTGAATA GGATATGCCA AACTGGGCAT CGTTGGGGAT 60

AGCGTAATAC 70

(2) INFORMATION FOR SEQ ID NO: 2773:

50 (i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2773:

5 AACATTGTAT TCGTGATTAA GACTTCGATC GGTTCAGTAT TCGGCAGATC CACATGTGAC 60
CATGCTT 67

(2) INFORMATION FOR SEQ ID NO: 2774:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2774:

CACCCTTGTG ATATCACATT TGTATGTGTT AAGAGGGAGC CCCTTTCCCG ATCAACTGGC 60
20 GATAAAAACA GTTGAAAGT GGGCGGGGGT TATTATTCTT GATGACGGCG GGGTTTTTTC 120

(2) INFORMATION FOR SEQ ID NO: 2775:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2775:

AACCGTTGCA GGTAAAGCTG GGCnCACCAT TCTTCTCTAT TAATGGTTCA 50

35 (2) INFORMATION FOR SEQ ID NO: 2776:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2776:

CATGTACGGT GTCCACACAA GAAGTATTTA GGTGGTTGTT CCCGATTTA ACCTGGC 57

(2) INFORMATION FOR SEQ ID NO: 2777:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2777:

5 AACGACCCCG GGTTCACCG GGTCCATTA AGCCAAGGGC CAGGGGACCC C 51

(2) INFORMATION FOR SEQ ID NO: 2778:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2778:

TTGTTCCGGC CTAAAAAATT TAAATTGAAC CCAAGGGTTG CCTTGGGTTG GGTAATCCAT 60
TTTTTGAATA AACCTTTGnC CCTAATGAAT TTTCCGCCA TTAAAGGGT GTCCGCCAAT 120
20 CCGG 124

(2) INFORMATION FOR SEQ ID NO: 2779:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2779:

GTAAATTTGG GAATTACCGG AAAATTAAGG AAAGGCCAGT AAGGGGTTTC CAGGCCAA 58

35 (2) INFORMATION FOR SEQ ID NO: 2780:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 371 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2780:

GCACTCCAGC CTGAGACCA GGGTGAGACC CTGTCTCAAG AACAAAAACA nCAACAnCAA 60
AAAAC TTGTT CAAAAC TCACTTCCTGCAGT AATCTTTCTT TGAACAAACT CACCCTCTAA 120
50 TTCCACCTG CAATTGTGTG TAGAAATCCA TTCTCGTGTG TAATTTTGGG CTTATATGCA 180
CACATTGAAA ATCCAAGAGC CAGAAAGAGC TCTAAGGAAT TATCCAGTCC AGCTCTGTGC 240

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AGCCTGGGCT AGGACCCAGA TCTTTCCCAT TTCCCTGTTC CAAAAATTTT nGGCACAGGG 360
TGGCCACCCT G 371

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(2) INFORMATION FOR SEQ ID NO: 2781:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2781:

GGGGTTGCCA AAGGGGTGTT AAATTTAAGT CCGATGAAAA TTAAGnAAAA AAATCCCATT 60
 TTCCCTTCCG GGTCCGTTGT TGGGGCCTTA ATTTCCCGCC AATCCAAGTT TGGTGAATGA 120
 AATTAATTAC CGT 133

20

(2) INFORMATION FOR SEQ ID NO: 2782:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2782:

GTTCAAGTTG ACGCTGGATC ATCTGGTACA CACGTATCCT GCATACTATA GATGTCAT 58

35

(2) INFORMATION FOR SEQ ID NO: 2783:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2783:

GCTAATTATA GGCCGTCAGG CATTACGnGA TCGAATCTGG CAACTCACAA 50

45

(2) INFORMATION FOR SEQ ID NO: 2784:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2784:

GCCnChCTCT GTGACACTGT GTATATACAC CCGCGGGAAT ATCTCCAACG 50

5

(2) INFORMATION FOR SEQ ID NO: 2785:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2785:

15

CTTTGTCTGA CATATTGGGG CAGTGATTTT TGGGACGGTT CTACATGTCG AGTACTTTAG 60

TCAGAGTTGT GAGTAGCGGA CGGGTnTACT TGATATACCC TTAATGTGTA T 111

20

(2) INFORMATION FOR SEQ ID NO: 2786:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2786:

30

CATGATGATA CTGTCATGTA CGTTGTACGT GAACGTACAG TTACGTTGTC 50

(2) INFORMATION FOR SEQ ID NO: 2787:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2787:

TCAGCAAGTA GTAAGGATAT CAAACTATGA TCTATTTGAT GTTATGCCAT AA 52

45

(2) INFORMATION FOR SEQ ID NO: 2788:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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GCATCATGGA ATATTAAAC AGCTGATATG TTTGAGTAAT GATTGATTGA CGAGATATGC 60

GGCA 64

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(2) INFORMATION FOR SEQ ID NO: 2789:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2789:

15

TGAGAGAAGT CACAGTCGCC AGCGCAAAG AACCCGnnAA GATGTGnGCA 50

(2) INFORMATION FOR SEQ ID NO: 2790:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2790:

CAGTGTATGG AATCTTGTTT GAGTGTGAGA GTCAAAGACT TGGTGATTGA ATGGAAAAAT 60

30

TGAA 64

(2) INFORMATION FOR SEQ ID NO: 2791:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2791:

ACAAnGGGTG AAGTTCTCCC ACATGCTGTA TACCGTGGGA TTATTTTAA 50

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(2) INFORMATION FOR SEQ ID NO: 2792:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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ATTCCTATTC AACACGGAT ACATAATCTT TTATATCTTC CTTCTAGTCA TATGATACTG 60
GAATAAGTGA TATTTCTTAT AAT 83

5 (2) INFORMATION FOR SEQ ID NO: 2793:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2793:

CATATGTCAT CGTACGTAAT CATCGATGAA ATATCAACAT CTCGACTTAA TAGGTCAACA 60
AGAT 64

20 (2) INFORMATION FOR SEQ ID NO: 2794:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2794:

30 CCCTACTCCG CGCAATAACC GCATTACCAG ATGCGCTTCC ACTGAGGAAC GACGGAT 57

(2) INFORMATION FOR SEQ ID NO: 2795:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2795:

AGATAAAGTG TCATCTATAT CCATCTATCA ATATAGATAT GTTTACGGCC GATTTCATC 60
45 CGCAA 65

(2) INFORMATION FOR SEQ ID NO: 2796:

(i) SEQUENCE CHARACTERISTICS:
50 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2796:

TATACGCCTC ATTACACCCA ATTGGACCCT TTACGTATGG AGTACATTAT AGAATCGA 58

(2) INFORMATION FOR SEQ ID NO: 2797:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2797:

nGCTAAGAAT TTATAAGAGG TTTCGGCAGA TATATATACG CAAGTATCTG 50

(2) INFORMATION FOR SEQ ID NO: 2798:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2798:

AAGCAGTCTT TCACAAAAAG TGAATAATCA CTAGTTCATT AATTTCATT TGAACCTTCA 60

TATAATGCAT ATTACTTAAT GTACAAGCAA AGATGTATTT ACCTATCAAA GAATTnC 118

(2) INFORMATION FOR SEQ ID NO: 2799:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2799:

CCATAGAACC TGTGAATACC TATACATATC ATACTGTGGA ATTCGTTACG AGG 53

(2) INFORMATION FOR SEQ ID NO: 2800:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

CCAATTCAGA CTGTTATTCT CTCTTCGTGA TAACCCGTGA TGTTTGTCTG C

51

(2) INFORMATION FOR SEQ ID NO: 2801:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2801:

GGGGGnGCAT ACCGCACCGA AGCATCAGAC GATGTGAGCG ACCTACCTCC

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(2) INFORMATION FOR SEQ ID NO: 2802:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2802:

CCGTAGCGCA CATATGACGA GACCAAGGAT AACGTGCAAn GnCATATTGT

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(2) INFORMATION FOR SEQ ID NO: 2803:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2803:

40 CACGTCATGA ACGTGCAATC AACACAATCA TTTACGAGAT GGACCAAGAC

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(2) INFORMATION FOR SEQ ID NO: 2804:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2804:

TATGGTGTIT ATTTTAGCGC TnGTTGTGCT TTGTCTTCAG CATCTATAAC CTAGTGCGAT

60

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CTATTG

126

(2) INFORMATION FOR SEQ ID NO: 2805:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 88 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2805:

AAAAGCGCAT ATGGTGT TTT TCTCATATCA CTCCAGGACT CAGCAGCTGG AAGGAGTTAA 60
15 GAAGTAATAA GGTGCCACCC TAAATCCA 88

(2) INFORMATION FOR SEQ ID NO: 2806:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2806:

TGGATCCGGT ACCAAATAGG GACTACCGGG AATGTCCCGG GGGGCCTAAT GCCGAATGGG 60
30 GCAACG 66

(2) INFORMATION FOR SEQ ID NO: 2807:

- 35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2807:

CCCGCTAACG TGGGGAAAGT TTTGAAGTTA AGAAGGAATG GATTCCTAAC GGGGCGGGGT 60
45 CCAAAC 66

(2) INFORMATION FOR SEQ ID NO: 2808:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2808:

ACAAAGCAGT ACTGAACTGG TTTCGTTGGA GCCCGTGTG CTGTTTATTC ACGGCA 56

5 (2) INFORMATION FOR SEQ ID NO: 2809:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2809:

AGGGGGCGTA CAACATAGAT TTGCGAGATA CTCAGCATT CACTTCCATT TAACTTATTA 60

TCC 63

20 (2) INFORMATION FOR SEQ ID NO: 2810:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2810:

30 TTAGGCGCCT GTTCCAACCG CACCCATATA AGGCGGTCGG CTGCACGCAC GACGTATG 58

(2) INFORMATION FOR SEQ ID NO: 2811:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2811:

AAACCCCAA GGAATTAATT TTCCGGTTTT CCAACCCCTT AAAAAGGGAA AGGCCAAT 58

45 (2) INFORMATION FOR SEQ ID NO: 2812:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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CATCATTAAG GCAAAAACTT TCACAAAGTC ATGAGGCGCA AAAGGTATTA TTATAACACA 60
TCCCGCGTTG GG 72

5 (2) INFORMATION FOR SEQ ID NO: 2813:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2813:

15 CCATTTAAG CGGTACGGGG CTTGGTTCAG GAACGTCGTT AGACAAATTC GGT 53

(2) INFORMATION FOR SEQ ID NO: 2814:

20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2814:

30 TAGTACCCAA TTTCCAGTCG AACCAGGATG GGACCAGAAG CCAAACCAAC GTT 53

(2) INFORMATION FOR SEQ ID NO: 2815:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2815:

40 GAAAAAAGG CCTTGTTTAC CAAAGGGGCC AATTTTTTCG GTTCAAGGTC CAAACCTACC 60

TT 62

45 (2) INFORMATION FOR SEQ ID NO: 2816:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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TCTGAATGAC GCCGAAATCC CATCTGAATT CATGGGATTT TCCACTTTCA

50

(2) INFORMATION FOR SEQ ID NO: 2817:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2817:

15 CGTTACTAAA GCTACATAGT GCGTCATTTA AGATTATAGC AAGTAGCATA T

51

(2) INFORMATION FOR SEQ ID NO: 2818:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
20 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2818:

CATTCACCAT AATATTCATT GTTCATTAG CATATCAGGC ATGTCACGTG CACA

54

(2) INFORMATION FOR SEQ ID NO: 2819:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2819:

40 GTGTATCAAA TGAGCATGTT nCAATGGTTC AnCATGGCGT TTATGGCACT

50

(2) INFORMATION FOR SEQ ID NO: 2820:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
45 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2820:

ACAATTGCGG CTGCTCATTG TGAGCACGAC TTTATCATGG TTGGGTTTCAG

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2821:

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CAGTAGTACG TAAAAATGAA TCACTTGAAG ATGCGTACGT AGATTTTAAA CGTCAGTTCT 60
AAAAAGTGGG CAATCCAAGA GACGTAACGG AATTTnCGAA AA 102

15

(2) INFORMATION FOR SEQ ID NO: 2822:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2822:

25

GAGTACTTAA TCCGGCACCG TTTACTTCTG GGGGCATCGA CTAAGTGGGG CGGCC 55

(2) INFORMATION FOR SEQ ID NO: 2823:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2823:

ATTGGTTTCT CATAAACACT TTTCTATGAA TTTGTATGTA TTTGTTTATT AAAATCTCTA 60
ATTCTTATGG A 71

40

(2) INFORMATION FOR SEQ ID NO: 2824:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 134 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2824:

CCATTGAGTG TGAGTATATC ATCGATCAAT ATGCAACATT TATCAGGTGC ATGTTGCTTA 60

55

TGGATAATTG AACA

134

(2) INFORMATION FOR SEQ ID NO: 2825:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 57 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2825:

15

CCAGAATGAT GAGCTACAGG ATCAGCCCAG ATATGCAGGT AACCGGGCCA ACCATTG

57

(2) INFORMATION FOR SEQ ID NO: 2826:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2826:

CAATAATGCT GAACAGCAAC GCATCTCATT CTAAAATCGC TCAGAATCAC ATCCCATGCA

60

CACATAATAA GTGGCACTTA GCTTAAAT

89

30

(2) INFORMATION FOR SEQ ID NO: 2827:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2827:

CGGATTAGTG GTGTAAACTG GGTGACCCAT ACCACACCTC GCGTGTTGTG AAAAAAGGAC

60

TTAA

64

45

(2) INFORMATION FOR SEQ ID NO: 2828:

50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

55

TATACAGAAA ACAGCGTGCC GTTATCCATT ATCACATGAC ATATGTAGTC C

51

(2) INFORMATION FOR SEQ ID NO: 2829:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2829:

GAGATACGGT CTCGTATAT GATATGTGCA TATTTAGATA GTCATTTATG AGAGAACGTG

60

15

GACGTGAG

68

(2) INFORMATION FOR SEQ ID NO: 2830:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2830:

TGATGATTGT TTATGATACG ATATGTAAAT GATAATCATC CAGGAGGTCT AGCATGGT

58

30

(2) INFORMATION FOR SEQ ID NO: 2831:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2831:

40

CCTAACAAAC ATAATTAAAC CCATAAATGC ATCCAATGCG GTTAAACCAT GAAA

54

(2) INFORMATION FOR SEQ ID NO: 2832:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2832:

55

(2) INFORMATION FOR SEQ ID NO: 2833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2833:

GTCTGCTACC CTTTCAGAGC AACATGCTGA GTGTATAATG CCGTGATAG GGGACAATGC 60
CATTCACTA 69

(2) INFORMATION FOR SEQ ID NO: 2834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2834:

AACACCAGCT GGTAAGTATC ACGTTACATT TTGTGCTTC ATGATTAATA AAAAC 55

(2) INFORMATION FOR SEQ ID NO: 2835:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2835:

AGAGCTTGGA TGTCGTTTCGT AATTGATGCT CTAGCTCCAT GGGGCCCATG 50

(2) INFORMATION FOR SEQ ID NO: 2836:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2836:

TTTCGTCACT ATTGCTCATG CATAGACATT TGCAATACCG GCAAATGACG ATGGnATATG 60

TTAATGGTCA ATACAGGG

138

(2) INFORMATION FOR SEQ ID NO: 2837:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2837:

15

GTTGGCAACT TCAGTCGCTA CTTTAACGCA TCTCACAGTC CTCCTCCCAA AGAGAACGTA

60

T

61

(2) INFORMATION FOR SEQ ID NO: 2838:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2838:

30

ACGTGAATCC CGTGAGGCCA ACAGTGATTT GGATAATTAC ATGGATGTTT GACTAATGGT

60

CATTACACC CAGATCAG

78

(2) INFORMATION FOR SEQ ID NO: 2839:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2839:

45

ACTTAAATC TCCTCTTGCC TAACTTCCAC ATTCTTATCG ATATGAATAC ACCATACGTT

60

TTATAGATAA GTTGATGTTG ATGCATATGT

90

(2) INFORMATION FOR SEQ ID NO: 2840:

50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2840:

TATATTTAGT CTGTTATACA AGGTGTATCA CAGCGGTAAT ATGCCTCTAC ATGGCCATAT 60

5 G 61

(2) INFORMATION FOR SEQ ID NO: 2841:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2841:

GGGCCCCGGC GGCAGGGAGG AAGGGGGCAA GGGCGGCGCC AAGACCACGA CCGGCACC 58

20 (2) INFORMATION FOR SEQ ID NO: 2842:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2842:

30 TGTACAGGTG CAGTTAGACC GCCTGACGGA ACGAGACGTG CAATTGCCAG CAACGCACAA 60

(2) INFORMATION FOR SEQ ID NO: 2843:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2843:

AAACATGTGA AGTGATCGAG GTATGGACGG AGTAATGATC GCACAAGACA TAGCATCCCC 60

45 GT 62

(2) INFORMATION FOR SEQ ID NO: 2844:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2844:

ACGATTTAGT TTGAATTCT ATTAGGTTT GGTGATTCTA CTACTTCTGA TA 52

(2) INFORMATION FOR SEQ ID NO: 2845:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2845:

GATTATCACA ATTATGCAAA GTTGTCTAAT CGTTAGACCA ATTCTGTTC AACACCACA 60

ATC 63

(2) INFORMATION FOR SEQ ID NO: 2846:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2846:

CGTTATATAA GAnCGACATG GAAGCATGAT GAAATATTGA ATACATCATA 50

(2) INFORMATION FOR SEQ ID NO: 2847:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2847:

CCACAGGTGC ATCCGCCTGG TATGGAGCCG GCCAGTCTTC ACTGCTTTCA C 51

(2) INFORMATION FOR SEQ ID NO: 2848:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

AAAACTGTCC CAAGCTGTTT TTATTTAGAG CAACCAATCC AATTAAACC CCCCACCATT 60

ATTTTAAATA ATACCATTCC AGCGAAAGCC CTTTCCAnGG TTTTGAATA TAA 113

5

(2) INFORMATION FOR SEQ ID NO: 2849:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2849:

15

CATCTGGAAC TTTTAAATTC CAGAAGGGTT CCAGAAGGTT TCGAAATCCC TCCTAATGGG 60

CTCCATTAAC GGATTTTAAA TTTTAAATA ATTTTAGGCC AAAAAATTAA TTTCCAGGAA 120

20

AAGTAAGTTT CCAACCCGGG TAAGAAATTA CCnAA 155

(2) INFORMATION FOR SEQ ID NO: 2850:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2850:

30

CACAACTAA CATAGAAGGG CCATCATCAG GTGCTATTAA ATATCTACGC TAGATTGTAA 60

ATCA 64

35

(2) INFORMATION FOR SEQ ID NO: 2851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2851:

45

AATTATTCAT CAATAGCTCT TTACGATTCA CAAATCTAGG TACTTTTCAG ATCT 54

(2) INFORMATION FOR SEQ ID NO: 2852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2852:

AAGCCCCTTT AAAGTGGGCC TTAAAGGAAC GGTGGCGAAA ATCCCCAAAT TCCGGGCA 58

5

(2) INFORMATION FOR SEQ ID NO: 2853:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 103 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2853:

15

AAAGGTTTCC ATTCGGTCCC ATTAAGATTT TTTTGGAAT TCCATGGAAG GATGGTTGGT 60

CCTTTAGGCC TGGTAGGTTA TCCTTTTTGn AGGTGGTATC CAG 103

20

(2) INFORMATION FOR SEQ ID NO: 2854:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

25

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2854:

30

GGCCACGGTC ATTCCTCCAA GCCAACCAGT GGACAAGATG GGTGGAAGGC GCAGG 55

(2) INFORMATION FOR SEQ ID NO: 2855:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2855:

TATTTGGCAT TCAAATAACG TAAACGGATT TTGAAGTAAT TTACATAAAG AGG 53

45

(2) INFORMATION FOR SEQ ID NO: 2856:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

50

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2856:

ACAATTGAC AATGACTGGG ATGCTGACAC TTGATATGAA GACAATTGAA GAT

53

5 (2) INFORMATION FOR SEQ ID NO: 2857:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2857:

AACTGCGTTA CATGCTTTC TTTTAACTGA ACCCAGAACA ACGGTTTCGG

50

(2) INFORMATION FOR SEQ ID NO: 2858:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2858:

30 CTTTnnTAnC TTCATCTCTA TTATTATTGT CCGAATTACT ACGTGGACAA

50

(2) INFORMATION FOR SEQ ID NO: 2859:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2859:

TCCAGGTCGA ATTTATTGCC AATTAGCCTC CCGGGTTAAA AGGGTGGGTG TCGGGTAAAA

60

TCGTAC

66

45

(2) INFORMATION FOR SEQ ID NO: 2860:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

50 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

GGTATCCAGT CCCCCGGAGG GGTGACAAAC TTCCACGCCC AGTGGGGGGA CTACCGTTTT 60
GGACCAAAGC CC 72

5 (2) INFORMATION FOR SEQ ID NO: 2861:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2861:

AGTGTGGAAC AATTAAAGAT ATTGAGTGAC AGGATTGCTT AAGGGCCGGT CGGAACAG 58

(2) INFORMATION FOR SEQ ID NO: 2862:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2862:

TTAGCGGTAA ATCCGAAGAA CTAAGAAGAC GTCAAGAAGG GGATATACGC 50

30

(2) INFORMATION FOR SEQ ID NO: 2863:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2863:

GCAAAAnTGA GAGCTCAAnC TGCAnnaAGC AAATCAACGA AAGATTAGGT 50

(2) INFORMATION FOR SEQ ID NO: 2864:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2864:

55

AACTATTCTG GATTGTGCA GTGGCTATGG GGATGAGTGC GTTCCCCTCT TTCATGACGC 120
 AGGCGAACGC CAGCAACGCA ACCACTGATC AATGCTGAGC CAGCTGTAGC CGCCCAGACG 180
 5 GAACAAAATC CGCAGTGGGG GCAAGTGATG CCGGGCGTGC AnGGCGCTGA TGnCAgTTCG 240
 TGGCAG 246

(2) INFORMATION FOR SEQ ID NO: 2865:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2865:

20 ACAGATGATA CCTCTTGATC ACTTGCCAGA GATCGTCTAA GTCGTCCTTG 50

(2) INFORMATION FOR SEQ ID NO: 2866:

- (i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2866:

30 AATACCACGC TGACCTTAAT AAGCCATCAT GGGGGAAATC ATGACCGCAA T 51

35 (2) INFORMATION FOR SEQ ID NO: 2867:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2867:

45 CAACTTGGTA AGTGGTCGTT TTGGGCCCCA CCCTACCCGT TTGGACCTGG 50

(2) INFORMATION FOR SEQ ID NO: 2868:

- (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2868:

5 CCCAACCCGG TTCCGGGCCT TAATTTTTTn CCTTTTAAAG GAAAAAAGG AAAAACCGGT 60
 TAATTCGGC CCAAAAAnCC CGGAAGTTGG AAACCTTTTT TTAATAAAAA TAATGGACCG 120
 TCCCAACCTT TGTGCCCCAA AGGTGGCCTA AAGGTTTAAA AAAAACCGTT AAAATCCATG 180
 10 GCCAGGATCC AGCCTAAAAT TGAAACCATT ATAATTGATA AAC 223

(2) INFORMATION FOR SEQ ID NO: 2869:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 66 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2869:

TGGACCTTTG GTAATATGAA TTGAATGGTG CTTTGTGGAA ATCGGGAATT CGCCTCGTGC 60
 CTTGTA 66

25 (2) INFORMATION FOR SEQ ID NO: 2870:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2870:

AAnAGCCAnG ATCATGGTAT ATCCATTAAG AGACGAGAAG ATCGATGCCC 50

(2) INFORMATION FOR SEQ ID NO: 2871:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2871:

50 TTATTTGGAC TTACAAGGAG AATAGTCAnT TCTAGGAAAG TGGTGCGAAA GTCACCTTACC 60
 AATATACGGG GATTATTCAT CCATCGTCGG TCGGTCATAT GATACGGAAT TAACACGCCA 120
 CTCCG 125

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2872:

CAACACCTGA CGTGTATAGA ACTCATCTCT TCAATAACGT CGCTGTCAGG TTACGAAGTC 60
 GA 62

(2) INFORMATION FOR SEQ ID NO: 2873:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2873:

TATACATTCC ATTAAACACC TTAACACATG CAAGTTACTT CCTCCTCAAG CATC 54

(2) INFORMATION FOR SEQ ID NO: 2874:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2874:

GCTGAAAGGA GACTTCTGCA GGTGTGATCA CAAACTGCAC ATCTACACAA GCCATT 56

(2) INFORMATION FOR SEQ ID NO: 2875:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2875:

AGCGCGACCG CGAGAAGGGA GGGGGAGCCA GAGCAGCAGC AGGCCCCAGG GCGAAACCCC 60
 CAAGAGGAGC GAGnAAGAAG GAGGGAAAGC CCAGCAGGGG CGCCCAGGCC AG 112

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2876:

GnGCGTTnnA nCGGTCGCGT AGAGATGTCG GGTCTGTAGT AGATCTGGGG

(2) INFORMATION FOR SEQ ID NO: 2877:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2877:

ACCTTGACTT TGCAGACGAT GATGCTTTTG GCTGGGATCT TCACCATCTG GCAACTGAAT

ATGGTTGG

(2) INFORMATION FOR SEQ ID NO: 2878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2878:

CTCCACCTGA TGCATGCCCC CATATCAGGA AAATGATAAC CTCGGACACC TTC

(2) INFORMATION FOR SEQ ID NO: 2879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2879:

GGGAACCTTG ATCTGCCCTT GAAATCCTGA AAAATGTTTG CAAACGGGAA TGATCTTGTG

CCTTGCTTTG AATGA

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2880:

10 AGAGAGGCCG AGATGGCAGA TGAGATTGCC AAGGCTCAGG TCGCTCGGCC TGGTGGCGAC 60
 ACGATCTTCG GGAAGATCAT CCGCAAGAAA TACCAGCCAA AATCATTTTT GAGGATGACC 120
 15 GGTGCCTTGC TTTCCATGAC ATTTCCCCTC AAGCACCAAC ACATTTTCTG GTGATACCCA 180
 AGAAACATAT ATCCCAGATT TCTGTGGCAG AAGATGATGA TGAAAGTCTT CTTGGACACT 240
 TAATGATTGT TGGCAAGAAA TGTGCTGCGG ATCTGGGCCT GAATAAGGTT ATCGAnGGTG 300
 20 GTGAnTGAAG TTCAGnGGTG GACATCCGTC TATCACGTTC A 341

(2) INFORMATION FOR SEQ ID NO: 2881:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2881:

30 GCGGTTACTG TGTAATGGCA TTAAATATGA AACGAGCCGA TGGAGCGTTG 50

(2) INFORMATION FOR SEQ ID NO: 2882:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2882:

45 CTCATCATTT GTAGTTGGAA AGGTTTATGT ACATTGGAA AACACCGACA CATGACGTAT 60
 CTCCATTGCA ATTACACAA G 81

(2) INFORMATION FOR SEQ ID NO: 2883:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2883:

5 TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 60
TTTTTTTTTT TTTTTT 77

(2) INFORMATION FOR SEQ ID NO: 2884:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 104 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2884:

20 ACGGTGTGCT TGATGCACTT GGAAGTGTGA GTTTGGGTGT GACTTTGCTT TGGCTTGCTT 60
GCTGAATGTT TTGACTATGC ATTGCGTATA TGACTTGnAG CGCG 104

(2) INFORMATION FOR SEQ ID NO: 2885:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2885:

35 AGCAACGTGT CTGTCAACGT GGTGTCATTG GAAAAGGCGT CATGTATTGn CCGGTGGGAT 60
TTACGTGTAG TCACACATGT GCCCAATTAT TGTTTTGAGG CCAACTTGAG TAGGTTGATG 120
GTTATGT 127

40 (2) INFORMATION FOR SEQ ID NO: 2886:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
45 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2886:

50 TGAGCGAGTG CTGTGTGAGC GCGAGGTTGT GAGAGTTAGA ACCTTGAG C 51

(2) INFORMATION FOR SEQ ID NO: 2887:

55

(A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2887:

10 TTGAAACCGC GAACCTGAGT TCTGGTTAAC TACAGTCTGG TATACACATT GAGGGAAACT 60
 TCG 63

(2) INFORMATION FOR SEQ ID NO: 2888:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2888:

25 AGTAnCATAC nCAACTATCT CAGCATACAA TATTGGnCAC CTCGCAGCTT 50

(2) INFORMATION FOR SEQ ID NO: 2889:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2889:

AAAAnATAATC CCGGTTTTAT CCCCTACCT AATTAGTGGG AAAAGTACCA ATTGCCAATT 60
 40 GGTAAnATAG GTTGCCATAA CGGCCTCCCA AAAGTAAATT CCCTTTTTTG GTTTA 115

(2) INFORMATION FOR SEQ ID NO: 2890:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 147 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2890:

AATCGGTCCG TTATACTCTT CATAATATTG TGGCGCAACC ATTTCAACTT TATCTTTTCT 60
 TATAAATAGC ATCATCGCAA TAnTAAAGAA TAATATCGGA ATGATTAAAG TAACGATAAG 120

55

(2) INFORMATION FOR SEQ ID NO: 2891:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2891:

```

AACACAACAA GTTGTTAAAG ATGCATTTTT ATCACAACAT AAATCTATTG GACGTAAAGC      60
TCAAGAAGCA TACTTATCAT ATCGTTTAGA ACAAGAGTAT AGTAAAGATG ATATCTTCCA      120
AGTATATCTA AACAAAATTT ACTATTCTGA TGGCGTAACA GGTATTAAAG CTGCTGCTAA      180
GTATTACTTT AATAAAGATT TAAAAGATTT AAACCTTAGCG GAAGAAGCTT ATTTAGCCGG      240
TTTACCTCAG GTTCCAAACA ACTATAATAT TTATGATCAT CCAAAGCTG CTGAAGATCG      300
TAAAnCACT GTTTTATACT TAATGCATTA TCATAACGC ATTACAGATA AACAGTGGGA      360
AGATGCTAAG AAAATCGATT TAAAAGCGAA CTTAGTAAAT      400

```

(2) INFORMATION FOR SEQ ID NO: 2892:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2892:

```

CCTAATTAAA CCTCCATCCA TCCTTTTGAA GGGGGATCTT TAATAAAAnCC GGAAAGTTTG      60
GGGGAAAAAT CCTCCATCCT TTGAAGGGGG GGGCTTTCCA ATGGCCTTTA AGAATGGCCT      120
TTTCCAAGCC AACTTTTAAT TCCCCCGGT      149

```

(2) INFORMATION FOR SEQ ID NO: 2893:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2893:

```

GCCCCAAGTA TTCTTGTAAG TATTATGATA CTCGGTnCTT TTTATGATTT ATGTTAATTT      60

```

TTATGTTAGT

130

(2) INFORMATION FOR SEQ ID NO: 2894:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2894:

GATGAGACCT GAATTGATTG CAACCCAAAT CGGCATATGC AAATTGCATT AAAGTTGGTT 60
CAACG 65

(2) INFORMATION FOR SEQ ID NO: 2895:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2895:

CGCACAAACAC ATTTAGCGAC TCAGATGTCG CGCGAATGGA CCGATATGGC GTGTCTACAC 60
ATTGTCATAT TGTACGAATA GATGAGAAAT TnCAAAGACC GA 102

(2) INFORMATION FOR SEQ ID NO: 2896:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2896:

ATTAAGTGAT GGGCTAATGT TTACGCCCCA ACCAAAGGTT TCAAAGAGC CCTTGTTGGG 60
CCTGTGTTG 69

(2) INFORMATION FOR SEQ ID NO: 2897:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2897:

ATTGAATTAA TGTCCCAACC AACGAATGG TTGCCCTTTT TCCATCCAAA GGGGGCTAAT 60
TGGGAAGGGT ATTGGTTCCC 80

(2) INFORMATION FOR SEQ ID NO: 2898:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2898:

CAAATCCTGG AGATGAGCGT AACCAAAAAT AACGTTGAGA AAATGACCAC ACA 53

(2) INFORMATION FOR SEQ ID NO: 2899:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2899:

ATCGTGAACC TCTCATCCAA TCACTCATGT GAGTGAATTG GATGACCTGA A 51

(2) INFORMATION FOR SEQ ID NO: 2900:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2900:

AGCTTTCAGG GCTATATCAG ACCCAGCAT TCATCCACGT GAATGAAACA CG 52

(2) INFORMATION FOR SEQ ID NO: 2901:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GGTACTGACA GAGGGACAAG GTGGAAAGGn TGCCAATGTA AGAATACGGT

50

(2) INFORMATION FOR SEQ ID NO: 2902:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2902:

15 TGTCTGGAAT TCAGGTGAAT TGATGCGGAG ATTTAGGTGA TTAAGGAGTG TTGATTATGA 60
AGATGACCAC TT 72

(2) INFORMATION FOR SEQ ID NO: 2903:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2903:

30 CATGCCAAAG CAGTAGGCAA GCCGCTTAGC AAGCCAAAAA CGTCAGCCCA 50

(2) INFORMATION FOR SEQ ID NO: 2904:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2904:

TTGATGTTAC CTGATCGCAA TCTTGACCAC CTGGCAGGGT CTCATTGTTG GGTATCGA 58

45 (2) INFORMATION FOR SEQ ID NO: 2905:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2905:

55

GCGGTCTAT

69

(2) INFORMATION FOR SEQ ID NO: 2906:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2906:

15 ATTCCATTAG GTTCAATTAA AAATTAACGG GGTTATGGTT CCGGTAATTC GGG 53

(2) INFORMATION FOR SEQ ID NO: 2907:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2907:

25 AAAGCTAAGA AAGGAGGATT AGCTGGTAGT GGAGGAATGT TAAGTGAGGC TGGTGAT 57

(2) INFORMATION FOR SEQ ID NO: 2908:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 86 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2908:

40 GGGAAATGGCG CATGAACGTG CACATCAAAT GACACTGCAG GAAATCAATT AGCACGGATA 60

TGGCATAAAG ACAATGGTAA AAGTGG 86

(2) INFORMATION FOR SEQ ID NO: 2909:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2909:

55

(2) INFORMATION FOR SEQ ID NO: 2910:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2910:

GAATTTGTTC CGAGGTATCG AGGACTACGC TTATAAGGTG CTTACAGATA CATTTCATCAT 60
 TAATGGCGTG TGCTGCTGTA TGGGTTATAC TGTTACAGG TTTAAGAGA 109

(2) INFORMATION FOR SEQ ID NO: 2911:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2911:

TTGTCCCCAT AGGGAGAAAT AATCCGCCT GGGCAAAACC AAATCCACGA GCTTCTAAGG 60

(2) INFORMATION FOR SEQ ID NO: 2912:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2912:

TAGATGTATC CAGCTGACAT TAGCTATTGG TAAGGTAACG GCTTACCAGG CAACG 55

(2) INFORMATION FOR SEQ ID NO: 2913:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2913:

GCCATGAGGC CCACCCATCC ATGTTTATGG ATGGTGGATT GGGGAATTAC TTGTTTCAAA 60

TCA

123

(2) INFORMATION FOR SEQ ID NO: 2914:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2914:

ATCCGTAATT CTGGCCTACC AAGGGTTTAG GCCAATGGGC CATTCTTTTA TTAAACCC

58

(2) INFORMATION FOR SEQ ID NO: 2915:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2915:

TGGTGCGACA GTGGTAGGCT TTTTACGGTn TGCnGGCGAG AGTTCTGTAG

50

(2) INFORMATION FOR SEQ ID NO: 2916:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2916:

CTGTTACGCT ATGCCCCCA GTTGTATGTT GAGTGGAATC GTGTTTTTCG ACCTGCCTTT
 GCTTTTTT

60

68

(2) INFORMATION FOR SEQ ID NO: 2917:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2917:

GGAAA

65

(2) INFORMATION FOR SEQ ID NO: 2918:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2918:

AAATTCCAAT CCTGGGAATG GGATTCCATG GTnTTCGGAA AAATCCGCCA CCCCAAAAAA 60
ATAAATGGGT CCCTTCCCTT GGAAATATTA CCTTTACCAG G 101

(2) INFORMATION FOR SEQ ID NO: 2919:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2919:

TAATAAATCC ATGACCACCG TCACGACGAT CTGACTGATA AACTAATGAC ATATGACTGG 60
TGTACACACC GTATG 75

(2) INFORMATION FOR SEQ ID NO: 2920:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2920:

CTTGGATTGA CCATCATTAG TTTTGGTCAC TCTAAGTTGT ACTGTCCGTT GTACAA 56

(2) INFORMATION FOR SEQ ID NO: 2921:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

GCTCATTGCT TGTATATTAA TCCCTGAAAT TGACCGTGTA TATCCCGTCG ATCTATCTTG 60
TCCTG 65

5 (2) INFORMATION FOR SEQ ID NO: 2922:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2922:

GCAATATTCT AATCTGTATG TTACAGCACA TGGATATAGC ACATCCGGGC 50

(2) INFORMATION FOR SEQ ID NO: 2923:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2923:

30 TGTGATTTAA CAGGATTACA CAGGTGTACC AGCCGATAGT TGATTAAGCT TCTT 54

(2) INFORMATION FOR SEQ ID NO: 2924:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2924:

ATCCTGGGAA GTGCTGAAAA ACCACTnCAC TAAAGGCATA GGAnCCACAC 50

(2) INFORMATION FOR SEQ ID NO: 2925:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2925:

(2) INFORMATION FOR SEQ ID NO: 2926:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2926:

TTGGTCACAT TTATTCTCGT GTTGTGCCGT TCTTCTTCAG TACTAAAGAC AAGGTGATTC 60
 GG 62

(2) INFORMATION FOR SEQ ID NO: 2927:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2927:

CAAAAGGCTA TCCCACCTGA TTTGCAAAG GAACTGGACT GCAAGGGAAG TCTCAG 56

(2) INFORMATION FOR SEQ ID NO: 2928:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2928:

TGATCTTGCT ATTTAGTTGC GGCTTGGATT CATTTGGCAT GGTTAAGATT AAATTAGATG 60
 CTTCAATTCAT TCAAGATTTC TTCATGTTAG CATTCCTTAC GACAATCGGT CTTGGTGCAT 120
 CATTGAAATT ATTTAAATTA GGTGGCAAAG TCTTGCTATT ATACTTTATG TTTTGTGCTA 180
 TCATTTTCAGT CATTCAAAC ATAGTTGGTG TATCACTAGC AAAAGTATTA AATATTAAAC 240
 CTTTGTTAGG ATTAACAGCA GGTCCATGT CTATGGAAGG CGGTCATGGT AATGCTGCTG 300
 CTTATGGTAA GACAATTCAA GATTTAGGTA TTGATTCGGC ACTGACAGCG GCTCTTGCAG 360
 CTGCAACTTT AGGTCTTGTA TTTGGAGGGC TATCGGTGGT 400

(2) INFORMATION FOR SEQ ID NO: 2929:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2929:

10 CTGAACCGAT GGCGCACTTT GCTACGCCAC CTACAGCAGA TCCCA_nGGGG GG_nGAAGCTT 60
 ATACTGAAGC TCTACGTTCA ACATTTTTC ATTGGGGATT CCATGCTTGG GCTGTTTATG 120
 GTGTTGTTGC GTTACGTTTG GCATATTGCG AATTCCGTAA AGGTGAACCA GGTTTATTAT 180
 15 CTAGAACTTT ACGTCCTCTT TTAGGTGATA AAGTAGAAGG TCCTATTGGG ATTTTATTG 240
 ACGTTTATC TGTATTTGCG ACAATCGTTG GGGTAGCCGT TTCGTTAGGT ATGGGTGCTC 300
 TACAAATTAA TGGTGGTTTA CATTACTTGT TCAATGTTCC AAACAATACG TTTGTACAAG 360
 20 CGATTATCAT CATTGTTGTT ACTATCTTAT TTATAGCAAG 400

(2) INFORMATION FOR SEQ ID NO: 2930:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2930:

ATGTAGATCT ATATGATGAC TTTTACAAG ATCCATCATC TGTACCAGAA GATTTAAAGT 60
 35 CTTATTCAGC ACAATTAAGA ATGATGACTC AATTGTACCA GCTTTAAAAA GTACAAGTAG 120
 TC_nAATAGC GACGGCACAA TTAAGCGTGT CATGCGTTTA ATTGATAATA TTCGCCAATA 180
 40 CGGGCATCTT AAAGCCGATA TTTATCCTGT AAATCCTCCA AAAAGGAAAC ATGTACCTAA 240
 ATTAGAGATT GAAGACTTTG ATTTAGATCA ACAGACTTTG GAAGGTATAT CAGCAGGAAT 300
 TGTTTCAGAT CACTTTGCCG ACATTTATGA TAATGCCTAT GA_nGCAATTT TAAGAATGGA 360
 45 AAAACGTTAC AAAGG_nCCAT TGCATTTGAG TATAC_nTAT 400

(2) INFORMATION FOR SEQ ID NO: 2931:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

GGTTATACAA TCTAGAATCG CATGATAATT TAATGCTACA AATCGATAGT ACAATATATC 60
TACCGTGAAT AACTGTGCAA ATAGTGACGT TGTAGCCGCC ATACGCATTT CATTTTCATC 120
5 AGTTCTGCCA TAAATCAATG CATAGTCTGC AATTTGAGCC ACTGGATTAT TAGCTGTACT 180
AGATATAGTT ATGATGGGAA TACTGTAATG TGTGGCCACC TGTGCAATTG ACTGCAATTC 240
ACTATGGACT ACCTTGGATT CGTCACAAAA ATCATGCAAT CTCTATCATC ATGCGTCGCA 300
10 AATGTTGACA CAAGTGAAAT GCGTTTCCAT GTAATAACCT GACATTTGAA GCCATACGAG 360
ATAACTTTGG AAAAAGATCA CCAATAGnCC AACTCGATGG 400

15 (2) INFORMATION FOR SEQ ID NO: 2932:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2932:

25 CTTTCAGTAG CAGCTACAAT TGTCTTTAAC ATTTAAGTTT AAAGCTGTAT GTGTCAACCG 60
CAAATACCGA TAGCCATTCA CTAATGAAGT TTCAACTAAT TTAGTACGAT CTGACAATAA 120
30 CTTTTTGTA TCTTGGGCTG CTTTCAGCTGA TACAGCAATA TTTCTCATTG TTTTAACAGC 180
TTCTTCAGGA TATAAACCAG CAGCAGTTTC ACCAGATAAC ATTACTGCAT CTGTACCATC 240
ATAGATTGCG TTGGCAACGT CACTAGCTTC TGCACGTGTA GCACGTGGGT TACGTTGCAT 300
35 AGAATCTAAC ATTTGTGTAG CTGTAATAAC TGGTTTACCT AATTTGTnAC ATTGTCTGAT 360
TAAATCTTTT TGAACCATG GGACTTTnTC AG 392

(2) INFORMATION FOR SEQ ID NO: 2933:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2933:

50 TGA CTATGGT ATCGCATGTT GTGTATCAGC GATGACAATT GGTAACAAA TGCAATTCTT 60
CGGTGCACGT GCGA AACTTAG CTAAAACATT ACTTTACGCT ATCAATGGTG GTAAAGATGA 120
AAAATCTGGT GCACAAGTTG GTCCAACTT CGAAGTATTA ACAGCGAGTA TTAGAATATG 180

55

ATTAAATGTT ATTCACTACA TGCACGATAA ATACAGCTAT GAACGTAATT GAAATGGCAT 300
TACATGATAC AAAAAATTGTA CGTACAATGG CAACAGGTAT CGCTGGTTTA TCAGTAGCAG 360
5 CGGACTCATT ATCTGCATTn AATATGCACA AGTTnAAACC 400

(2) INFORMATION FOR SEQ ID NO: 2934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2934:

AAAATATGCC ATGACTGGCA TGACAAGAAT TGGACGTTAG AAGCATCTCA AACTGGTACG 60
20 TTCAGAGGTC GTAACnTAA CTTCAATGGT GAAGGATTCT CACGTCAAAC ATTTAAAGTA 120
AATGCCGTTA GTCAAAAAGA CTACGACAAA TGGGTGAAAG AAGTTAAAGG TAAGAnAACG 180
TTAGATCAAG ATACATTTGA TAAACAATTA TTACCAAGCA CACCTAATAA AGCTTTAGAA 240
25 TTAAATGGTA CACATATGGC GTTGTGTTGAT CCAGCAGCCG ATCCAGAATA CATCTTCTAT 300
GCATATAAAC GTTTCAATTT CGGATTGAAG GTCCCAAACT TCACTAGTGA GGAAAATATG 360
30 TTAAAGGTGT ATCAGACAAA CCCTTAATAC CTGCTCGTGA 400

(2) INFORMATION FOR SEQ ID NO: 2935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2935:

ATGGAGTATA CAACTACTTC GGCATTGGCG CTTACGACAA CAATCCTAAC TACGCAATGA 60
CGTTTGCAAG GAATAAAGGT TrGACATCTC CAGCAAAAGC AATCATGGGC GGTGCTAGCT 120
45 TCGTAAGAAA GGATTACATC AATAAAGGTC AAAACACATT GTACCGAATT AGATGGAATC 180
CTAAGAATCC AGCTACCCAC CAATACGCTA CTGCTATAGA GGGTGCCAAC ATCAAGCAAG 240
50 TACAATCGCT AAGTTATATA AACAAATCGG CTTAAAAGGT ATCTACTTCA CAAGGGGTAA 300
ATATAAATAA AGAGGTGTGT AAATGTACCA AATAAAAGAT GTGAAACGAG AATTAAAAAT 360
GATGGTGTG ACTTAGGTGA CATTTGGCTG TCGTTTTACA 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2936:

```

10 AAACAATACA AACAAAAGAA AGTCAACCAA GGATGGATTG CTATTTTAAT CCTTGGTTGA      60
    CTCTTATTTT ATTTAAATTG TAGAACCTAG AAAATAAAGT TTAATTAAAA GCACCAATCA      120
15 TTTCTACTTT GAAATCTAAG GTTCTAAAA TAGCAATGAC TTTCTTTATA TCGGTTGTAA      180
    TTGCAGAATC AGCCTGAACG AAAAATCGAT ACATACCTAA TTGTGTTTTT AAAGGACGAG      240
    ACTCAATCCA GGGTAAATTA ATATTAAACA AAGCAAATGT ATTAAGCACA CTTGCTAACA      300
20 ACCCGGGTTA TCATGCATTG GTGTAATTAA AAACATCAAT GGTGTCGCAT TTTGATCAAA      360
    TGCTGCTGAT TTTTATAAC TAAAAACGTG TCAGGTATGT      400
  
```

(2) INFORMATION FOR SEQ ID NO: 2937:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2937:

```

35 TTATTATCTT GATACATTGA GTGTATATTC CATTTTCCAT GAGGCGTTAA ATAACGCATA      60
    CCAAAGCATC TGTACCACCT TTAATTTTCT TATCTCTATT CCCAAATACC ATTGGCGGCA      120
    ATGTCGGTTT ATATACTGGT AAGCTCTCCC CAAATTGTTG GAAACTTCG TGATCCACAT      180
40 AATAACTTTG GACGTCCTGT TAATGTTCTA AAAGGTACTA GACGTTCTAT ATTCGTTGTA      240
    AATGGTGGAA TATCGTCGAC CTTGTTTATT TGAACCGGGG AATACTGCTG TCGGTATTAC      300
    TTCTCGTGGT TGTGGAAGTT ATATTTAAAA ACGGAAATTT TCTCAGCAGC GntTTCGTTA      360
45 GGAAATATCT TTAAACGGGC ATTCCAGTTT GTTCnTCGGG      400
  
```

(2) INFORMATION FOR SEQ ID NO: 2938:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2938:

5 TATCTCTTAA AGCCGGTGAT GGTGGTAATG GTATTACCGC ATACAGAAGA GAAAAATATG 60
 TACCATTGG TGGACCAGCT GGCGGTGACG GTGGTAAAGG TGCTTCAGTC GTATTTGAAG 120
 TGGATGAAGG TTTAAGAACG TTATTAGATT TTAGATATCA ACGTCATTTT AAAGCAAGCA 180
 10 AAGGTGAAAA TGGCCAAAGT AGTAATATGC ATGGTAAAAA TGCGGAAGAT TTAGTATTAA 240
 AAGTTCCACC TGGTACAATT ATTAAAAATG TTGAAACAGA CGAGGTTTAG CAGATCTTGT 300
 TGAAGATGGT CAAAGAGCTG TAGTAGCGAG GGCGGTGAG GTGGCCnAGG TAATTCACGT 360
 15 TTTGCAACAC CTAGGAAACC CTGGCACCTG GACTTCATGG 400

(2) INFORMATION FOR SEQ ID NO: 2939:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2939:

25 CTAACCTCGA GTTCGTATTA TGCCCACCAC ATGTCTGCTG GCTTGTCGTA AATATTAACA 60
 30 GATTTCAAAG TTTGACAAGC TTTTGGAAA CCTTCTTCTA CTGACATAAT AGGATCTTCA 120
 TGTTCATAC TTAATACATA ATCATATCCA TTAATAATAA GTTGACTTAT GATATCTGCC 180
 CATACATATG GACTATGTCC TAAGCCAACT GTACGGAATG TCATGCTCTT GTCGCAACGT 240
 35 TACCATATGG TTGCATATCA GTTAGACCAT ACATATTTAC ATTTTCTTGG ATTAATATAC 300
 GTATCTTTAG CATGGAAGTG ATGAATTGCA TTTGCTTGGn CTAATATGCG AATCGCAGCC 360
 AATTGGGTCA ATAnCnTGGC CACC 384

(2) INFORMATION FOR SEQ ID NO: 2940:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2940:

50 TTTTCATATT TTCTATTAAT GATTCATATT GTAGGGTGAT TGCAATGTCA TCTAAGCCAT 60
 TTACAAGTTT ATTCTTCCAA GTTTCATCAA TTTCAAAATG GAAACGCTTG TCTGGTGATG 120

CACTTTTTTC TAAACGATA GGCAACATCG CATTTTTAGT GCAATTCATA TAAAATATGT 240
 CACTGAAACT TCCTGCAATA ATAATATGAA AACCATAGTC CTTAAGAGCC CAAGCAGCAT 300
 5 GTTCACGACT TGAACCACAT CCAAAATTAT CTCCAGTnAT TAAATnGGAG GCCCCTTTAT 360
 ATTGTGGTTT GTTAGGGTTG AATCAGGGTT TnTnGGAACC 400

(2) INFORMATION FOR SEQ ID NO: 2941:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 409 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2941:

20 ATCATAATCC ATCGTGCGTC CAAGAAGTAC TTGATTATTT AAAGTTTGTA TTGTGAATCC 60
 TGTGCACATT GTTCTCACTC CTCTGTACCT TCATTACTT TAATCACTTT CAAATAAAGC 120
 TGTTCACATT AAACATACTA TAAAAATCA ATTATACAAG CAATTAATTG ATATTCATTC 180
 25 TCAATAACTG TGGTATGATA TGTAAGGAAA TCATGACTTA TGTGTGAGTG AACGATCATC 240
 TATACATCCG TTCACTTCAT CTCATGACTT TCTATATTTA ATTTTACAA GGgAGTGACA 300
 TCTGTGAATa ACACACAATC TTCACCACGC gTAaTaTtAT TaTTGCGATT ATGTTGTCTG 360
 30 CATAACATAT GGTGTGTGCA CAATCATTAT TAnTATAGGA CCTCCGTTG 409

(2) INFORMATION FOR SEQ ID NO: 2942:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2942:

45 ATGAAGTGTC AAAAGGTTTA AAAACATCTG AAAGGGGTTC GCACATGTTT TAAACTTTAA 60
 AAATAAAGGT GGATGTCCAA AATGTCGACC AGCAATCAAC TATTATTTAA ACATGGTTTA 120
 TCCACATGAT CATGAAGATG AAAGAGAATC AAGATTTGCT AACGAACGTT ACCATGCGAA 180
 50 TATTCAAAAT GATGGTACAT TTTCTGTTAT ACCTCAAATG CGTGGGGGTG TTACAGATGC 240
 AGACCAACTG ATTCGTCTAG GAGAAGTGGC TAAGAAATAT CATGTGCCAC TAGTTAAAGT 300
 GACAGGTTCA CAACGTGTTG GTTTGTATGG AGTTAAAAAA GAAGATTACC AAATATATGG 360

(2) INFORMATION FOR SEQ ID NO: 2943:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2943:

ACCTGGAAAT GSTATGTGCCA TCTCTTTAAG CCAATCAGTA TCTTGAATAC CTTTCGTTCC 60
 AACTATGCAA TAATTAATCC CTGCGGCAAA GTAGTCCATG ATTGTGACTT CGTACGAATG 120
 CCACCACCTA CTTCAATATC TTTGGTTGTT AATCTCCTCA ATGACTTAAT ATAATCAAAC 180
 TCTCGGGCAT GCTGTGCCTT AGCACTCATC AAGTCGACGA TATGAATACG ATTCACACAT 240
 TCAAATTGAC TATAGTAAGC AATACTTTCT TCAGCCGAGC GTGGACATTT TTTCTTCACT 300
 ATCATATTTA CCCTCTGTTA ACCTCACACT TGTTGACCCA ATCAAATCAA TCGCTGGGCC 360
 ATAATTCAAT CATTtATAA ATCCCCCTTG TATTGGCCTG 400

(2) INFORMATION FOR SEQ ID NO: 2944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2944:

AACAAAAGGG GTCTATCGTC AATCGTTTCT TGAATAGTGT TGAAAAAATC GGAAATAAAT 60
 TGCCAGATCC TAGCGTCTTA TTCTTTTAA TGTGTGTGGG CTTAGCCATT ATGACATGGG 120
 TTATCTCATT ATTTAATGTA TCTGTTAAGC ATCCAGGTAC GCATCAAACC ATTTATATTA 180
 AAAATATAAT TAGCCATGAT GGATTTACGA TGATAATGAA TGATACGATT AAAAATTTCT 240
 CAGAGTTCCC AGCATTAGGC TTAGTACTAG CAGTGATGAT TGGTATTGGT GTTGCAGAGA 300
 AAACAGGATA CTTGATAAG TTAATGATTT CTGTTGTGAA TCGCGCACCA CGTTTCTAAA 360
 TTTACCGCTA TAATATTAAT GGGnATTTTA GGGAGTCAGA 400

(2) INFORMATION FOR SEQ ID NO: 2945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2945:

5 ATTTTACAAG TAACGGTGCA TCACCAGATT CTAATTTAAT GTCATGCTCA GCAGCATTTT 60
 GATAACCCAA CTTTTCAAAG TAGTCAAAAC AATGGTCTAC AACCAACCGTA CTATACTCTT 120
 GTGCTTTGGC CGCTCTTCTA CTGCTTGAAC CAAGCCACGA CCTAATTTTT GTCCACGTAA 180
 10 TTCAGGATGA ACTGATAAAG AGGCAATCGC CAAACCATAA TACGTCTTAT CATCACTATT 240
 AATTTCTACT TCAATTAATA AAACGTGTCC AACGACATCG TTATTTTCAT TTTTCGCTAT 300
 TACTTCTAAT TCAAAATTAT AGCAAGGAGA TTTTCTTAAA TGGTTTACTT TCGGCACGTG 360
 15 CCTGGCCAAC TCGTTTTTCAG GATTATCATC CAACTTTTCC 400

(2) INFORMATION FOR SEQ ID NO: 2946:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2946:

GGAAATAATT ACTTGAGCTA GATAAGTTGA CAGCTGTGCA ATTATTTTCA GCAGCTAATT 60
 30 GTAAAATTCG CTCTAATCTT GCTGATGAAT GTTCAGGCCC TTGACCCTCA TATGCATGAG 120
 GTAAGAATAA TGTTAATCCT GAACGTTCTC CCCATTTTGA GCGAGAACTG AATAAGAAGT 180
 TGTCAAAAAT CATTTGTGAC ATATTTGGCA AAATCACCAT ATTGTGCTTC CCAAATATTG 240
 35 AAGCTTTTTT TGTTTTCCAC ATTATAGCCG TATTCAAAAC CAACTACTGC TGCTTCTGAA 300
 GCGGAGAATT GTGTATATCA AATGTCGCTT TTTGAnCAGG AGCATGATGT AAAGGTGTAT 360
 40 ATGTTnCACc nGTTTGCTCA TCATGTnACA CGGCAGCCGT 400

(2) INFORMATION FOR SEQ ID NO: 2947:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2947:

AAGTGCATA AAAAAATCAC ATGACGATAC ATTGTCGTCA TATGACTTTA AATATTATTC 60

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TTCAATTGTG TCACCGATTT TTAATACATC TTCCACTTTT TCAATTCTAT TTTTGAAT 180
 5 TTGTGAAATG TGAAGCAACG CATCTTTACC TGGGAATAGG CCTACAAACG CACCGTATTT 240
 TTCAATACGT TTAACAGTGG CTTGGATAAG TTTGACCTAC TTCCGCTTCA CGTGTAATTT 300
 CCTCAATGAT TTCACGAGCA CGATTIATCA TAGCTTGATC AACAGCACCC ATAAAGATAG 360
 10 TACCATCCTG GnCCATATCn AATTTAACAC CnGGnTCCTC 400

(2) INFORMATION FOR SEQ ID NO: 2948:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2948:

TTTTCAAGT TTTGCTGAAG GCTTTACACA AGGCTATTTA ACAATGGATG CCATTGCAGC 60
 AATTGCTTTT TCAATGATTG TTGTTAATGC AGTAAACTA ACAGGCATTA CTAAAACAAA 120
 25 TCAATATTC AAACAACTT TGAAGTCTGG TTTAATTGCA GCCGTAGCTT TAATTTTCAT 180
 ATATATTTCA TTAGGTTATA TTGGTAATCA TATGCCAGTA AGTGACATGA CGTTAGATCA 240
 30 ATTGAAATCC AAAGATCGAA ACATTGGGAC ATATTTATTA ACGACAATGG CTTCAACAGG 300
 ATTTGGTCAT CCGGAAAATA TTATTGGGCA TCATTGTGGC GCTGGCATGC TAACTACAGC 360
 ATGCGGGCTA TGGTGAGTT CCTGAATATT CCATAGATCG 400

35 (2) INFORMATION FOR SEQ ID NO: 2949:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2949:

CATGGCTTCA GATTGTTTGA ATTGAATGGA CAATTTTGGn TTCTGTCCAA AATTCTTACA 60
 AAATCTTCTA CCGATAAACT ATCAAGTTCA ACTCTAATCG GAAAAACGAC CTTGCAATTC 120
 50 TGGTATCAAG TCACTCGGCT TAGATACATG GAAAGCTCCA GCACCTATAA ACAGCATATG 180
 TTCAGTATTC ACAGTACCAT ATTTGGTTTG AATAACGCTA CCTTCAAGTA TAGGTAAAAT 240
 ATCTCTTGA ACACCTTGTC TTGAGACATC TTGACCACTA TTATGATTAT TCGTCGCAAC 300

55

GTTAGCGCTT TCTTGATCAn TTAGTTCATC CGCATAACTA

400

(2) INFORMATION FOR SEQ ID NO: 2950:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2950:

15	TTGACTTTGT AACTAACTA CTCACTCGAC CGACTCAACT GTTTAAATGT TTCAGATGGT	60
	TTAACTCTAA ATACTACGTA TAAATCACCA GCAGGTCCTC CATTACAGCC TGGAGAGCCT	120
	TCACCAGCTA ATCTAATTG TTGTTTCATTG TCGACACCTT CAGGTACTTT CACTTCTAAT	180
20	TTAACTGTTT TATTTTCAGT ACCTTTTCCG TGACATGTTG GACAAGCTTC TTCAAATTCT	240
	TGACCACTTC CATTACATTT AGGACAACT TGTTCAGTAC GAACTCTACC TAAAATTGTG	300
	TTTTGTTCTA CAGCTACATG ACCAGCGCCA TTACAGTAAC TACAAGTCTT TTTACTTGTT	360
25	CCAGGCTTTG CACCATCACC ATGACATGTT TCGCATGThA	400

(2) INFORMATION FOR SEQ ID NO: 2951:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2951:

	CAATGATTTT AAAAGATGCA ATAAAACCAA ACTTAGTACA ATCAATTGAA GGGACACCTG	60
40	CATTAGTTCA TGGTGGACCA TTTGCGAATA TCGCACACGG TTGTAACTCA ATTTTAGCAA	120
	CTGAAACAGC ACGTGATTTA GCTGATATCG TTGTAACGGA AGCTGGATTT GGTTCAGACT	180
	TAGGCGCTGA AAAATTCATG GACATTAAAG CGCGTGAACA GGATTTGATC CGGCAGCTGT	240
45	CGTTGTTGTT GCGACAATTC GTGCGTTAAA AATGCATGGT GGTGTAGCGA AAGATAATTT	300
	AAAAGAAGAA AATGTAGAAG CAGTAAAAAG CAGGAATGGT TAATTTAGAG CGTCATGTTA	360
50	ATAATATTAA CAATTCCGTG TAGAnCCGGT TGTTGCCATA	400

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(2) INFORMATION FOR SEQ ID NO: 2952:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2952:

	TCAAGTAGCA AAAGAAACAG GTGCTTCAGT TATCGGTATT GATATTGGTC CACAAGCCGT	60
10	TGACCTAGGG CGCAGAATCG TTAACGTCTT AGCACCAAAT GAAGATATAA CAATTACGGA	120
	TCAAAAGGTA TCTGAACTTA AAGATATCAA AGATGTGACG CATATCATAT TCAGCCGACA	180
	ATTCCTTTAA AGTACAGCAT TTTAGAAGAA TTATATGATT TAACAAATGA AAATGTCCGT	240
15	AGTTGCAATG CGCTTTGGTG ATGGCATCAA AGCAATATTT AATTATCCGA AGAAACAGCG	300
	GAAGATAAGT GGGCCATGTG TGAATAAACA TATGAGACCA CAGCAAATTT TTGATATAGC	360
	ACTTnATnAA AnAGCCGGCT ATAAAGTnGG TATTACGGAT	400

20

(2) INFORMATION FOR SEQ ID NO: 2953:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2953:

	CGCAATTCAC AATAACATTA AATAATTTTT GGTCTCATAT TTTCAAAAAA CATACTGTTA	60
	TTATCCCATG GGnTTAAAAA TATCATTAGT ATATAAACGA AACACTTTAC GATAAATGAT	120
35	ATCTGCAAGC CAAGCTGTTA CAAATGGTAC AACAAAGAAC GCTACTACAA TTAGTAAGAC	180
	ACTCAACCAA GCAGAATCAA CCTCCATAAA TTTAAATGCA TTAATCGGTC CTACCATTCC	240
	TATAAAACCA AATCCAGCTG ACTCTTTCGT TCCATGAATA CCTACTAATG CTGATACCAA	300
40	ACCTGATACA ATGGCTGTCTG TAnGGGCGGG GnGCATAAGA ATTGGATATT TCACCATATT	360
	AGGTATCATC ATTTTAACGC CTCCAAAGAA GACCCGATAA	400

45

(2) INFORMATION FOR SEQ ID NO: 2954:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2954:

55

AACACTTTAA TGGAGATTTA GCAGGCACTG TTACACTGAC AGCAGGTTTA GGTGGTATGG 120
 GTGGTGCGCA ACCGTTAGCA ATTACTATGA ATCATGGGGT AGCAATTTGC GTGGATGTTG 180
 5 ATGAAACACG TGTGATAAG CGAATTGATA CGAAATACTG TGATGTTAAA ACAGCTGATT 240
 TAGATGAAGC ATTAAAATTA GCAGAAGAGG CGAAAGAACG TGGGAGAAGG ATTATCAATC 300
 GGGTTAATTT GGAAATGCTG TAGACATCCC ATCCAAGCGG ATTCTAGGAA AAAGGGTTTT 360
 10 AAAATTGGAC ATTAATTACT GGnCCCAAAC CAAGTGCCCC 400

(2) INFORMATION FOR SEQ ID NO: 2955:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2955:

TTCAGAATAC GAGCAATGTC AGTTGCAGTG TTTAATAAAT TTTGTTGCT ATTTTGTAGG 60
 25 CATCTTCTAA AGTGCTAGGT GAAGAGATTA TAGAATAGGC ACTATCAATA CCGAAATCGT 120
 AAACATGTTG ATAATTTTCG CCTAGACTGC CACAAATCGC GATGACAGGA ATATGATATT 180
 30 GTTTTGCAGC TAACGCAACG CCTACGGGTG TTTTACCAA GATGGTCTGA TAATCCATGC 240
 GTCCTTCTCC AGTAATAACG AGGTCTGCAT CTTTAATTCT TTGATGAAAA TCTGTAATGT 300
 CAAAGACGAC ATCAATACCT TTTGTTAAAG TTGTCTCACA AAACGnTAAT AATGCTGCGG 360
 35 CCATACCGnC AGTGCACCAG AACCTGGTAT TTGGTTnACG 400

(2) INFORMATION FOR SEQ ID NO: 2956:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2956:

AATACGTCCT TTATATAATG TTAATAACCA GTTAAACAAT TTCACACCAG TTGGAATACC 60
 AATCAGCATT GTTGAAATTG AGAAGAATGA GTTGATTAAC GCACCATTAC CCATTGTGAA 120
 50 GAAATGGTGA ACCCAAATA AGAACTAAG GAACGCGATA CCGGCAGTTG CCCATACCAT 180
 ACTTTGATGT CCGAATAAAC GCTTACGAGC GAATGTCGGG GATAATTTCT GAGTAAATAC 240

55

CCAAAGCATT GGGCATACCG CCATGTGGCA CTGTGGAAGA ATGCTGTGTC CAATATTCGG 360
 nTCATTGGTn CATTAAATGGC TAACGCTAAC GGTTTAAAGG 400

(2) INFORMATION FOR SEQ ID NO: 2957:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 394 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2957:

TAGTAATTAA TACGATGTCA GCACCTACTG ATTTTGCTTT GTCTGCTAAT AATCTTAAAT 60
 GTTCCGTGGA CCTGAACCAG AGATAATTAC AAATACATCA TTCGACTTAA TCGCAGGTGT 120
 CGTTGATTCT CCAACAACAT GTGCCTGTTT GCCGAGCTGA TTTAAGCGCA TTGCAAAACT 180
 ATTCGCCACG AATCCTGGAA CGTCCTTTGC CAGCTACAAA TATATGTTCA GCATGTAGTA 240
 TTTTGGGATG CAAAAGTTGG AAAACTCCAT CCGnTTCAAC ATGTGACAAA GTCATCTTTG 300
 AATTCATCTA GAnTTAATTG ATAGTCACTA AnTTTAGCCA TATTACTTAC CTTCGGTTGC 360
 CAGCGCGACC ATTGTTTCGC AGCTTCTTAC TGGG 394

(2) INFORMATION FOR SEQ ID NO: 2958:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2958:

AATTATTCTA CCTATAATTA AAAATGCTGG CAAAGGTGTA ATGATGATGA GTAATGAACC 60
 TACAACATTT AATATCAATC CTACATAAGT AATTTTGACG CGACCAAATT TATCAGCAAC 120
 ATCACCAGCA CCTACGATAA ACAAACCAGC AAATAAGGCA GATAAGCTAA CAGCGATTAT 180
 TTATCGTTCC AACGTCACCTA CTATATGTTG ATTGTAATGG GACAACAAGA TTAACAAGTG 240
 ACTGCGCGAA TAGCCAAAAG GTAATAACCC CTAAAACGAT ACCCAAAnGC AATCGGTTGT 300
 TCACCTCTTA AATTGTTTTG ATGTGTCCnT GGATTAGGAT AAGCCTCCTA TGTTTAGGAA 360
 AAACAATTTT TAATATGGTA TATTAAGGAn ACATTTTCCTT 400

(2) INFORMATION FOR SEQ ID NO: 2959:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2959:

10 CTCCTTTCTC AACATCAAAG AACATATGGT TTTGTTTCAA ATATTCTTTT ACTAGCGCGA 60
 TATGTTTCGTC TGATCTACCA GTTAACCTCA TATATTTAAG AGATTCATCA TCAACTGGGA 120
 AGAATCCGCA AGTTGCTCCA TACTCTGGTG CCATGTTTGC AATTGTAGCA CGGTCTGCTA 180
 15 GTGGTAAATG TTGTACACCT GGACCAAGA ACTCCACAAA TTTACCAACA ACACCTTTTT 240
 TACGTGGCTC TTGAGTTACT CTTAACGCTA AATCAGTTGC TGTTCGCCTT TGTGGTAATG 300
 AATTTACTAG TCGTACACCA TTAACCTCTG GAATTGGGGA AATAGGAGGG TTGTCCAGGC 360
 20 ATTCCAGCTT CAGTTTCAAT ACCACCAACA nCCCTCCTAG 400

(2) INFORMATION FOR SEQ ID NO: 2960:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2960:

ACGTCAAATG TAATCACAAT CGGAAAGTAT CGTGACAATG CATATATAAC AGGGAGGGTT 60
 35 TAAATATGAG TTAATAAGGG GATTTTTAGA TTTAGGTGCA CTGTTTATTT TACCGGTTGT 120
 CATATTCTTG CTTGGCCTAT TCTTTAGGCA GAAAATTGGA GCGGCATTTA GGTCTGGTTT 180
 AACAAATAGGT GTGGCTTTTG TAGGGATTTT CTTAGTCATC GATTTATTAG TTAAAAATTT 240
 40 AGGGCCAGCA GCACAAGCGA TGGTTAAAAA TTTAGGCGTC AntCTGAATG TGGATTGATG 300
 TAGGTTGGCC AGCAACATCA TCTATCGCTT GGGCATCATC TGTnCGCnCC ATTTTATTAT 360
 TCCACTCGGG ATTCATAGTT 380

45

(2) INFORMATION FOR SEQ ID NO: 2961:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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5 GGCATTTGGT CGAACTTACG AAGAATCATT GTTAAAAGCA ATTCGATCAC TTGAGTATGG 60
 TGTGCATCAC TTAGGATTAC CAAATGGTGA AAGCnTCGAT CTTGATTATA TTAAAGAACG 120
 TATTTACACAC CAAGATGATG GACGATTATT TTTTCATCGGC GAACAATTAG AAGAGGCACA 180
 ACAGTAGAAG AAATTCATAA TATGACTCAG ATTGATTACT TCTTCTTACA CAAGTTCCAA 240
 10 AACATTATTG ATATTGAGCA TCAATTAAAA GAGCATCAAG GTGATTTAGA ATATCTTAAA 300
 TATGChAAAAG ATTATGGnTT TAGTGGTAAA ACAATAGCGC ATCGCCTTAA TATGACGG 358

(2) INFORMATION FOR SEQ ID NO: 2962:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 364 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2962:

25 TTTGGGCATC ATTAGGAAAA TTCTTTGAGC AACTTTTAGTG TCTACTGGGT AATACAATTT 60
 TATCACCATG TTTTCTAAT AAATCTTTTG CGAATCGATT TTATCTTCTT CTAATAATGA 120
 AATACCAATT TCTTTACCTT GCGCTTTTAA GAAAGTATAA GCCATACCTC CGCCGATGAT 180
 AATTTTATCA GCTATGTTAA CTAAGTTTTT GATGACATTA ATTTTGTGAG ATACTTTTGn 240
 30 GnCACCTAAA ATAGCAACAA CTGGTTTATG TGGATCGTTA ACTACGCCGC CAATAAACTT 300
 AATTTCTTTA TCCATTAAGA ATCCAGCTGC AGTTTCTAAA TGTGTAGAAA TACCAACATT 360
 35 ATn 364

(2) INFORMATION FOR SEQ ID NO: 2963:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 372 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2963:

50 GTTGATTCTT TGAAAGATAA TAAAAAATTC AAAGAAATGG GATCTAGGAT TCCTAAAGGT 60
 GTCTTACTTG TTGGACCTCC AGGTACTGTT AGAAACATTA CTTGCTAGAG CGGTTGCAGG 120
 TGAAGCTGGC GCACCATTCT TCTCTATTAG TGGTTCAGAC TTTGTAGAGA TGTTTGTGG 180
 TGTGGTGGC AGCCGTGTTT GTGACTTATT CGATAATGCT AAGAAAAACG CGCCTTGTAT 240

55

TCATGATGAA CGTGGAACAA ACCCTAAACC AnTATTAGTT GAAnGGATGG TTTnCGGTGG 360
 AAAATGAAGG TG 372

5 (2) INFORMATION FOR SEQ ID NO: 2964:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2964:

TTAGCAGAAC GCCCACAAAA CCTATCTCTT GCTGTAAAAG AATTTGTGAA nCTGCTGGCT 60
 TAAACGTGT TGGCATAATT GCAGCTTTAG GAGCTACAGT TATGTTAGGT TTAAGTACAA 120
 20 TTAAAAAATT ATGCCGTAAA TAGAGCAAGA CATAACAAT AATTTAGGAG TCTGGAACAA 180
 TAATCAATGT TCTAGGCTCC TAAATGTTAT ATTGGCAGTT CTGAAACATT TATAAATCTT 240
 TGATTATGAA CTCACAACAG TGCTCTATGC TTTTATAGAT TTTAATAAAT TAGCCATTTT 300
 25 AATTGCACCT ACTGCTGCTT CACACCCTTT ATTGCCAGCT TTCGnACCTG CnCCTTCCAC 360
 AGCTGGGCAA TACTGCCAGC CG 382

(2) INFORMATION FOR SEQ ID NO: 2965:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2965:

GGGAATCATA CAATCATTAC CAATAACAT GTTACTTATC ACATGAAAGT CGGTGATGAA 60
 40 ATCAAAGCAC ATCCTAATGG TTTTATAAT AACGGTGGTG GACTTTATAA AGTTACTAAG 120
 ATTGTAGATT ATCCTGGTAA AGAAGATATT GCGGTCGTAC AAGTTGAAGA AAAATCAACG 180
 45 CAACCAAAAG GTAGAAAATT CAAAGATTTT ACTAGCAAAT TTAATATAGC ATCAGAAGCT 240
 AAAGAAAATG AACCTATATC AGTCATTGGT TATCCAAATC CTAATGGAAA TAAACTACAA 300
 ATGTATGAAT CAACTGGTAA AGTACTATCA GTGAATGGAA ATATAGTGAC ATCTGATGCG 360
 50 GTTGTCCAAC CTGGCAGCTC TGGTTCACCT ATATTAAATA 400

(2) INFORMATION FOR SEQ ID NO: 2966:

55

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2966:

10 TGGGGATTCA CAGGCTAATA CATTTGACTT TATTAGCTGG TGGCGGTAAC GCGCTGAAC 60
 TTAAATGCG ATTCAAAGTG CTGCAATTAT AAGTGCAATC CCATTCTCCT TTGTCGTCAT 120
 ACTCATGATG GTAAGTTTCT ACAAGGATGC GAACCAGGAA CGTAAATTCC TAGGTTTAAC 180
 15 ATTGACTCCG AATAAACATC GCTTACAAGA ATATATCAAG AGTCAACAAG AAGTTATGAA 240
 TCTGACATTC TTGAAAAGCG TCAGTCACGT GAAATATAGA GAAAAAAGAT AACTAATAAA 300
 GTTTAGTTAA GTATTTTAAT AACAAAGTAGT ATGTCATTCT AGTAGCTAGA ACGGTnATAC 360
 20 TACTTGnTG TTTTGTGGA AATTGAGTAT TTCAAAGGTT 400

(2) INFORMATION FOR SEQ ID NO: 2967:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2967:

ACGAGGAATT AGTGAAGTAC AATATTATCG GTGGTTTTGA TTTAGGTGTT GTTTCAGACG 60
 35 ACTTTAAAAA TCACATGTTA ATAGCTGTAA CTGAATTAAAG AACAAAAGAT GAAATCGATA 120
 CATTTGTAGA AAAGGCTGGT GAGTTAAATG ACTAGTAAAT CAAGTCCATT AATTTTTGAA 180
 AGATCTCGTG AAGGCAGATA TGCATATTCA TTACCAAAAA GTGATATTAA AACAAATTCT 240
 40 GTTGAGTCAT TGTTAGATGA TAAATTTATT CGTAAAAACA AAGCGGAGTT TCCTGnAGTT 300
 GCTGGAAC TA GACTTnGTAC GTCATTAATC CTGGACCTTT CCAAATAAAA AATTCCGGnG 360
 GTAGACACCG GGTTTAACCC ATGGGGT 387

45

(2) INFORMATION FOR SEQ ID NO: 2968:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 806 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

AACAAAGTGCA AGTGAGTCAA CATCAGAAAG TGCCTCAACA TCACTCAGTG ACTCAACAAG 60
 TACAAGTAAC TCAGGATCAG CAAGTACGTC AACATCGcTC AgTAACTCAG CAAGCGCAAG 120
 5 TGAATCCGAT TTGTCGTCAA CATCTTTAAG TGATTCAACA TCTGCGTCAA TGCAAAGCAG 180
 TGAATCCGAT TCACAAAGCA CATCAGCATC ATTAAGTGAT TCGCTAAGTA CATCAACTTC 240
 10 AAACCGCATG TCGACCATTG CAAGTTTATC TACATCGGTA AGTACATCAG AGTCTGGCTC 300
 AACATCAGAA AGTACAAGTG AATCCGATTC AACATCAACA TCATTAAGCG ATTCACAAAG 360
 CACATCAAGA AGTACAAGTG CATCAGGATC AGCAAGTACA TCAACATCAA CAAGTGACTC 420
 15 TCGTAGTACA TCAGCTTCAA CTAGTACTTC GATGCGTACA AGTACTAGTG ATTCACAAAG 480
 TATGTCGCTT TCGACAAGTA CATCAACAAG TATGAGTGAT TCAACGTCAT TATCTGATAG 540
 TGTTAGTGAT TCAACATCAG ACTCAACAAG TCGGAGTACA TCTGGTTCGA TGAGTGTGTC 600
 20 TATATCGTTA AGTGATTCTGA CAAGTACATC AACATCGGCT AGTGAAGTAA TGAGCGCAAg 660
 CATATCTGAT TCACAAAGTA TGTGAGAATC TGTAATGAT TCAGAAAGTG TAAGTGAATC 720
 TAATTCTGAA AGTGACTCTA AATCGATGAG TGGCTCAACA AGTGTCAGTG ATTCTGGCTC 780
 25 ATTGAGCGTC TCAACGTCAT TAAGAA 806

(2) INFORMATION FOR SEQ ID NO: 2969:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2969:

ACCATCTACT CCGTTAATAG TTAACTGTT ATCATTGGTG TTTGGACTTT CAGCCCTTGC 60
 40 ATCTAAAAAT ATAAGCTGAT TAAAATCTGT TATTACTTCT TCCTTGTAAC CATCTATGAT 120
 TTTTACAAAA GATTGCATTA ATTAGTCAAA CCTCCCATAT AATTATTTGC ATTTGCTCTA 180
 45 TGCCCACTTT GTTTTGACAA TATTTTTTCT AAACCTCTAA TTGCATCATT AGAACCTAAG 240
 GATTATCCTG AGAAGAAACA GTTTGAATCA ACGCATCTGT TAATTnATTn CCTTTATCAC 300
 TTAACATAAC AATTTGGTTC AACAAATTTn AACTGTAGAA GTATCATTAT T 351

50 (2) INFORMATION FOR SEQ ID NO: 2970:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2970:

5 AGTGCTTGAT GAATTTTGAC CACAAATTCA AATGTATCAG GCGTTTCTTT TATCCATTTC 60
 AATATATTTT TTTCCGGTTG TATCGCATAG TATGTCGCAT CTAATTCGAC AACCGGAAAA 120
 TGTCCAGCAT ATGTTTTAAG TTTATCGGTT TGGCGTTCTA AATCTTCATA TAATGAATAG 180
 10 TGATCACCCC AACCTGTAA TCCGATGTTT ATCATATATA TCACCAATGT CATCATACCA 240
 TATAACTTTT ATCATAATCA TTTCAGCGAA CTTTAGTTTG ATGTTTTTGC TTGATTAAAA 300
 TCTTTTCGGC GAnCCTCAGC TTGATGTTTT TCGTTGATTA AATGGTAAAT AGnnACGCA 359

15 (2) INFORMATION FOR SEQ ID NO: 2971:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2971:

25 CAGACGGTCA AGAATCTTAT ACTTATCAAA ATTTATACTG TGAAGCGAGT CTATTGGCTA 60
 AAAGACTCAA GGCTTATCAA CAATCTCGTG TTGGGCTATA CATAGATAAT TCGATTCAAT 120
 CGATCATTTT AATACATGCA TGTGGTTGG CAAATATTGA AATTGCGATG ATTAATACAA 180
 30 GGTGACACC TAATGAGATG ACGAATCAGA TGAAGTCAAT CGATGTACAA TTGATTTTTT 240
 GTACCTTGCC ACTGGAATTA CAGGGTTTCA AATTGTATCG CTGGGTGATA TTGAATTCGC 300
 35 TGGAGGGATA TTACAnCGAn CAGTTGTTGG GCAACACAAT GGGTATCCAT TTGAACCATC 360
 GGATGnAACT TTGTGCCGAA GGTCGCCTCC ACATnTAATG 400

(2) INFORMATION FOR SEQ ID NO: 2972:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2972:

50 TCAACCGCTT TACAGCCAAC CGGCGACGCT GACATGGATC GCCTGGCCCA TGCCACGCC 60
 TTGGCGCCAT CATTATTAAT TGCTGCAGTT ACGGTATCTT TAATTGCGTT AAATAAACCT 120

55

AAATCACCGA AATGTTATTC GCTTAACGTT TTGTTGTTGT TATTTTAAAA TAAATTTGAT 240
 GCAATTAGTT TGTTTATCCG CACAACATCT TATAATGTAC TTAAGTGTAT TTTAAAGAGA 300
 5 AAAGAAATAC AGTTAGGCAT TCAAAACTGT ATTTAACACA ATTAAGTTGC CTGAATTCGT 360
 ATTTAAGTCT TATTGAACCT TTTTnAGATA An 392

(2) INFORMATION FOR SEQ ID NO: 2973:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2973:

20 ATTGCAATGA TAGCAATCGG AATCGCACCT GCTAAAATAA ACGTTGTGCC ATCCGTCGCA 60
 TTTGTACCAC GAATCACAAT GTCACCAAGC GTAGGTGCTC CTATAAATGA TCCAACGGCA 120
 ACAACACCTA TCGCAACAAC CAAGGCAATA CGAATGCCAC CGATAATAAC CGAAACAGAT 180
 25 AACGGTAATT CAATCATTCG TAGCACTTGA TTGCGTGTCA TTCCCATACC TTTGCCAGCA 240
 TCCTTAATAT TCGCATCAAC ACTAGCTATA CCAGTATAAG TGTTTTTATA ATTGGAAGTA 300
 ACGCATATAA AAACACTGTT AAACACTGT TCTGAnCTAG CCTGACTACA TTAAATAGTn 360
 30 ACATTGCATG ACTGGACTGn TGGATATATT GCATGGATnC 400

(2) INFORMATION FOR SEQ ID NO: 2974:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2974:

GTATTCTTTA GGTAATGCAA CTTTAAATCC TTAAATATCT TTACCAATTT CAGATGTAAA 60
 45 GTCTACATCA TCAACTGGTG CACTTGTAGA GTCATTAACA TCTGCACCAG AAATAGCTTC 120
 TAATACGATT GCATTATCTT TTACATTTTC AGTCAATGGA CCAATTTGGT CTAATGAAGA 180
 TGCAAAAGCA ACTAATCCAA ATCGAGATAC ACGACCGTAT GTTGGTTTCA TACCGACAAC 240
 50 GCCACAATAT GGCAGCCGGT TGTCTAATTG AACCACCTGT GTCTGGAACC TAAGCTAAAT 300
 GGTACTAAGC CAGCTGCAAC TGCTGCTGCA GATTCCACCT GAnGGAACCA CCTGGGCACG 360

55

(2) INFORMATION FOR SEQ ID NO: 2975:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2975:

GAGATCGCGG GTTCGATTCC CGTCGAGACC GTACAAATGC CTATCCAAGA GATAGTTTTG 60
 TnTTGCGTTT AATATTATAT TAATAAAAGA TATATGGACG AATGATAATC ATATTGATTT 120
 ATCTGTTCGT CCATTTTCTT TAAAATGTAT GAACCTCAAG TAACTTAGTG GTTGGATATG 180
 AAAGATAAAC GTnGACAATA AAATCTTTAT TAGACGTACA AACATATGCT ACTGTCAACA 240
 TATTCTTCG TTGTGATATG CCACCAGTCC TCCATAACAT CAATTGTTAA AGTAACGAAT 300
 AACGAATAAT GATATTTnAT TTCTGAGCCA TGACGTGCCA CTAGAAGTTG CCCATTATCC 360
 T 361

(2) INFORMATION FOR SEQ ID NO: 2976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2976:

TGCTGCTTCT GAAGCGGAGT AATTGTGTAT ATCAAATGTC GCTTTTTGAT CAGGAACATG 60
 ATGTAAAGGT GTATATGTTT CACCTGTTTG CTCATCATGT AACACGGCAT GCCTATGACT 120
 GAATGTACCA CGTTCACTAT CTGACCAGT TAAGCGAATC GGTGTACCAT CTTGTAAAAT 180
 TGTCGCAAAT GCAAGTnGTT CTGCTTGTC CCAATCAACT AAACCATCTT CTTTATTAAA 240
 CGGCTCATGA CGCTTCTCAA GAACTTTGTT TAACTTTTTn CAAAATGTTA AAGCCATCCG 300
 GATATGTAA CAATGCATCA TTATTTCTTT CAAGTGATCC AAAAGTAAAG GnTTGT 356

(2) INFORMATION FOR SEQ ID NO: 2977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2977:

CTTTAGAGCG ACACCTAGTC ACTGCAGCAA GCTATTTCTT TATTTGCTAT GCTATAnATC 60
 5 GTTAATTACT AGACCTATTG CTGGTAGATT GATGGATGAT AAAAATGAAA ATATTATTGT 120
 CTACCCAGCA TTTATCATGC TTTTCCTTTC ATTTGTATGC TTAATTTCAA GCTATCAAAG 180
 CTGGTTAATA TTAATTGCTG GTGCTTGCCT AGGTTTAGGG TATGGAAATT TATCATCTGC 240
 10 AATGCAATCT ATTGCGATAA AAGTCTCACC CCCGATTAAA TATGGTATCG CGACATCTAC 300
 TTTTACGTT GGTCTAGATG CCAGGTGTCG GCTTCGGTCC AGCATTCTCT GGGTTAnTTA 360
 15 CGCAGnGTTT T 371

(2) INFORMATION FOR SEQ ID NO: 2978:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 . (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2978:

TTGTAATTTT ATGATTACAC CTCAATTGTT CTGTTGTTA AAACCTCAATA TTTAATTGTC 60
 TGCGCTCAAT AATTTGTTGT TTAAGTTGCT CAATATGATT TGATTGGAAT TCTTCCAATA 120
 30 ATGCTTTTGC TATTTCAAAT GCTACGACAT GTTCGCAGAC GATACTTGCT GCAGGAACAG 180
 CACAACATATC AGAACGTTCA ATGTTGCTT TAAAGTCTTC TTTAGTATTA ATGTCTACTG 240
 35 AATTTAATGG nTTATATAAC GTTGAATTG GnTTCATTAC ACCATTACGA TAATTGGCAT 300
 CCATTGACAT ACCGCCTCTA ACCACCTAAG TGATTAGAnC ACGATAATAC CAATTCACTA 360
 TATAT 365

40 (2) INFORMATION FOR SEQ ID NO: 2979:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2979:

TGATTATATA AATCTAACCA GCCAAGTTTC GTCTGCGGTG AGACATTGAC ATTAATTGCT 60
 GCAGATAATG ATTTAACAAC ATGTGTGGCA TGTGATTCAT TAACGATGAC AATATCATGT 120

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TGGCGATGGG TAACATTGTT AACATTGCTT CATTAAAAAC GATATCGAAT TGATTGTCAT 240
 CAAAGGGCAA TTTAACAGCA TTCGCTTGTT GAACTTGAAT ATATGATTCA nGACCTGCTG 300
 5 CGGAAATGTT TTCCGTGCTT TTTCTAAGCC TTCnTATTAT ATCAACGCCT GAnGTGACAC 360
 CAnAGTGTGA GCCAGATAAA TAGAGGTGTG CACAGATACA 400

(2) INFORMATION FOR SEQ ID NO: 2980:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2980:

20 TTTCTGCTTT TGATAATCTT TCATCAATGC AAAAGCTACA TTGGACAGTC CTATAATGGA 60
 AATAATGTTT ACAATTGCCA TTAAGCCCAT AAATAAGTCT GCCGTATTCC ATACTGTTTC 120
 TGTTTTTACA ACTGCACCGA CAAAGACAAG TACTACAACA AGACATCTAA AGATAAATAA 180
 25 TATTACACGG TTTGTTGATA AAAATTCAAT ATTAGATTGA CCGTAATAGT AATTACCTAC 240
 AACAGATGAA AATGCAAACA GTGnAACGCT TATTGGTTAA GAAAATACCT CCAGCAGAAC 300
 CTAATGCTC CTTAAGTGCC GATTGGGTAA CTGCAACACC nTGGAGGGCG TTTATCACCA 360
 30 AATTThCGTC CCGAATATAG TAAA 384

(2) INFORMATION FOR SEQ ID NO: 2981:

35

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2981:

AATTCTAACG ATATCACCAT TTTTACAACC ACGTTCTCTA AGCGCATCAT CAATACCCAT 60
 45 CGAACGCATT TGACGAGCAA ATCGACGTAC TGCTGGATCA CTGTTAAAGT CAGTCATTTT 120
 AAACATTCTT TCAATAGCAT TACCACTTAC CACATAAGCA CCATCATCAT CTCTTGAAAA 180
 TTGTAAATTT ATCTTGTGAC GGTGTATGTT TATATAATAC TCGGTTAATG CCAACTGACT 240
 50 CCTCTTCTTC AACTGTGGAG TCAACATCTT TATATTCTTC TGAATTTATC TGCTTATTGC 300
 ATATGAATAA TTGnnCAATG ATTATCACGC GTTATTGTTG GAAACTGGGA TTAAGTGGCA 360

55

(2) INFORMATION FOR SEQ ID NO: 2982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2982:

CCTCAACCGC TTTACAGCCA ACCGGCGAGC GCTGnACATG GATCGCCTGG CCCATGCCCCA 60
 CGCCTTGGGC nCATCATTAT TAATTGCTGC AGTTACGGTA TCTTTAATTG CGTTAAATAA 120
 ACCTTCCATT GAAAACACTC CTTAAATTT AAATTGAAG ATAACAAAAA CGTGCGTACT 180
 TThTGAAATC ACCGAAATGT TATTCGCTTA ACGTTTTGTT GTTGTTATTT TAAATAAAAT 240
 TTGATGCAAT TAGTTTGTTT ATCCGCACAA CATCTTATAA TGTACTTAAC TGTATTTTAA 300
 AGAGAAAAGA AATACAGTTA GGCATTCCAA AACTGTGATT TTAACACAAT TAAGTTGGCC 360
 TGAATTCCGT ATTTGAAGTC CTAATGGAA 389

(2) INFORMATION FOR SEQ ID NO: 2983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2983:

ATATTCCTAT GACAATGTTT AGGCAACGAT TCCAAGGATT AAGAAAAGAT CAACCGGTAT 60
 ACTTATGTGA TGCCAATGGG ATTGCTAGCT ATAGAGCCGC TCGTATTTTG AAAAAGAATG 120
 GATATACAGA TATCTATATG TTAAGGCG GCTATAAAAA ATGGACTGGA AAAATAAAGT 180
 CTAAAAAATA GTTTTTGTAA ATTTAATATA CGATTTAATA AAATCTGAGT GTTAATTGAT 240
 CATCAATAAC AATACTCAGA TTTTAATTTT TTAACAAAGT CTGTTACTAT ATTTCTCTAG 300
 CTTCACTGAT CATTAAACCT TAGTTTCAGC ATAATTAAGG AAGGTCCGnC CCATTTCCAT 360
 CGnGnTCCAT TACCGCCAC 379

(2) INFORMATION FOR SEQ ID NO: 2984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2984:

5 ATGCTGAAAA TATGGTGCCG TTTATATGAA TCAATTTGAA TCCGAACATA ATCCGGATAC 60
 ATATTTTCAT ACATTGGGAC CCGAATTGAC TTCAGCATT AAGCAAATTG ATTATTTTGT 120
 GGCTGGTATT GGCTCTGGCG GTACATTTAC AGGTACGCAC GTTATTTTAA GCAACATCAC 180
 10 GTGCAATGTT ATGCCGTTGA GCCAGAAGGG TCCGTGTTAA ATGGAGGGCC AGCTCATGCA 240
 CATGACACTG AAGTATCGGT TCTGAGAAAT GGCCGATATT TTTAGAGAGA CGCTTGTAGA 300
 TGGGnTATTT ACGATTAAGA TcnAGATGCC TTTCCGAATG TCAAAGTTTG CTATAATGAn 360
 15 GGTGTAGTAA GCAG 374

(2) INFORMATION FOR SEQ ID NO: 2985:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 464 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2985:

GGAGCCACCA TTGGAGCAnG TTACGGTGGA AAAGATACGG nAAGGTTnGT ATGACTGTAn 60
 30 GTCTTGATA GAGTAACAAA CCTAATTTGT TAACTCTAGG CCCCATATGT CGCAGTACCA 120
 TCTGCATGTG TTGTTAcATT GTATGCATTT GTTTTACTTG GCTTCTTGtA TGTCGGGCGA 180
 GCTCCGTATG AACTTTGACC GTTTGCATGT GTTGTTACGT TGTATGCATT TGTTTTGCTT 240
 35 GGCTTGTTTT GTGTTGGGCG AGCGCCATAT GATACTTGGC CGTTTCCATG TGTTGTTACG 300
 TTATATGCGT TTGTTTTGCT TGGCTTGTTT TGTGTCGGAC GAGCTCCGTA TGATACTTGG 360
 CCGTTTGCAT GTGTTGTTAC ATTGTATGCA TTCGTTTCGC TTGGCCTCCT GTATGTCGGA 420
 40 CGAGCTCCGT ATGATACTTG ACCATTGCAT GGGTGGTACG TnnG 464

(2) INFORMATION FOR SEQ ID NO: 2986:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2986:

AACTATTATA TTAACATACA ATGTAGGGAT GTGATGCGCG TGAAGTTTAG GGATAAAGAT 120
 AATCGTCAAG TTAATTGAC ATTTAAAAAG GATAATGAGA TAGCAGATGG CAATCATGTG 180
 5 CTAGCTATTC CAACGTTTAA AAATCAATTG CTTTMTACCA AACATAATTT ACGGGGGATT 240
 GAATTCCTG GTGGTAAAAG GGAACGCGGG GAAAAGTAGT GCTGGAAGCA GTTACACGTG 300
 AATTATATGA AGAAACAGGC GCCAAATTGA AAAATGnTTA TTACATAGCA CAATGTnCC 359

10 (2) INFORMATION FOR SEQ ID NO: 2987:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2987:

TAGAATTCTT CTAATGAATG AGCTTCTTTA GAATGATAAC CATAACGAAT TCCGTCAAAA 60
 CGAGAAAGGT TTGACGAAGC TTCTGATGAT GCAATCACGT AATATGATGG AATACCAAAT 120
 25 TTAGTATTTG GCAATGATAC TTCCTCAACG ACAGCACCTA AAGATTTTAA AGTTTCTACA 180
 GCGTTTTGAA CTGCTTCTTT TACGTCATCA GCTACACCTT CACCTAAGTA TTCTTTAGGT 240
 AATGCAACTT TTAATCCTTT AATATCTTTT ACCAATTTCA GATGTAAAGT CTACATCATC 300
 30 AACTGGTGCA CTTGTAGAGT CATTAAATC TGCACCAGAA ATAGCTTCTT AATACGGTTG 360
 CATTATCTTT TACAnTTCGG GTCATGGnCC CATTTTGGTC 400

35 (2) INFORMATION FOR SEQ ID NO: 2988:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2988:

45 ATTCATTCAT AATTATCAAT CCTTTGTGTT AAATTACTAT ATAAATAGTG TACGnATTTT 60
 CGAAATTTGT GATCATAAGT TTATTCAATG CTAAACAATA AGGTTGAGAC ATAATCGTAT 120
 CTCAACCTTG AAATTATTAT ACGTTGACGT CACTAGTCAT TCAGTTTTCT TAATGCTGCT 180
 50 ACAATCTCTT TTTTAGTATC TTGTACTTCA GAAGCTTGCT TAATCACTTT TGCAGGTGTA 240
 CCAGCAACAA CTGCACCAGC TGGTACATCT TGTGTCACAA TCGnGCCACT GGCAACAATA 300

55

nGATTATAAC CGTGGAG

377

(2) INFORMATION FOR SEQ ID NO: 2989:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2989:

15 CCAGGnACCT GGACACGCCG GGTCTTATCA TCAATAATAG TAGCATGACA AATCTACTAT 60
 TTTTTCGCTA ATAAGTGGAT GTAATGCTAA TAATGTTGCT GTAGGGAAAC AGCCAGGATT 120
 AGAAATGAGC TTCGTTCCAT TGTATCAAAA CGATTGCCAT TCTGAAATGC TGTAATAGT 180
 20 CATGATTCAA ATCATCTTGT GCCTGCAGCA GTTCTTTTGT AATATGCTTC ATATATTTCA 240
 CGnTTCTTAA TTCTAAATGC GCCAGATAAA TCGATAACAT GAATACCTTT TTCTACTAAG 300
 GGAGGGATAC ATGTTTTACT TACGGGTGCT GGTGTCGCAA AGAAAATTAC ATCAAn 356

25

(2) INFORMATION FOR SEQ ID NO: 2990:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2990:

TCATTTTCCA AGTGAGACTC TGCTCTTGCT TTGGCTAATT TAGCTCTTTC AACATCAATT 60
 TCTCTTGCAAG TTTCTGCAGT CTGAACAATG ATTGAACTT TATCTTTTCT AACTTCAACA 120
 40 AAGCCATCGC TTACAGCAAT ATATTCAGTT CCATCGTGGA AATTTCACTT TTACAAAGCC 180
 TGTTTTTAAA GCAGCTACAG TTGGGAATAT GTCCACTCAT GACACCTATC TCACCAGCTG 240
 TTGTTTGCAT AACACGAGT TCAACATTAT CACGATTGTA AACAGAACCA TTAGGAGTGA 300
 45 CAATATCTAG GTTTAAATGT CCATTATCCA TTCCnCCnGA ATTGGnTGA 349

(2) INFORMATION FOR SEQ ID NO: 2991:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2991:

5 ATGGCCACGT TCATGCCAAT AGCTGTCGTA GTCGCATTTT CACGTTCTAG TATTGCATTT 60
 TTTAAATGCG ATGTGTGCTC TACATAACGG CAAATTTTAA GTTTATGAAT CAACATATCA 120
 ATTGCTTCGT TTCGAGACAT GTCGTGGATC AGTAATTATC ATAGTTTGTT GATCAAAAAC 180
 10 ATGAGAAGGT TTATTGAGAT GTGAATGTTT CGCGGTGTTA TCTACATTGT CAACCTCTGT 240
 ATCATGTTGT GTAATATCTG TATCATGAAG TTGCGGTTGC GCTGGTGCAT CTACTGCTAT 300
 AACTGGTGTA TTGCGTTTAA ATAATAGTAC AGTAGTnCAT TGTnGACAAG ACTnACCGAC 360
 15 TTA 363

(2) INFORMATION FOR SEQ ID NO: 2992:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2992:

AAGTTTATTT TAAATTCGT AATAAAAATA ATAACTCAT CGAACGATTT AATGGTCTAG 60
 30 GTTTCATAT CAACTATGAG TACATTAAAT TCAAATTCGA ATCACGTAAC GTAAAAGATC 120
 AAACAATCCC TGAATAAAAC ACCAAGCAAA TACCCTACAG TACATCATTA GCATGTATTG 180
 TGGGTTTTTC TACTTTTTGT AAATATTGAn AATTATnAGT AGTTGTTTTT TACTATTAGG 240
 35 GCAGAATGCT TTACAATAAC ATGCAAGTGT CAATTAAGGG GAGCACTTGC ATAAATAGTA 300
 TAGGnGAGTG AGTAGTCCTG GCCATTCCTT GGAATTCCTT AATCGGCAC 349

(2) INFORMATION FOR SEQ ID NO: 2993:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2993:

50 TTTGTGCAAT AAGCGTTTT TGTTGTTTG CTTTTGTTGC TAATTCATCT TTCGCAACAT 60
 CTTTAATTGT TGTATCTGCA GTAATACCTT GAATATCAGC AACTGCTTGA TCTTTAATTT 120
 GCGTAACATC ATTAGTTGTT TGTGCATTTA AGATATCTTG ATACGCTTTT TCTTTAGCTT 180
 55

TTGCTTGATT TTGAGTTGTC ACAGCTTGAT CAACATCATT TTTAGCATTG ATTTAACCGC 300
 TGTGCTGGTT GCGGCTTGAA TTGAATCTTC CAGGCTTCGC TGACTACACA TACACAGTGA 360
 5 GnGnAATATT TCGGCTGAAC GCGTGCATGT GAAnGCTCT 399

(2) INFORMATION FOR SEQ ID NO: 2994:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2994:

AATGACAGGA ATCGTCGTTG CCTTTACTAA TTGACCAGTT AATTCAAAGT TAGGTCCGGA 60
 20 CATTTTGCCA TCTTTAGCAA TATCAGTATA TATAATGCCG CCAAGAGGTA TATCCGATAA 120
 CCGTCTCACA AACTAAATAA ATTTAACTCT GTGTCCTCTT CCCATCCGTT CACTTTAATA 180
 TCTTCTCCAT AGGCATCAAC AGATAAATAA ATGCGACCTG GAAATGTATG TGCCATCTCT 240
 25 TTAAGCCAAT CAGTATCTTG AATACCTTTC GTTCCAATA TGCAATAATT AATCCCTGCG 300
 GCAAAGTAGT CCATGATTG TGAATT 326

(2) INFORMATION FOR SEQ ID NO: 2995:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2995:

CTAATGCCGA TGAGCAAAAC ACAAGCATTG GAAATTATTA AAAAAGTTAG GTACGTATAC 60
 AACATTGATT TTGATAAACC GAAGTTAGAA ATGTGGATTG ATGTATTAAG TCAAAATGGA 120
 45 GATTATCAAC CAACTGTAAA AGCGGTAGAT GTTTATATCA ACAGTAACAA CCCGTACCCG 180
 CCTAACTTAC CAGCAATCAT GCGTAAGGAA CCTAAAAAAG TATCTATCGA GCCAGTAGAT 240
 AACGAAACCG CTACACACCA TGGGAAAATG CAGAATGACC CGAATTGTCA GACAAGGAAA 300
 50 ATAGCGCTAG ATAGTTCATG AATAGTTGGC AGATTGGGGC GAACGATGAT ACGnCATTCG 360
 ATTGAAGTCA TATCGTCGTA CTTAACACCG GACGTTnGAA 400

(2) INFORMATION FOR SEQ ID NO: 2996:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2996:

10 GAATGTAAGT GTCCCTTAAG CATAGTGCTC CCACCTTAAA TTTTGTTACA TACTTTTCATG 60
 GAATGTACGA GAAATTACAT CTAATTGTTG TTCACGTGTT AATTTAATGA AGTTAACAGC 120
 GTAACCAGAT ACACGGATGT TAACTGTGGG ATATTCTTCT GGATGTTCCA TTGCATCTAT 180
 15 TAATGTTTCA CGGTAAATA CGTTAATATT TAAGTGGTGA CCACATTGCA TTGCGTAACC 240
 ATCTAACATA CTAGTTAAGT ACGGTTTGAT CTCTGGnTCT TTACCTAATG ATTTGGnACG 300
 ATACTGATGT ATTGAAATAC CATCCTTACA GCATCGTAAG GGGTCCTAGC CACAGAACTT 360
 20 ATGAAGAAAT GCACCTTTTn GGCACnGGCA TGCATGGGGT 400

(2) INFORMATION FOR SEQ ID NO: 2997:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2997:

ATGATATTAA CCTGTTTACA AGATGGTTGA TACTTGCGCA TGA_nATTGA ATCTTCAACA 60
 35 CCATATTATT ATGGTACATA CGAAACTGAA AATGAATCCA TAGTTACTGA CAAAGAAAAA 120
 ATCTTAGTAT TAGGCTCTGG ACCAATTGCA ATCGGCCAAG GTGTAGAATT TGA_nCTATGCG 180
 ACAGTTCACG CCGTTTGGGC AATTCAAAAA GCAGGGTACG AGGCGATAAT TGTGAATAAC 240
 40 AATCCAGAnA CAGTTTCAAC AGATTCTCAA TTTCTGACAA ATTATACTTT GAACCTTTAA 300
 CTGAnGAGGA TGTGATGAAT ATCATTAATT TTGGA 335

(2) INFORMATION FOR SEQ ID NO: 2998:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 397 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2998:

GCAGTAACTA ACTTTTGTAC AAAAGGATCA TTTTATCAA CATAATGTGG TGGTTGGACT 120
 TTACCTAATT TCACTTCAAA GtATTGTTGA ATCTCATTTG CAAAACGATC CATAGCTTTT 180
 5 TCAAATTCAA ATCCTTCTGG GTAGCGTAAt TGATACCGAA AAGACCTGCG TTTTCATTAT 240
 CATATGTAAT AACACCAATG TTAGTTGTCA CGTCACCCAT GgACATCTGT ATGGgAATTT 300
 CATTCCCAnC TTTTTCACCA AAATCnGGAA TTGAAATAAG TGAGCGATTA CGAAATGGCG 360
 10 ACAAACGCCT GTGGCATTGA TnGAGCAAGA TTnAAGG 397

(2) INFORMATION FOR SEQ ID NO: 2999:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2999:

AAAGCTGTGT TGGTAAAGAG TTTTGTGCGAT TTGGTACGCA ATACACGACA CGACTTGGCA 60
 25 TTCGTTTAGA AAAACATTT GAATACATCG ATACACCTCA TAAATTCAAA ATGGGTGTAT 120
 CAGGCTGCCC AAGAAGTTGT GTTGAATCAG GTGTTAAAGA TTTTGGTATT ATCTCAGTTG 180
 AAAATGGGAT TCCAAATCTA TATCGGTGGT AATGGTGGTA CAGAAGTTGA AAAAGCTGAA 240
 30 TTTTAAACAA CTGTAGAAAC AGAAGATGAA GTAATCAAAT TATGTGGTGC TTTGATGCAA 300
 TATTGAnCGC GAAACAGGTA TATATGcGG AAAGAACCAG CGCCCAGGTT AAGAAGACCT 360
 35 GGATTTGAAA ATGTnAAAAG AAGTCCTTAC CTGGGCCCCG 400

(2) INFORMATION FOR SEQ ID NO: 3000:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 506 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3000:

AACGGTAGTA TTACAGAAAG CTCTACTTAT GGTGATAATG ATACACCAGC GCCACCAACT 60
 GACGAATTAG GTGGTAGTTG GACACTATGG AAAAATTTAG CGCGACAAAG TCCTGAATTT 120
 50 GGTAATCCTG ATAAGTTTTG CCAAAATATT CCTAAAAAAA GTTGGTTTGT TTCAGCAACT 180
 TCTACAACAA ACAATAAAGA GATTATCGAT ACAATAGAAA GTATTTGTAA ACGTGACCCA 240

AGTTTTACAA TCAATCGTCA GCMACAGTTT aAAGACCAaC CTGrAAATGA AaTATCTACA 360
 TGGATTTATG CCTTATATyC AGATGTAAaC GGCGATTATA TTAAAAAGCC AATTACAGAA 420
 5 TGTAGTGGTA ATGAAATATG CCAAGnATGG CTGTATCnCT TnGGTGTATC AACTGACAAG 480
 ATTGAAGACT TAGCAAAACA TCGGTC 506

(2) INFORMATION FOR SEQ ID NO: 3001:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 353 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3001:

20 ATTGATGGCA TCGAAAAACT TTAATAAGAC AACAAGTTGA TGAGATATAT GTATATAGGT 60
 TTGGCATGGA TTTCGATTGC AGTTAATTAG AATAGCTCAA TGCTATAAAT GTAAGTAGTT 120
 GATATGAAGA AACTAATGAA CTAAATGCAA GTATTGTCTA AAACAATCAT TTTATTGAAA 180
 25 TTTAGTAGAG CTGAAATTAA TATAACGTCG TTAATTGAAT AACGCTTATG TTATAAGAGC 240
 ACTCATACCA nACCATAATC ATCTATAGnT ATAACAATTC ACGTATAAGG GGCTGTGTTT 300
 30 GGCATAGCCC TTAGGTATAC ACCTAATTCC CATTAAAATA GTAGGGGnTT AAA 353

(2) INFORMATION FOR SEQ ID NO: 3002:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3002:

40 CAACAAAATG TCTATATGGT AAGTGGTAAA ACGAAAAATG ATGAAGACTA TTCATCAACT 60
 ATTTTATATA ACAACGAAAA AGAATTACAA AAAATTACTG ATGCTGCTAA AAAGCAAAAC 120
 45 GGTGTAAAAT TAACGATTAA AGAAGAAGAA AAACAAAGTG TCTTTGTGAG TATACTTTCA 180
 ACATTAATTC CAGTTGTAGT CATAGCGTTA TTATTTCTTC TCTTCCTAAG CCAAGCACAA 240
 50 GGTGGCGGTA GTGGCGGTCG TATGATGAAC TTTGGTAAAT CTAAAGCAAA AATGTACGGT 300
 GATnAATAAA CGTCGTGTTC GTTCTCTGA TGTAGCCAGG GGCCAGATGn AGGAAAACCA 360
 AGGnTTAATT GGAAATTGTT GGTTCCTTGG AAAGGTAATG 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3003:

10 ATAACATCGG CACAGCAGCT AAAATAACCA TACCCAAAAT GAnTGTATCT TTAAACGTGC 60
 ACCGTAAAGn CTTCCGACTA GCCATGTATA AGCTTTGGCA GCAGATAATT GCTTCGTTGT 120
 15 AATGAGTAAT CCTTGGACAA GCGCAATAAA CAACGTTTGC ATCGAAATAC CGATGATTAT 180
 GAGTGTGTGC GGGCGTATTT GTCCTTTCGT TTGAAACACT AATAGTATCA TCATTGCAAC 240
 TGCGCCACCT AATACTGCAA ATAGTGGAGT AAATGTATTG TTAAAGGCTG AAAATGCAAT 300
 20 AAAGACAACA GCACTTAAGC TAGCACCACC TGTGATACCG CTAATATCAG GTGAGGCCAA 360
 TGGnnTTTTT TTATACATTT TGGCAACATT TAACCAC TTC 400

(2) INFORMATION FOR SEQ ID NO: 3004:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3004:

35 CTAATAACAA ATGCGATGAT GATTAATACT AATTTACCTG CTGCTAATAC AGAATCTCCA 60
 AGGAATGAGA AGAATGGTTG ACGTTCAACT TCATTGTTTT TAAGACTGTA GATAATATCT 120
 TCTTTCTCTT CAACACTTAC TGGATTCAAC AAGCATGACA CAATAATCGC GTTAACGGAT 180
 40 ATTTAGTGGA ATTGCCGTTA GTACCAGTTC TCCTGGTACC ATTTGTACAT ACGCACCTAC 240
 AATAGCTCCC GATACAGAGC TCCATTGACA TCATTGCGAT TGTTAATACA CGCATTTCAT 300
 TnCAGACGTT TTAGTTGCTC ACTTGGATAC GGGCTAAngC TTnCGTGAAT TGCC 354

(2) INFORMATION FOR SEQ ID NO: 3005:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GGTCAGCTTA TTGAACAAGG GACACGTGAA TCAGTCTTGC ATCATCCAGA ACATGTTTAT 60
 ACGAGATTTA TTATCAACGA AGAAGAAGAT TAATGATCAT TTTAAACATG TGATGAGGGG 120
 5 TGATGTACAT GATTAAATTT AAAGATGTTG AAAAGTCATA TCAAAGCGCA CATGTTTTTA 180
 AGCGTCGTCG AACACCTATC GTGAAAGGTG TGTCAATTGA GTGTCCAATC GGTGCGACGA 240
 TTGCGATTAT CGGAGAAAGT GGTACGGnTA AATCGACGTT TGAGTCCTAT GATATTAGGT 300
 10 ATTGAGGAAC CGGATAAAGG TTGTGTACCC TTAAATGATC CACCGATGCn TAAGAGGAAG 360
 TGAGCCGCCA CChATTGG 378

(2) INFORMATION FOR SEQ ID NO: 3006:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1785 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3006:

25 AChTTAGTTG GCCAAGCCTT TATCCGGAAT TATTGGGCCT TAAAGCCCCC TTAGGCGGTT 60
 TTTTAAGTCT GATGTGAAAg CCCCgGCTCA ACCGTGGAGG GTCATTGGAA ACTGGAAAAC 120
 TTGAGTGCAG AAGAGGAAAG TGGAATTCCA TGTGTAGCGG TGAAATGCGC AGAGATATGG 180
 30 AGGAACACCA GTGGCGAAGG CGACTTTCTG GTCTGTAAct GACGCTGATG TCGGAAAGCG 240
 TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC GTAAACGATG AGTGCTAAGT 300
 GTTAGGGGGT TTCCGCCCCT TAGTGCTGCC AnTAACGCAT TAAGCACTCC GCCTGGGGAG 360
 35 TACGACCGCA AGGTTGAAAC TCAAAGGAAT TGACGGGGaC CCGCACAAGC GGTGGAGCAT 420
 GTGGTTTAAT TCGAAGCAAC GCGAAGAACC TTACCAAATC TTGACATCCT TTGACAACTC 480
 40 TAGAGATAGA GCCCTTncTT CGGGGGACAA AGTGACAGGT GGTGCATGGT TGTCGTCAGC 540
 TCGTGTCTGT AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCTTAAG CTTAGTTGCC 600
 ATCATTAAGT TGGGCACTCT AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG 660
 45 ACGTCAAATC ATCATGCCCC TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA 720
 AAGGGCAGCG AAACCGCGAG GTCAAGCAAA TCCATAAAG TTGTTCTCAG TTCGATTGT 780
 AGTCTGCAAC TCGACTACAT GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACG 840
 50 GTGAATACGT TCCCGGGTCT GTTACACACC GCGGTCACA CCACGAGAGT TTGTAACACC 900
 CGAAGCCGGT GGAGTAACCT TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG 960

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TATATTCGGA ACATCTTCTT CAGAAGATGC GGAATAACGT GACATATTGT ATTCAGTTTT 1080
 GAATGTTTAT TTAACATTCA AAAAAATGGG CCTATAGCTC AGCTGGTTAG AGCGCACGCC 1140
 5 TGATAAGCGT GAGGTCGGTG GTTCGAGTCC ACTTAGGCCC ACCATTATTT GTACATTGAA 1200
 AACTAGATAA GTAAGTAAAA TATAGATTTT ACCAAGCAAA ACCGAGTGAA TAAAGAGTTT 1260
 TAAATAAGCT TGAATTCATA AGAAATAATC GCTAGTGTTT GAAAGAACAC TCACAAGATT 1320
 10 AATAACGCGT TTAAATCTTT TTATAAAAGA AACCGTTTAG CAGACAATGA GTTAAATTAT 1380
 TTTAAAGCAG AGTTTACTTA TGTAAATGAG CATTTAAAT AATGAAAACG AAGCCGTATG 1440
 TGAGCGTTTG ACTTATAAGn ATGnnnGATA TGTGAATAT CCATATCTAA AGCTAGATCT 1500
 15 AAACCTTGTT CAAAATCTTC AATCGTCTGT TTCGGTAAAT GATACATTAA ATCTAAACTG 1560
 ATTGATTTAA TACCTGCGTT TTTAGCATTT AACACCGAAG TGTAAATATC TTCAGTATTG 1620
 20 TCGCTTCTAC CTAAAACAGA CAATAACTCC GGCTTGAATG TTGAACGCC CATTGAAATC 1680
 CTTTTACTC CATATTTCTC TAATAGTTGG ACTTTCTCTT TAGTTAACTC ATCAGGATTT 1740
 GCTTCAAATG TATACTCGCC TGTGATTGTA AACGTATCAC GTATT 1785
 25 (2) INFORMATION FOR SEQ ID NO: 3007:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3007:
 35 TGCAAAAAAC ACAATAACGA TAAATGTTCC CATTGATCCT ACAGCATCGC GAACATTTTA 60
 CCTAAGTCTT TTGTATTTTT AATTTCTTTG CTTAAAATCC CATAAACTAA TCCAGGTACT 120
 40 AAAAATACGA CAAGAATAAT TAATCCGACA CCGTTAATTA ATGGCGATCG TCTAGTAAGC 180
 TGCCTGTTTT AGCATTTCCT AAAAAGCTAT GTCAGGAATG GCTGTAATAA TTAATAAAAT 240
 AATTGnGCTA TGAAGTATA TTTGCCATTT TAAAAnATGT GCTCTTTGTC AGAATATGTC 300
 45 AGATGTnCTC ATGGCATCAT GCATTAACT GCATCATATT TTCCTAATCT AGGATAATGA 360

(2) INFORMATION FOR SEQ ID NO: 3008:

- (i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3008:

TTGCCTTCAA ACACATACTT GTAGTCGGAT GATCACCTGT TCCAAAAGnC ATACCTGGGT 60
 5 CGAGCTCAAT GCAAAGCTCT TCATCCGCTT CTTTAGCATA TGTTTCCCAA CTAGGAACTA 120
 TTGTGAACCTT CTTGACGCT CGGGAATGGA TGGAAATAGT TTTTCCATTC ATTTTCCCAA 180
 TCCGTCTCTG CAATAATTTG CTCACTGAAT TGAACGTTAT GTTGATCAAG TTCATCTAAA 240
 10 TTTAATAACT CATCTTTGAA TTTGCTGTCG CAACTGTATC ATCATAAGTG CATTTCAGTA 300
 AAATAGGCTT nGCAAnCTTA CTCCTTATC TGGGATAAAG CCTCGGTTTT 350

(2) INFORMATION FOR SEQ ID NO: 3009:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3009:

25 TCTTATATCA CCAGGAATTA ACACTGCCTT TTGACCACTT TCTTCAATCA CTTGGCGTAC 60
 TTCTTGTGCA TCTTGTTCTT CACTCGGAAG ATAGTTAATC GCTACATCTG CACCTTCTTT 120
 AGCATACGCA ATTGCTGCTG CACGCCCTAT TGCTGAGTCA CCACCTGTGA CTAAtATTTT 180
 30 ATAGCCTTGT AAGCGTTGAT GACCTTGTA AGACGTTTCG CCACAATCGG GTGCTGGCGT 240
 CATTTCAGAT TGTAACCCG GTACCTCTTG TTCTTGTTTT TCaTAATCCG TTGTTTTAAA 300
 TTTTGTTcNa GGaTCTkGAG CkGCCaTTTT TtGACAyCtC CGTaTnCGCT TAATGGGTAT 360
 35 CATTTACCCC AATCTTCCTA AGG 383

(2) INFORMATION FOR SEQ ID NO: 3010:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 388 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3010:

TAATTCAACG GGAATTTTCC CTTTGAAGTT AACATAACGG TAGGCTGCTT TAACAGCTTC 60
 50 ATCATCGGGC GCTTCGACAT CTTCTAATTC ATATGCAATG CCCAATGTTT TCCACTTATG 120
 AACACCTAAC TGATGATATG GCAGAATTTT AACTTTTTCG ACGTTATCAA GAGAATTAAT 180

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TGTCGAATCC ATACCAGGTG GTTTCATATC TGACAGTTTG CGCGCGAAGT TAAAGGATGT 300
 GTGTATTAGG GCTTTCCTGG TCCATCCAAA TAnGGTTGGT CCATTAAATCC ATAAGGTTTT 360
 5 AnAATCnAAA TAATAATCCA GTCCGGTA 388

(2) INFORMATION FOR SEQ ID NO: 3011:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3011:

ACTGCTGTAA CGTCAGTTGA TCTTTTCATT CTTGGTTTAA TTTCTGAGAC GTTACTTGGT 60
 20 TGnGcAnGC CACCAATTGC CATAACGACA GATTGGAAGA ACAATGCATC AGTTCCACCA 120
 ACACCAAAGA TGTCACCAAG TACAACGAAA CCTACATATC CAACTGTAGA TACAATTAAA 180
 ATACCCATTG CTTTTTTAAA TTCAGGATTA TCTGATTGAC GTnCATTTTT AGCTTTAAGT 240
 25 GAAGTAAGTG CTACACCAGT AACTAATAAT ATCATGGCGA TTAAACCAAA GATAATTTGA 300
 GTCATTGAAG ACCATTACCC TAAAAAGATA ACGCTGGAAT AATGGTGTAC CCAACTAATT 360
 GGCATACCTG GTAGGAAACT GGGCATAGGT ATTTGGATAC 400

30 (2) INFORMATION FOR SEQ ID NO: 3012:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3012:

TTATCGGATT CGTTAATACT GGCGGTTTAC GCAATAGTTT AGATGTAGAT GATAACAATG 60
 TGCCTATTAA ATTTAAAGAA GAGTTCGAAC CTAGAAAGTT TGTTTTCACT AACGGCGAAA 120
 45 TTAAATACAA TAGCAATTTT GAAAAAGAAG ACGTACCGAA TGCATCAAAC CAACAAAGTG 180
 CGTCAGATTT AAGTGATGAG GAACTTCGCG GAATGGTTGC GAGTATGCAA ATGCAGGTGG 240
 CACAGTAAAC GTATTAACAA TGGGATTAGC TCAACCAAAC GCTATGTTAA CACCACAGTT 300
 50 GACTGACTGG AACTACCAA ACCAGTACTG AGGGGnCGTT AATAATGAGT GTTTCCACTT 360
 AAGCATAAAC TTTTGTGGT CTAAACGGC ATTAGTGTCG 400

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3013:

```

10  GGCTGTAATG AAAATCCAAA AGCCAAGCTT ATTTAATTCG CCTTCATGTG TCGTGGAATC      60
    AATAGTGTTC GTATCATGAC TCATGACTTA CAGCCTCCCT TTCTTTAATA CGCGCTTCTC      120
    TTAATCTAGC TTCAGTTTCT GCAACTTCAG CAGCAGGGAT ATGATATCCG TGATCGATTT      180
15  GGAAACTGCG ATAAATCATA GTACCAAAAA TACCGAATAA ACAAATTAAT GCTGGAATTA      240
    CAGTTTCGAA AATTAAGAAG AAACCGCCGA TAGTCATAAA GATACCAATC CAGAATCCAA      300
20  CAGGAGTAAT GGTTCGGCAT ATGGATGGCC TTGGnAATAA TGGGTTGnCC TAAGTAATGG      360
    CCGACCAAGG TCCTTTCCAn ATCCACCAA      389
  
```

(2) INFORMATION FOR SEQ ID NO: 3014:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3014:

```

35  AATCGCTTCG GTTAACTGTT CTAACCATTC GTAATAAACA TGTGTATGAT CAAGCTGAGC      60
    TTTAATTTTT TGTGCTCTT GTGTTTCAGC TTCAGTTAAA TCACTGCTTT CAAGTAATGG      120
    ATTGATAATA GCTTGAGCAT CTTTACTGC TCGACATTG ATGTCAATT CACGCTGGAA      180
40  TTTTITAGTG AAAAAGTTTC GGAAAAAGAT GAAAAAGTCT TTCTCGGCGA TAAAATGTGT      240
    TTGCGGCTCC TCTCGTAAAT TGTGGTTAAC AATATCAAAT TCCTGCAATT CCTAACGCAG      300
    CACTCATACT nGTTGnCAT TGCAATGATG ACGCATTAC AGGGCAACTG CTCAACACAT      360
45  GGGCATAAAG TTCCCACTC ATAGGCAACA ATCATGGCGG      400
  
```

(2) INFORMATION FOR SEQ ID NO: 3015:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3015:

nCCTATCTCT GGTGAGAGT CTTTGAGCTG AAAAATGTGA CACACAAAAT TGCAATGGnA 60
 5 TCAACAAATG TTTCCCATG TGGATGGTCT TGAATAAGTA TTTGGTGTTT AACTTGGTGA 120
 TTTGCCATGA CTAATACCAT GTCATTTGTA CTTGTATCGC CATCAACAGT AATCATATTA 180
 AATGTATGGT CAGTCGAAGA TTTTAATAAT TGATGAAGTG TATTCGATTG AATCGATGCA 240
 10 TCGGTTGTTA TAAAAGCAAG CATGGTAGCC ATATTTGGGT GAATCATACC TGAACCTTTG 300
 GTGCTACCAC CAATTGTAAC GGTTTACCAT CGATTTTAGT GATACAGCGA TATGTTTTGT 360
 ACAGGTATCA GTGTTAAAA 379

(2) INFORMATION FOR SEQ ID NO: 3016:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3016:

CATATAAATT GCTAACGTGC CACCATTAC TAAGGAATTG ACATCCACTT CATTTTCTTC 60
 TGAATCTTTA AAGTGACCTG TAGAAAATGT CACACTTTTA GCAACTGTAC GCATTGTCAA 120
 30 ACCTGTCTGC ATAGTAGCAA CTGCTGCGCT CGCTGATGTC ACCCCTGGTA CAATTTCAAA 180
 CGCAATATGA TGTTTATTGA GTATGTCGAC TTCTTCTTGC ACACGACCAA ATATCGCTGG 240
 ATCGCCTACT TTAAGTCTAA CAACCTTGTT ATATCGACGC GTGCTTCCAC GATACAGTCA 300
 35 TTATTTTCTT GCGGAAAAT GTTTGGAAAC GGCTTTTACC AACAGGTAA TTCAGAGGCA 360
 ATCGCAATGn AAATTACGGn TCACnAACGG TCATTGGATG 400

(2) INFORMATION FOR SEQ ID NO: 3017:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3017:

CCTTTTTCTC TTCTTTCATA TCTGCAAACG TGCATCAATT TTAGGATCTA AATCTCCAAA 60
 TGCTTCTGCA ACTGGTTCAG AGCGTTCATA ATACATACGA ACTTTTGGAT ATAACGCTTT 120

TCATTTAACT GTTCATCAGT ATATTTATCA TATGCTTTTG TTGCTTGTTT TAATTCTGCT 240
 TTAACACCAT CATCTTTTTT CGATGTCTTT GAATCATCCT TCTTACTATC GTCGTTCCCC 300
 5 ACATGCAGCA 310

(2) INFORMATION FOR SEQ ID NO: 3018:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3018:

TCGCTTTGTA AATTCTGGAA CAAAGnCAGT CATGACAACA ATTCGTGTTG CACGTGCATA 60
 20 TACTAAAAGA AATAAAATTA TAAAATTTGC TGGATCTTAT CATGGCCATT CTGATTTAGT 120
 ATTGGTTGCA GCAGGTAGCG GCCCATCTCA GCTCGGTTCT CCAGACTCAG CTGGTGTTC 180
 AGAAAGCGTC GCACGTGGAA GTCATTACTG TACCTTTCAA TGATATTAAC GCCTATAAAG 240
 25 AAGCAATTGG AATTTTGGGG TGATGAAATT GCCGCAGTAT TAGTAGAACC AATTGTTGGT 300
 GAACTTTGGG AATGGnnaAT GCCTCAACCT GGGATTTTTTA GGAAGAGGGT 350

(2) INFORMATION FOR SEQ ID NO: 3019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3019:

ATATCATGTG CCAGTGAAAG CGGCACTGGn CGGATATGGC GCACATATGG ACATTATGAA 60
 40 AGAGTACCAA TTAATCATTT TAGCGCCACA AGTTGCGTCT AACTATGAAG ATATTAAGCA 120
 AGATACAGAT AGATTAGGTA TTAAATTAGC GArGACTCAA GGTGCTGAAT ATATCAAATT 180
 45 GACACGrGAT GGCCAAGCAG CCCTTGATTT CGTTCAACAA CAATTTGAAA ATTAAGAATA 240
 GGAGTTTTTC ATATGACTAA AACATTACCT GAAGGATTTT ATTTTGGTG GAGCAACAGC 300
 AGCATATCAA GCAGGAAGGT GCGACCAAAT TACGGGATGG GTTAAAGGTC GCGTGCATTG 360
 50 GGGATACGGT ATTTTAGGAA GGAAAACCTTA TTGGTACCA 400

(2) INFORMATION FOR SEQ ID NO: 3020:

(A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3020:

10 ACGTTCGTCT TACGTTTAAC GCCATACGGT GTATTAGCAA TTATGGnCCA ACACATTATC 60
 GACAAGTGAC TTTGGCGCCA TTTGGACTTT AGGAAAAATT CTTAATCGCA TCGTACGCTG 120
 CATTAAATTAC GATGTATATC ATTCACTTAA TTATTTTAAG CCTGTTAGGT ATTAGCCCAA 180
 15 TTCGCTATGT TAAAAAGACT TTGGAAGTAT TAATCTTTGC ATTCACATCA CGCTCAAGCG 240
 CGGGTGCCCTT ACCAATGAAT GTACCAACAC CAACCAGACG TCTAGGCGTG CCAGAAGGTA 300
 ATGnCAATTT CGCTGCGACA TTTGGAATGG CGATTGGACC AAATGGGTGG GCAAGnAATT 360
 20 A 361

(2) INFORMATION FOR SEQ ID NO: 3021:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3021:

CAATGACCAT GACCAGTTGA TTTGGAACAA TGATTGACAT TGGAGCTATG CATCAAGTTT 60
 35 GTCTTTAAGA CTAATAAACC CACGAACCAT GTTAACCCCG TGGTGACCA TCACCAATTG 120
 nCTCGATCTA ATTCAGTTAA TTCAGATTCA TGTTTTTTAA ACGTTTCTTC TAAATTTAAT 180
 AAACGTGnCT TTCATATCAT TCACTTTCAT TTGTGnCCAC CTCATAAATG TATATTATCA 240
 40 TATTCACTCT TATTAAAGTA TGA CTGTTGT TGGTGCTAAA AATGCTCAA ATATTCGGTT 300
 TATTAGGCAC GATAGTTATA GAAAAACCTG ACAGTCTAAA GATGTCATAT AATCAC 356

(2) INFORMATION FOR SEQ ID NO: 3022:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3022:

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GTGTTTGGTC CAATATCCAT ACCTTCTTGG nTCTGCTGGA ATTGAATCAG ATGGTACTAC 120
 AGTGATTTTG GCATCATTAG nAAAATTCTT TAGTCAACTT TAGTGTCTAC TGGTAATACA 180
 5 ATTTTATCAC CATGTTTTTC TAATAAATCT TTTGCGAGTC GGATTTTATC TTCTTCTAAT 240
 AATGAAATAC CAATTTCTTT ACCTTGCGCT TTTAAGAAAG TATAAGCCAT ACCTCCGCCG 300
 ATGATAATTT TATCAGCTAT GTTAACTAAT AA 332

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(2) INFORMATION FOR SEQ ID NO: 3023:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3023:

AAAGGTATTC CACAAGAATT AGCTTTGCAA AAATGCCAAA GCAAACAGAA GATGGnACAA 60
 TTTAAAGTgn CCTACAATCA TGAATGAGGA GGACGCGTAA GATGAGCATT CGCTACGAAT 120
 25 CGGTGAGAA TTTATTAAT TTAATAAAAG ACAAAAAAAT CAAACCATCT GATGTTGTTA 180
 AAGATATATA TGATGCAATT GAAGAGACTG ATCCAACAAT TAAGTCTTTC TAGCGCTGGA 240
 TAAAGAnAAT GCAATCAAAA AAGCGCAAGA ATTGGATGAA TTACAGGCAA AAGATCAAAT 300
 30 GGATGGCCAA T 311

(2) INFORMATION FOR SEQ ID NO: 3024:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3024:

ATTAGACATT ACAAGGTGCA GTACGTGCAA CATATTAGAC ATATTGAATT AAGTGGTCAT 60
 45 GnAAGGTATT GACAGTTAAA AAAGTTGAAC AATTAGAAGA AATCGAGGGC TTAATATTAC 120
 CTGGTGCGCA GTCTACAACG TTACGTCGAT TAATGAATTT ATATGGATTT AAAGAGGCTT 180
 TACAAAATTC AACTTTACCT ATGTTTGGTA CATGCGCnGA TTAATAGTTC TAGCGCAAGA 240
 50 TATAGTTGGT GAAGAAGGAT ACCTTAACAA GTTGAATATT ACTGTACAAC GAAACTCATT 300
 CGGTAGACAA GTTGACAGC 319

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 320 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3025:

GGTGCCAAGC AATAAATATG ACTATGCTCA AACTGAATTA ATGGTGGGTG TGTCGCCATC 60
 GTAATTGGAT CGTCTGAAGG CGCATATAAA TGATAGTGCT CTTGAATAA AGGTAGCATA 120
 TGTAAATTGTT TGTGTTTACG TATTTCTGGT GGTAAGTTCC GTGAAACCCA ATGTCTATAT 180
 TCCCATTAA TACGCTATTT ATAAnTGTGT CATGTTCTAA TAAGCTCGGT ATGACATGTG 240
 TATCAATTTTG TAAAATGAAC GTTTGGATAA GnGGGAGTAA CATGTGGGAT ACGTCACTCT 300
 CATCAAGCCA TGTAAGATACn 320

(2) INFORMATION FOR SEQ ID NO: 3026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3026:

TCTCAACAAA TGCATCCAGT ACTTAAATTG GCATTATAGT AATTTAAGnA CAATATATCA 60
 ATATTTCTCC TTATCCAGCA ACAGCAAATT TATTGGTAAG GTGTACGATT GAACCTTTAG 120
 TCAATGAAGC AGGTACATTT GGATTGGCCA GGTGGATTTA CTTCAACTGA GCGCTTTGTG 180
 AGAATGGGCA TTTATGAAAG CAAACATTGC TCAAACAAT GATAAAGAAA TGGATTTAAT 240
 GAATGCATTT TATTTATTAG ATGCGGTAAA TATACCGATT GGAATTGTAC GTCCGCATGA 300
 TGCTGACAAT CACTATACGA TGTATCCA 328

(2) INFORMATION FOR SEQ ID NO: 3027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3027:

ATTGAAAATA TGTGTTCTnT GTAAAATTTT AATCGTTCGC CACGATGCTG TTGATAAAAA 120
 TTCAAAAACCT GGAGTTGATC TTCTAGTTCA ACATAATCAT CGTAATTAGA CATGTAACCT 180
 5 TTGATTAAGA TTTCAAGTAC ATGATCTTCG ATAGTATTGn TTTTAACTTG TTGTTGAGCC 240
 GCTATATCTT CCATCGTGGA ATTGTTCAAG CAATTTTGTA TAAGTAATAT AAGTTTCGATT 300
 TAATGAATGT AGGTTTCATT AT 322

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(2) INFORMATION FOR SEQ ID NO: 3028:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3028:

CAAGAATCTT ATACTTATCA AAATTTATAC TGTGAAGCGA GTCTATTGGC TAAAAGACTC 60
 AAGGCTTATC AACAACTCTG TGTGGGCTA TACATAGATA ATTCGATTCA ATCGATCATT 120
 25 TTAATACATG CATGTTGGTT GGCAAATATT GAAATTGCGA TGATTAATAC AAGGnTGACA 180
 CCTAATGAGA TGACGAATCA GATGAAGTCA ATCGATGTAC AATTGATTTT CTGTACCTTG 240
 CCACTGGAAT TACGAGGGTT TCAAATTGTA TCGCTGGATG ATATTGAATT CGCCChCCGG 300
 30 GChTATTACA ACG 313

(2) INFORMATION FOR SEQ ID NO: 3029:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3029:

CTTCCAAAGA AAAGACCACA GTTTTTGACG CATCAATATG GTGCAATTTT AGAGACACTG 60
 45 TAGTTGCAGA AGATGGTTCA GTTGGACTTT GAAGACAATC GTTATACAGA AACACGCGTG 120
 CCGCTTATCC AATTAATCAC ATTGACAATA TTGTAGTACC ATCTAAAGCA GCACATCCAA 180
 ATACAATTAT TTTCTTAACT GCGGATGCAT TTGGTGTTAT TCCACCGATT TCAAAGTTAA 240
 50 ATAAGACCAG CAATGTATCA TTTCTTGAGT GGTTCACCTC TAAATAGCTG GnCAGAGCGT 300
 GGTGTGACAG ACCTGACCAT CATCTCAACA TGTTCCGnGCA CCGTCTTCCG TACATChACT 360

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(2) INFORMATION FOR SEQ ID NO: 3030:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3030:

TGATGGATTG GCTAGCAGGT GTTTACATTA ACTCATTAAA TGTTATTCAC TACATGCACG 60
 ATAAATACAG CTATGAACGT ATTGAAATGG CATTACATGA TACAGAAATT GTACGTACAA 120
 TGGCAACAGG TATCGCTGGT TTATCAGTAG CAGCTGACTC ATTATCTGCA ATTAAATATG 180
 CACAAGTTAA ACCAATTCGT AACGAnGAAG GTCTTGTAGT AGACTTTGAn ATCGAGGCCGA 240
 CTTCCTTAAA TACGGTAACA ATGACGACCG TGTAGATGAT ATTGCAGTTG ATTTAGTAGA 300
 CGCTTCATGA CTAATTACGT GGTCAATTAAA CATATCGTGA TTCAGACCTT CCATGGGnGT 360
 ATTACCATTA CTTCAACGTG GTnTCGGGTA GAAACTGGGT 400

(2) INFORMATION FOR SEQ ID NO: 3031:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3031:

nGCGTTTAAT CACATCTTTT TGATAATGTT CCCTTACCAT TTCTTCATGT GCATCTGCAT 60
 AGTCTTTTCC AAATGGCAAA CTAAACTGAT ATGCAACTTT TAAATAGGCA TCTATATGCG 120
 ACTCGTCAAC GATGGCAATT TCAACGTChA GTTACGCGGA CAAATTGGCA AGCGCATCAC 180
 TTTCTATGGC ATACAATTCC ATAATACCTA GTTCAAAATT CATATCTTTA AAACATAGCC 240
 ATCCAATGGA TTATCAAGTT GTTCATTTTC CGGGAAAAC nAAACGCATA AATGATTTGG 300
 AACCTTGATT TGTATGTGA 319

(2) INFORMATION FOR SEQ ID NO: 3032:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3032:

5 AAGAAGTGGC AATTATGATT GATGCTCTAG CTGACAAAGG GAAAAAAGCA TTAGAAGCAT 60
 TATCTAAAAA GTCACAAGAA GAAATTGATC ATATTGTTCA TCAAATGAGC TTAGCAGCTG 120
 TTGATCAACA TATGGTGCTA GCAAATTAG CACATGAAGA AACTGGAAGA GGTATATACG 180
 10 AAGATAAAGC GATTAAAAAT TTATACGCTT CTGAATATAT ATGGAATTCA ATAAAAGACA 240
 ATAAGACAGT AGGGATTATT GGTGAAGATA AAGAAAAAGG ATTAACGTAT GTAGCGGAAC 300
 CAATTGGTGT TATTTGTGGT GTTACCGCCC AACCACCAAA TCCCTACGTC CGACCACCTA 360
 15 TTTTAAAGC CGATGGATTT GCCATTTAAG ACnGGGAATC 400

(2) INFORMATION FOR SEQ ID NO: 3033:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3033:

25 TAGCGGTAAT CGAAATTGGG GACTAAATTT CGCAAAAGCG GGTCGCACGA TATCAGAAGA 60
 GTATAATGTC CCTTTATTAA TGAAGTTTGA GTTACATGGA AAAAACAAG ACGTTATTGA 120
 30 ATTTAAGAAC AAGGTGGGTA ATTTTAATGA AAACCATGGA AGAGAAAAAG TACAATCATA 180
 TTGAATTAAA TAATGAGGTC ACTAAACGAG AGAAGATGGA TTCTTTAGTT TAGAAAAnGA 240
 35 CCnGAGCTTT ACTAGCTTAT TTAGAGGAGT AAAnGACAAA ACATCTTCTT CGACACTGAA 300
 TCG 303

(2) INFORMATION FOR SEQ ID NO: 3034:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3034:

50 CTnCGCTATT TTGTAGGACA TCTTCTAAAG TGCTAGGnGA AGAGATTATA GAATAGGCAC 60
 TATCAATACC GAAATCGTAA ACATGTTGAT AATTTTCGCC TAGACTGCCA CAAATCGCGA 120
 TGACAGGAAT ATGATATTGT TTTGCAGCTA ACGCAACGCC TGACGGGTGT TTTACCAAAG 180

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TGATGAAAAT CTGTAATGTC AAAGACGGAC ATCAATGACT TTTGTTGAAA GTTGTCTCAC 300
 AAAACGnTAA TGAATGCTGC GGCCCATGAC CGGCCAGCTG 340

(2) INFORMATION FOR SEQ ID NO: 3035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3035:

AAAGAACATG GTGTAGCAAT AGTCTCTGGA GGTGGAAGCG GACATGAACC TGCGCATGCC 60
 GGTTTTGTG CAGAAGGTAT GCTAGATGCA GCGTTTGTG GCGAGTATTT ACATCACCTA 120
 CACCTGATAA AATATTAGAA GCTATTAAAG CAGTAGATAC TGGTGATGGT GTATTACTAG 180
 TTGTAAAAAA CTATGCAGGT GACGTGATGA ATTTGAAAT GGCACAAGAG CTTCCAGAAA 240
 TGAAGGTAT AAATGTTCAA ACTGTTATTG TTCGTGnCGn CATTGCTGTG ACAAACGnGT 300
 ACA . 303

(2) INFORMATION FOR SEQ ID NO: 3036:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3036:

GGGGAAAGTA AATTAACAGC TGTGTAGAAT AATTAAGGTT TTAATTTATA TAGAACAACT 60
 TATTGTAAAC TTTTCATTTT TTAAGTTTA CAATGGTGCT ATAATAATGG TCATGAAATA 120
 CGAAAGGAAG GAAAAATGA CnACAAAACA GTTAGTATAT ACAGCTTTAA TGACAGCGAT 180
 TATCGCTAGT TTA_nGATTGG TACCGGTAAT TCCACTACCA TTG_nCTTCAG TACCAATTGT 240
 ACTTCAAAAC AGTGGTATTT CTTAGCAGGG GCGATTTTAG GACGTAAATA TGGCACATTA 300
 AGTGTTATCG TCTTT 315

(2) INFORMATION FOR SEQ ID NO: 3037:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3037:

5 GCACCAATTG ACGAAGGAAT ACCGAATCCC ATTGTTCTTA AACCACCGCT TGTAACCCAT 60
 TGTCCGTGAT TTTTAAATGG ATAAATTTGA GCTGCCACACA TTTGATGTTG TCCCACGTCT 120
 GTAGTAACAA TTGCTTCACC ATTTGTAATT TTGCCGATAT ATTCGATTGT TTGTTGTGGC 180
 10 TTACAAAATA CTTGATCTTC TTCACCAAGT TTAATGGGT GTTCTGCTT ATTATTTTGA 240
 CAATGTTTTAA CCCAGTCACT GTGTTCTATA GTCTCAACAT TTTTATCATT TAAACCTCC 300
 AAAAAACCTT TACAnGCCnG CAAAAAACC 330

15 (2) INFORMATION FOR SEQ ID NO: 3038:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3038:

GTGAGTCCAC ATAATAACTT TGACGTCCTG TTAATGTTCT AAAAGGTACT AGACGTTCTA 60
 TATTCGTTGT AAATGGTGAA TATCGTCGAC CTTGTTTATT TGAACCTGGG AATACTGCTG 120
 30 TCGGTATTAC TTCTCGTGGT TGTGAAGTTA TATTAAAAA CGAAATTTTC TCAGCAGCGC 180
 TGTCGCTAGA AATATCTTTT AACGGCATTTC CAGTTTGTTT TTCGAGATCT TCATATGGAT 240
 TTTTGTGnAT AATThACCAT TCGTAGCAGA TGGAAATACT TGAGTATnGG CATCAGCGAC 300
 35 ATTGACGTGC TGTATCAATA CGTGGACGAT TCGC 334

(2) INFORMATION FOR SEQ ID NO: 3039:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3039:

GGTCTGATCG TGGTGAATGA AAAAGGTTCT TCTCTGTAAT GAATTATCTC TTACCGATGC 60
 50 AAGATATTAT GAGCATGCAT TGCTCAGCAA ACGTTGGTGA AAAAGGCGAT GTTGCAATTAT 120
 TCTTTGGTCT ATCTGGCACT GGTAAAACAA CCTTTATCGG CTGACCCACA CCGTAAACTA 180

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ATGCAAAAGC AATTAATCTT TCCAAAGAAA AAGAnCCACA GnTTTTTTGGA CGCATTCAAA 300
TATGGTGCAn TTTTAGAGAA CACTGTA 327

5 (2) INFORMATION FOR SEQ ID NO: 3040:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3040:

GTGATATTCA CGAnCGTTAT TTTCAATATT TGATAAGTAG AAAnTATGAC GATCTTCATG 60
 AACAGCATCT TGTTCCTTCGT CAAATTCAAC GTCATCAAAA CGTTTGAAGA ATGTTTCATA 120
 20 TGCATCAACA GATACTTCAG TACGGTTATT TAATAATGCT TTATGTGCAG CTTGGATCTA 180
 AATGATCTTT GTAGCCTTCA ACTnAATGTC GCACTATAAA ATTCACCAAC TGAACCTGAG 240
 CCATAACTGA ATAAACCGAT TGTTTCCACC AGCTTGTGAA TCTCGATTTT CAAGTGAATG 300
 25 ATATT 305

(2) INFORMATION FOR SEQ ID NO: 3041:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 317 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3041:

GTTGTGTACC TTAAATGATC AACCGATGCA TAAGAAGAAA GTGAGACGTC ATCAAATTGG 60
 TGCTGTATTT CAAGATTATA CGTCATCATT ACATCCATTT CAGACTGTTA GAGAAATCTT 120
 40 ATTTGAAGTG ATGTGTCAAT GTGATGGACA ACCTAAAGAA GTTATGGGAA GTCCAAGCAA 180
 TTACATTGTT GGAAGAAGTC GGTCTATCTA AGGCATACAT GGATAAATAT CCTAATATGT 240
 45 TATCAGGTGG AGAGGCGCAA CGTGnTGCAT nTGCGCGTGC AATATGTATT GAACCCnGAA 300
 ATATATTTTG TTTGGAT 317

(2) INFORMATION FOR SEQ ID NO: 3042:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3042:

5 AATCTTCGAA AAATAATGCA ATGCAGATTC CGAAAAAAC AATATGATAG AAACACCTCA 60
 ATTAAATACA ACGGCTAATG ATACATCTGA TATTAGTGCA AACACAAACA GTGCGAATGT 120
 AGATAGCACA ACAAACCAA TGTCTACACA AACGAGCAAT ACCACTACAA CAGAGCCAGC 180
 10 TTCAACAAAT GAAACACCTC AACCGACGGC nATTAAAAAT CAAGCAACTG CTGCAAAAT 240
 GCAAGTTCAA ACTGTTCTC AAGAAGnAT TCTCAAGTAG GTTATTAAAA CACGGATGGT 300
 GCTAATAGCT TnGCAACAAC GTGGGCTTTA AAATTCTCCA ACTTTAGTTT T 351

15 (2) INFORMATION FOR SEQ ID NO: 3043:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3043:

25 ACGnCCCTTAC TGGnTACTTG GTTGATAAGT GTTAATCCAA ATGACGTCCT GCTACGTACA 60
 GCTTTACGAA TATTTAATGC ACGTGTGATA TTTTGAGAAA ATACACCGCC TGGCTAAACC 120
 30 ATACTCAGAA TCATTAGCTA TATCAATTGC TTCTTGATCG TCCTTCACTT TAATCACTGT 180
 TAACACTGGT CCAAATATTT CTCTTGTGC TAATTTGTGA TGATTGTCTG GCACnCAATT 240
 AATGTCGGCT CAAAGAAGAA CCCTTTATCT AATCCATTTT CAGTTAAGCG ATGACCGCCT 300
 35 GCTAAAATTT GTGCATCCG 319

(2) INFORMATION FOR SEQ ID NO: 3044:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 342 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3044:

GTCAATAAT CTAACATTTG TGTTATCTGT TAATTAACTG GnTTTTACCT TAATTTGTTA 60
 CATTGnTCTG TATTAAATCT TTTTGTAACC ATTGGTACT TTTTCAGGTG GAATTTCAAC 120
 50 ACCCATGTCA CCACGTGnCA ACCATTAAAC CATCAGACAC TTCAAGAATT TCCGCAATAT 180

55

AAATTCACGA ATTTCTAAAA CATCACTAGG TACGACGTAC GAAACTTGCT GCAATGAAGT 300
 CAACATTTTC TTTAATACCG AAACGGATAT CTTCAGCATC TT 342

5 (2) INFORMATION FOR SEQ ID NO: 3045:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3045:

TAATATCATG TTGTGCTTTT AGTGCTTCGG CAATTTGTTT TGTACTTACT GACCCAAACA 60
 ATTTACCACC TTCACCAGTT TTTGCTGATA CTTCAACTTC AATGTTTGAT AACGTTTCTT 120
 20 TTAATGCTTT ACATCTTCAA TTTCTTGTTG GCGTTCTTGT TTTGCACGTT TTTTCTGTAA 180
 CTCTAATTGT TTAAGGTTAC CTGGTGTTGC TTCTACAGCA TAATTCTTTT TCAATAAGAA 240
 GTTATTTGGC ATAACCTACT GGTACTTCTT TAACTTCACC TTTTTTACCT TTACCTTTAC 300
 25 CTTTAACAnC TGTGTAAAAA TTACTTTCAT GCAGnTCACT CCTACTTAAA TGTTCCGTAA 360
 TGCCTGTTGT AATGTGCCAA CGCCnCTCGA CGTGACACCT 400

30 (2) INFORMATION FOR SEQ ID NO: 3046:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 306 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3046:

40 AATCACTGTT TCATTACTTG TTCCAAATCT GnATTCAAAC TATTGTTCAA AGATTCTAAT 60
 TCCGCTTTAT TTTTATCTTT AATCGCTTTT GTCATCGCAG CATCTTTAGn CATCGACTTn 120
 CTGTTGCAAT AGTTTAATTT TAGAACCCGC ATCTTTACTA GCCAATTTCT CTTCATAAGC 180
 45 AATTAATGAC TTCGTTAATT GCGAAAGTGT ATCTTTTGA TTATCATTCG CTTTTCATC 240
 TTCAAGCTTT CTCACATCTG CATTTGACAG CATTACTTGC ACTATTATCT TCAAGCGATA 300
 50 ATTTCT 306

(2) INFORMATION FOR SEQ ID NO: 3047:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 306 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3047:

	ATGGATCATA TTAGCACGTA AAAGAAAATT CTGTTTCATTA TGAAGAAGTG CCAGAnGTTG	60
10	AATTTAAACG CACATATGTA TGTGAAGATA TGTCTAAATG TATTTGTTTA TACAACGCAC	120
	CTGATGAAGA AGCGGTAnTC GCGCGCGCAA AGCAGTTGAT ACACCGATTG ATGGCATCGA	180
	AAAACTTTAA TAAGACAACA AGTTGATGAG ATATATGTAT ATAGGTTTGG CATGGATTTC	240
15	GATTGCAnTT ATTAGAATAG CTCAATGCTA TAAATGTAAG TAGTTGATAT TGAGGAACTA	300
	ATGAAC	306

(2) INFORMATION FOR SEQ ID NO: 3048:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 287 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3048:

30	GACAGGCTAC GAGATATTTT AAACAAATTT ACATCAAATC CAGTATTAGG TGTTATTGCA	60
	GGTATCGTTG TAACTATTTT AATACAAAGT AGTTCAGGTA CGACATTATC ACAATCGGAC	120
	TGGTAACnCT GGATTTATGA CATTGAAACA AGCCATTGGA GTGATAATGG GTGCTAATAT	180
35	CGGAACAnCG GTAACGTCAT TTATTATCGG TATAGATTTA GCGCAATATG CAATGCCAAT	240
	TTTAGCATTG GGTGCATTCT TGAATCTTTT TCTTTAAACG CTCTAAA	287

(2) INFORMATION FOR SEQ ID NO: 3049:

40

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3049:

50	CATATAAATA GCGnTACATC GCGCCATTCT TGATCTGnAC ATATCTTTCT TAGGTCCAAC	60
	CGTGAATGAT TACGTCCATG ATAACGTACA AACGCAATTT CATTTGTGAT TCGATTGACT	120
	AAAGGTACAC TGCCATCTTT CACTTGTGGT TCATCAACTA CTGCATGAAT GATTTGATGT	180

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AATTCTACAC ACATTGGAAA GCTTGTAATG CTGTCTTACA TACAAATATA TTGATATTTG 300
 TGCATGCAGT CAACCAGGCG GAAATGACCA TACCATGCTA ATTTTCTGGT AnGAAGGCCT 360
 5 ACATATCTAA A 371

(2) INFORMATION FOR SEQ ID NO: 3050:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3050:

CGCCAAATAA AGATAATACA CGTATTGGTG AAGATATAAC TGTAAGTGA CATATCTTAA 60
 20 TTGATGGCGA AACACGCCG ATTACGAAAA CAGCAACATA TAAAGTAGTA AGAACTGTAC 120
 CGAAACATGT CTTTGAAACA GCCAGAGGTG TTTTATACCC AGGTGTTTCA GATATGTATG 180
 ATGCGAAACA nTATGTTAGG CCAGTAAATA ATTCTTGTGC ACAnATGCGC AACATTGAAT 240
 25 TTCCAATTTG TTGGAnCATA TGGGCTAACA AGGTGTTTAG GCATATCTAC TCGTCTTATT 300
 GGGTGCATAT GTAATGGCAA GCA 323

(2) INFORMATION FOR SEQ ID NO: 3051:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3051:

CCGnACCAAT CGGTTTACAG TTCATTGGTA AACCATTGCG ATGAAAAAAC GTTATATCGT 60
 40 GTCGCTTATC AATATGAAAC ACAATACAAT TTACATGACG TTTATGAAAA ATTATAAGGA 120
 GTGGAAATCA TGCATTTTGA AACAGTTATA GACTTGnGTT CACGTAGAGT TAAAAACGGA 180
 45 CTCAAAAATG TTTCTCCATC ACCAGCGCAT TnGAGCAGA ACCTAACTCA AATACGAATG 240
 GTATCGCTTA GCATATCCAG TGCTTACCAG TTGTTAATAA GCGTGCGTAG ACGGGCATGC 300
 50 GTGCTGCAAT GCCTAAATAG GAACG 325

(2) INFORMATION FOR SEQ ID NO: 3052:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3052:

CTTTTAATCG CTTGAAAAC TTAGGTAAGA CAATACAAGT AGCTACAAAG CCATATATTA 60
CTGTTAATTG ACCTATGAAA AAATATCCGC TAACGGGTGC CGTCAATCCT GCGATAGCAA 120
TACCAATAAA AAGTACAGTC CACGAAGGAT AAACATTTTC AAGTGAAAAA TCTTTTAAAT 180
ATTTTATTGA AAAAATAATC ATATGCGTCA TAATTCCCAC AAGGCATAAA ATCCAAATAG 240
GCGTATTAAG CTATTGTAAA GTTTGTTACT AAAAAATGTT TTAAATAGTG TnCTAAAAAG 300
CCGGCATGAA AATGTGTGAC CTGATGAACT GAGGCTGTTA TTGTCTTCAC TTATTAAATT 360
TGTCTAGTCT AAAGGTGATC CAATCAGAAG CAAGTCCGCA 400

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(2) INFORMATION FOR SEQ ID NO: 3053:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3053:

AATGAGATGC GAAGGATGAT CAGAGAAAAA GTCTCTCAAT CAGGTGTGAA AGTCAGATGG 60
TTATCACAAC TTTGGCGTAC GTTTTCGATA TAATGCACTA GGTGATTTAA ATACGAGCAA 120
TATTGTTTCT TCAAAGAAA GTTTCGGTAT TACTGAAGTG TGAAATCTGT CTCTATGCAT 180
GCCGGATCGA CATTAGCATT ACTAATCCAG AGAAAGCAAA AGGTATTGTG TATACACCAG 240
AACATTGCCA GCGAAAAGTA AATGGTCACA GCTGTAGAnC AAGGTATTTA TAATGGGGGC 300
GGTAAAGCAG AAGGCCCTA TGTAGCATTT CnTAAAGnTG GGAAAAGGTA AAGCAGCATT 360
ATCGGTG 367

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(2) INFORMATION FOR SEQ ID NO: 3054:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 382 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3054:

TnATTTATCT nAGCTCATGA CATGATGGCT GTTCACATTG CAAGGCGTTG ATGATnAAAT 120
 AAGGAAAGGC ATTAGGAAAA AGCCACAGGG AAAACATTTT AGCAGCAGGT TCTTGGAATC 180
 5 ATATATTCAA GTTCAACAAG CGAATGCTGT TAAATTGCCC TTTGGATGAC AATCAATTCTG 240
 ATATCGTTTT AAATGAAGCA ATGTTAACAA TGTTACCCAT CGCCATAAAG GAAAAAGCAT 300
 TACGCGAGTA CTACCGAGTC TAAAGCCTGG GGGTATCTGT TAACACATGA TATTGTCATC 360
 10 GTTAATGAAT CACATGCCAC AC 382

(2) INFORMATION FOR SEQ ID NO: 3055:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3055:

CTTAAGATTA GGTGTGCTTA ATTAGTACTG GCTGGGAACG ATAAAGGCAT ATTGCAAAAA 60
 25 ATAGAACATC CATATCCATT AAATGTATTT ACGCTAAATA TTGnCGACTT ATATTTTTTAG 120
 ACATAGAGAA GAGACAAGAC AATTTTTTAAC GATGCAACGA CAGTTAGGCT GAGGCAGTTA 180
 AAACAAATAT TTGATACACA TGTTGnCAGA TAAAAGTCAG TGTTCCTATC AAATGcNAAT 240
 30 TTTGTACTAC TAAAAGCTCA GCAGCGCAAC AATTAGGACA ATACGTATAT GAACAAGGGA 300
 TTTAAACCTC GCTTTT 316

35 (2) INFORMATION FOR SEQ ID NO: 3056:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3056:

45 GTTCACCATC CGTTTATTTT AATGAAAAAA TCGACAAAAA TGGTCGTGAA AACTATGATG 60
 CAACAATTAT TCCAAACCGT GGTGCATGGT TAGAATATGA AACAGATGCT AAAGATGTTG 120
 TATACGTACG TATTGATAGA ACACGTAAAC TACCATTAAAC AGTATTGTTA CGTGCAATTAG 180
 50 GGTTCCTCAAG CGACCAAGAA ATTGTTGACC TTTAAGTGAC AATGAATATT ACGTATACTT 240
 AGAGAAAGAC nGCACTGAAA AACTGACCA GCGTATTAGA ATCATGACGT TACGTCCAGT 300

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CTTAGCAGCG TGGGnCGTAT

380

(2) INFORMATION FOR SEQ ID NO: 3057:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3057:

TATGTGATGG ACTTAAAAA ACGAACTCAA TTAATACAAT GGGCTCAAGA AAAAGAAGAA 60
 CGATTTATTA TAGAAGATGA TTATGATTCC GAGTTTAGAT ATTTGCGCAA ACCCATTCCA 120
 GCAATTCAAG GTCTATATTC AAGAGGAGAA AAAGTGATTT ATATCAGTAC ATTTTGCAAA 180
 GTCTATTTTT CCTAGCTGTT CGAGTTGGCA TATATGGTGT TACCCTATTC TATnATGGAA 240
 AAAATATCAT TTCTnCAAAA TCCACCATTG GAAGGGCAAC ACTGGTAACC TGTTTCATAT 300
 GGCAAAACCT TATTGGCAAC GTTnAT 327

(2) INFORMATION FOR SEQ ID NO: 3058:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 284 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3058:

CGAAAAAGGA GAATGAAACA TGAGGTAATA CAACATTACA TGCAACAACA ATTTATGCGT 60
 GTAAGACATA ATGGAAAGCA GCTATGGCTG GAGATGGGCA AGTAACGCTT GGTTCAACAA 120
 GTCATCATGA AACAAACGGC AAGAAAAGTG CGACGTTTAT ATGAAGTAAA TGTTAGCTGG 180
 TTTGCGAGTA TGTAGCAGAT GCGTTTACTT ATTTGAAAAA TTCGAAACAA nATTACAACA 240
 GTTTAGTGGT AACTTAGAAA GAGCnGCTGT TGAATTGGCA CAAG 284

(2) INFORMATION FOR SEQ ID NO: 3059:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AAAGAAGCGG ATGAAGAGCT TTGCATTGAG CTCGACCCAG GTATGGCTTT TGGAACAGGT 60
 GATCATCCGA CTACAAGTAT GTGTTTGAAG GCAATAGAAA CATATGTATT GCCACAGCAT 120
 5 TCAGTAATTG ATGTTGGTAC TGGCTCAGGT ATATTAAGTA TTGCAAGTCA TCTAATCGGT 180
 GTAAAACGTA TTAAAGCGTT GGATATTGAT GnaATGGCAG TGAGTGTAGC TAGAAGAnAA 240
 CTTCAGAAGA nATCATTGTG AACGTTGAAT TGGAAGCTGT TCCAGGTAA CATATTGGAA 300
 10 AG 302

(2) INFORMATION FOR SEQ ID NO: 3060:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3060:

TTTTTAAnGA CACATTGnGC TGTGTTTAAT GCATGAAAGG AACCACTGAC ATGCATnAAA 60
 25 TCTTTGAATG GTTCTTTATC AATTCCTTCC CCCCTCTCAT GTTTTGTATC TTAAATCAA 120
 TATAATTCAA AAAGGGTCGA GGATATGAAA TCACATCTTC GACCCTTTAT TTAATTTTT 180
 AATTCAGCCA CACGCAAACG GTTATTGCT CTCTCTAAAG CTCTTTCGGC TCTATGGAAT 240
 30 ATCAGTATTG TCGTCAATCA TTTTCCAAGT GAGACTCTGC TCTTGCTTTG GCTAATTTAG 300
 CTCTTTCAAC ATCAATTTCT CTGTCAGTTC 330

(2) INFORMATION FOR SEQ ID NO: 3061:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3061:

CGATCAATCA ATATAATTCA CGGCGCAAAA CGTTTATTTA GCATGTTCTT GCAGACTCTG 60
 AAACCTGGCAT TAAACCTTCC ATTAAGATTT TTACCATTTCT AGGCATTAAT ACCATTACTG 120
 CAGCCATTGA CATTCTAAA TTAATGATGT CTCCAGGTTT GTAACTGCT AACACACCAA 180
 50 TACCTAAmCC TAAAATTAAG CCGACAAATA TAGACTCTCC AAATGCGCCA AAACGTTTTT 240
 GAATTGnTTC AGGATCAGCA TCTAACTnAT TCAGACCGGG TACTTTTTGT AACAATTTAA 300

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(2) INFORMATION FOR SEQ ID NO: 3062:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3062:

TATAAAATCA ATGATTTTAA CAAATAAAAA CGTACCGCAA ATACTGCAAA TAACAGCAAA 60
 TACTAGTTTT AATAAAATAT GACCGGTTGG AAAGAACAAT AAAGCAATTA AAATACCTAG 120
 TTTAGCCCAT TCCATCGTTC CAGCTGTAGT CGGACTAACA AACTTATTTT GCATCATTTG 180
 TTGGCATTAT CAAGCCTGCT GAAAGCCAAC GAACTTCCAG CAATTAAAAT ACTCATCGTC 240
 CTTGGTATTC GGGCTTGGAG AATAAAATGA TTCCGCTGGT GACTCAGTTG AAATGTAGTG 300
 AAATCTTTGA ATTGGATAGT TnCACTGCAC ACCTGATGGn AnCAACGGAA 350

(2) INFORMATION FOR SEQ ID NO: 3063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3063:

TTAGTGATTT TAACGTGTAT CGGTAATTTT AAATAAATGT TTAATGCTTT TGAAAATACA 60
 GTTCTAACCG AAGACGTCGG GTACACTGAA TCACCGGAAA CGCCAAGGTC TTTTATTAAA 120
 CCTTGTTCAC TATATTGCAT ATACTGTGGA TGCTGTCGCA ACACATTGAT TTGATAAGGA 180
 TGTGTTGGTA ATAAAATAAA ATCTTTGGGT ATCTCTGATA TATCTATGTC TGCTAATTGG 240
 ATACnACACT TTCTCAACCT GGATCCTTCC TTTTACCTnC CACCATAGCC GCGTGGAnCA 300
 GGAAACCATC CTGGGATGCA CCAGCCAAAA TAAATGCCAA TT 342

(2) INFORMATION FOR SEQ ID NO: 3064:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GTCCAGCTCC AGAACCAAAC TTAACAGTAT TATGGTCAGT ACGTTTACCT GACAACTTCA 60
 AAACATACTG TGCAAAAATG AGTATTAAAA CAAGTTCTAT CCAATATGAA AATGATGACA 120
 5 TTATGCGTGA AAGCTATGGC GATGACTATG GTATCGCnTG TTGTGTATCA GCGATGACAA 180
 TTGGTAAACA AATGCAATTC TTCGGTGCAC GTGCGAACTT AGCnAAAACC TTACTTTACG 240
 CTATCCATGG TGGAAGATT GAAAATCTGG TGCACAAGTG GGCCCAACCT CCGAGGGATT 300
 10 nACCAGCGGA GTAATT 316

(2) INFORMATION FOR SEQ ID NO: 3065:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3065:

TGATTGCGTG GATCAGCAAC TTCAAAGATT AACAAATAAT ATTACTTGGG CAGATAACCG 60
 25 CGCTGCAAAA TATGCAACAG TAATAAATGA AGTGCATGAT GGGCAATGCG ATTTACCAGC 120
 GnACAAGCAC AnCGGTTTCA TCCTATGTCG CCATTAGCGA AGATTTTTTG ATGAAACATG 180
 ATGGCCAGAT GTATTTCCAC GTACTGCTAA GTTTGCAGAT ATTAAACAT ACATTTCTAT 240
 30 CATTATTGAT ACATATATCA TTGATTATTC CATGGCTTCC GcNACAGGGA TGTTAATTAG 300
 AACATAGATT GGAGTGAGGC AT 322

(2) INFORMATION FOR SEQ ID NO: 3066:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3066:

45 TATAAAGAAT CCTGCCTTAC CTAAGAACAC TTGTCTTGTC GTTAAGACTG ACTCTAGACT 60
 CTTATGTTTA TTATCAACCG TTAATAAACT TACCATCAAG AGTGACCTA CCCATACTGA 120
 CAGTGACAGTA TAGAATGGTG TCATACCTGA ACCATAATCC TTAAGTGGGA AAACATCAAC 180
 50 AGTCTTCTTA TTAATAGATT GCAATAATAC CCGCTGCTTT TTCAAATCAT TCTAnTGGTC 240
 GATTAATTGT CGACGCATCA TCTTGTCAAT TCTTGAAATT TATTCGCTTT TCAACTTTCA 300

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CACGCTGACA TAC

373

(2) INFORMATION FOR SEQ ID NO: 3067:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3067:

TTCAGAGTTC GGAACATAAG GCGCTACAAT GTTGTGTTGC CAGTAGTTGA CTGAATATGC 60
 GTTTGTAACA AGCTTTTTTC GATTCTAGTC AACAGTAATT AAATTTATGA TATGGGCAAT 120
 ACTTTGTAAT ACTAATATTA AATGGCGACT TTATTTCACT ATGTTATAAG AGTGCCATTT 180
 GTTGATAAAG GnATACTAAA GGGTATCGTT TGGAAATTTTA GTAAC TAGAT ATGTTCCGGT 240
 ATAGACCGnA TTGTGGATAC GTAAATTTAA TGcATGAAT TTAAAATGA AAACATGACA 300
 TTAAATGAAT C 311

(2) INFORMATION FOR SEQ ID NO: 3068:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3068:

TATGATTATC TAGTAAGTAA ATTGCTGACG CGCCGAATAC CGCAAAGAAT ATAAAGCAAA 60
 CTAACGCCCG GACAAAAAGT ACACCTAGGA ATAAATTCTT TAATCGTACG TCCTTTTGAC 120
 ACACGTGCAA TAAATACCT ACAAATGGGT GCCCAGGnTA TCCACCATGG CCCAGTAAAA 180
 GATTGTCCAA TTTTGTAACC ATTGGGAATT TTTGACCACC TGTCGGAATG CGTAAACTCA 240
 TACTTAAAGA AATTGTCATT ATAATTACCT AGACC 275

(2) INFORMATION FOR SEQ ID NO: 3069:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 321 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AAATGGGTTT TGTGACATTA ACGTCTACAA AAGATGGTTC AGAAGAAACA CACGAGGCTG 60
 ATGGTGTATT CATCTATATT GGTATGAAAC CATTACAGC GCCATTTAAA GACTTAGGTA 120
 5 TTACAAATGA TGTGGTTAT ATTGTAACAA AAGATGATAT GACAACATCA GTACCAGGTA 180
 TTTTTCAGC AGGAGATGTT CGCGACAAAG GTTTACGCCA AATTGTCCT GCTACTGGCG 240
 ATGGTAGTAT TGCAGCnCAA GTGCAGGGAA TATATTGACA TTAACGATCA GCCTAAnTCC 300
 10 GAGCnGATTA GATGTGAGCG G 321

(2) INFORMATION FOR SEQ ID NO: 3070:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3070:

GTTTGACCTG CATATTTGAC AGTCATAACC TTTGTATCAC CATTATATTA ATATCAAAAT 60
 25 CTTGGAACGT GTTATTTGAG nTGACATTTA ACTTCGCAGC ATTATCAGCT GTTGAACCTG 120
 ATGTATACGT TCGCAACCC ATAACATCT GTGTTACAAT GCACCAAACG CACCTCCACC 180
 30 AGCTACATTA GATGGGCAGC TTCGCCTTGC AGCTGATTGG TTTAGATGAT TGTGATACGA 240
 TCCAATTTGA AGCCAAATnG TACTTAAGCA CAATCCTACT GCGGACCGTT TAACCCTGTT 300
 TCACCTATAC ACTGnTGAAA GGCAAACCGT ACCACTCACC ATTTCCATGC CTTCCATATT 360
 35 TGGTTACCAA ATTTACTTTT CCCnGAAAAA TGAAACTCTT 400

(2) INFORMATION FOR SEQ ID NO: 3071:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3071:

TGGCCATTTG TCATTGCATT TTTACCGTGG GTGTTGATTA TTATTCCTTA CTTACTATTT 60
 50 AAATCGGATA CACTAAATAT TATTCATACG GGTGATAATA TTGCACGAGG TCTAGGTGTA 120
 AGGTTAAnCA GAGAACGTTT AATATTATTC TTTATCGCAG TGATGTTATC ATCTGCTGCT 180
 GTAGCATAGC AGGTTCAATT TCGTTTATCG GATTAATGGG TCCGCATATT GCCAnACGTA 240

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(2) INFORMATION FOR SEQ ID NO: 3072:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3072:

GACTCCCTGC AGGTCGACGT CTAGAGGATC CCCCCACAGC AATTCACCTTA TACATGTAAC 60
 AGTGTGAAAT AATAACGTCA CAACGGCATA ATACACATTG CAACGTCCCA ACAACATATC 120
 ATAGAATCGT AACGGCATGA CATCAACACC AAACCTGGGC TATAACACCA TAACAGCGCA 180
 ACGCCACATC ATAGGCACTA CATCAAGTCG CATCGTAGCA CCAGCACATC AAAGTAACAT 240
 GGGCATCAAC ATCAAACCGG TCTATAACAC CATAACACCG GCAATGCCAC ATTCATAGGC 300
 ACTACATCAA GTCGGCATC 319

(2) INFORMATION FOR SEQ ID NO: 3073:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 282 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3073:

ATATACGCTT ATCAGCTGGA GCTCAATAGA TGGAGGATGA TTATGGGGCT ACCGGTTCTG 60
 TCTATAGCAC TGGTCTATCA GCTATGTGGA TTACAATCGG TTTAACATTA GGTGCTTATA 120
 TAAATTACTT TGTTGTTGCT CCTAGACTTC GTGTTTATAC CGAATTAGCT GGAGATGCAA 180
 TTACATTACC AGATTTCTTT AAAAATCGTT TAAACGATAA AAATAATGTG TTAAAGATTA 240
 TTTCTGGATT GATTATCGTA GTATTCTTTA CATTATATAC nn 282

(2) INFORMATION FOR SEQ ID NO: 3074:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3074:

AATCGAnAAA TCATGGATGT ACTTGAATCA AATGCAAACA GCGAAGTGTh TTGAATTGCA 120
 TGGTAGCGTT ATAGACGAGC CAGTAGAAAT TCAATCAATT AAAGTATATG TTCCTAACGA 180
 5 TGATGAAGGT CGTACGACAA CTGTAATTGG TAATGCTTTC CCTGACTCAG AAGTTAAATG 240
 CATTACACCA GCAGATATCA TkGCTTCAAT GAGTTACTTC TTTAACTTAT TAAGCGGtAT 300
 TGGGtATACA GATGATATTG GACCATTaGG TAACCGTCGT TTACGTTcTG tAGGkGGaAT 360
 10 TACTACmAAA CCaATTCCGT ATcGTTTTAT CCAAGA 396

(2) INFORMATION FOR SEQ ID NO: 3075:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 376 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3075:

ACCTACATTT GCAGTTGTCG GTGTATAACC GGCTGGTGTT GAAAACTCTA CACTATAAGT 60
 25 TCCATTGCTT AAACCAGTGA ACTGATATTT ACCATTTTCA TCTGTTGTCG TACGATCTAA 120
 TTCTTTACCG TTACTATCTT TAAGAATGAC ATAAACACCT TTAATCCCTT TTTCATTGGC 180
 30 ATCTTGTTTA CCATCTTTAT TTGTATCTCC CATACATAGT CACCTAGATT ATATTChTTT 240
 GGGCGCCATA GCAGTTGATG AGCATTCACTA TTGAAAAACT ATTGACCACT ATATTAGTTT 300
 GCAGTGCTAA GnATAACATT TCCATACGTG ACATACTGAT AGACTGTGAG TGATGTATGC 360
 35 GCTGhTGCTC ATAACG 376

(2) INFORMATION FOR SEQ ID NO: 3076:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3076:

TTACATCACC AATTAGACGT TATCCTGATT TAACAGTTCA TCGTTTAATC CGTAAGTATT 60
 50 TAATTGAGAA ATCAATGGAT AACAAAGAAG TGAAGCGTTG GGAAGACAAA TTGCCTGAGT 120
 TAGCTGAACA TACTTCTAAA CGTGAACGTC GTGCTATTGA GGCAGAACGT GATACTGATG 180
 AATTGAAAAA AGCAGAATAT ATGATTCAAC ATATTGGTGA TGAATTTGAA GGTAATGTCA 240

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AAAGCnGnGA TATACGTTTG AGGCGCAATG C

331

(2) INFORMATION FOR SEQ ID NO: 3077:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3077:

15	AATCATATGC ATCGATTTC AGCAACAGCA ACCATTTCATC CTATGTCCCA TTAGCAAATT	60
	TTTTGGATGA AACATGAATG GCAAGATGTA TTTCAACGTA CTGCTAATTT GCAGATATTA	120
	AAACATACnT TTCTATCATT ATTGATACAT ATATCATGAT TATTCATGGC TTCCGCAACA	180
20	GGATGTTTAT TTAGAAACAT TAGATTGGGA TGTTGAGGCA TAGAACTGCT GGGTATTTCC	240
	AAGGAAATGT TGCCGGAATT ATTCCAACAA CTATTGATGT AAGTATGAAA GAACGTATGC	300
	AACATAATGG GCTAATAAAG TACACCGTnT GTTAATGGTG CnATG	345

(2) INFORMATION FOR SEQ ID NO: 3078:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3078:

35	GATTATCAAG CGATTGATCA AGTATCATCA TTGTTGAAAG AAAAATATGG CATTGCACAT	60
	TCAACGTTGC AAATTGAAAA CTTGCAATTG AATCCATTAG ATGAGCCATA CTTCGACAAA	120
40	TTAACATAAA TAAACATTG TAGCGCCTAA AACATTAATC TATGTCATAG GCGCACGTTT	180
	CGTTTTTATAC TTATGTTGCA TCATTTAAAT GATTTTCGTC AATTTCTTTG ATGCTATCTA	240
	CATCTAACAC GAGGTTAACT TGC GTTGATT TTGATAAAGT GATCATAGCT TTTAGTACTT	300
45	GAGGATTTTT ATTGTTGCTG TTACGAATGT GGTTCATGTTT AATGCGGGAC AGTAATTTAA	360
	GTTGTTTTTT TACAATTGAG AGTGTGATAT TTCGATTCCG	400

(2) INFORMATION FOR SEQ ID NO: 3079:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3079:

5 AAACGTTTAA TATACACTTT TACACGTCGC CTTCAATTGAA GCGAATTGCC ATAACCTTCA 60
 CATTATATAT AGTTCTTTCC ATATAAATGT CCAAATTTTT AGAACAACGC AATAATAAAC 120
 CATCCACCTA ACTTATCAAA AATTTAAGTG GATGGTTTTT CATTTTCATT TATATTTATA 180
 10 TTAGTGTTAA TCCAATCATA GATTTATCTA TATGCACTGC TCTATACaTT TCCTCaTTTA 240
 ATTTGcYTTA CTTTCATTTA TATCATTATC AGAACACTTG GCGTGTCATC GnTATTATTT 300
 CGCATCTTTG AnACGTTTA 319

15 (2) INFORMATION FOR SEQ ID NO: 3080:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3080:

TCAAATGCAT CTAGGnCACA TTATTCTATT TGGGCATTCT TAGTGCTGTT CTTATTTGCG 60
 GCTTTAACGT CATCTATTTT TTTATTAGAA TTAAATGTTT CTAAC TTCAC GAAGAATGAC 120
 30 AATACAAAAC GTAAAAAGT CGCAGTGATC GGTAGTATTT TAGTATTTAT CATTAGTATT 180
 CCAGCAACCT TATcTTTTGG TATCCTAAAA GATGTAAGAT CGGTGCGGGA ACGATTTTTG 240
 ATAATAAGGA TTCCACCGTT CGAATGTAAT GAAGCCATAA GCGGG 285

35 (2) INFORMATION FOR SEQ ID NO: 3081:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3081:

ATCATAGCGT TTCTCCTAAA AATTACGATT AATCAAAGTA TGCCATTATT TAACTTTAGT 60
 TTCTTCAGAA TTATTTGCCC CATTATCATG TTTTCTTCT TTATTAAACAG CATTTTTATC 120
 50 ATTTTTAACA AGATACAATT TACCAATTAA TGGGCGGTGT GCGTGCTGGT ATGGGTTATA 180
 CTGGTTCACA CGATTTAAGA GAATTACGCG AAGAAGCACA ATTTACACGT ATGGGTCCTG 240

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CATTCTAATT AAGATAAAGG AGAACGACAA ATATGGGAAA TGGCAAAGGA CCAAGAGTTA 360
 ATCCTTGCTCT TAGGACTTTG GTAGGCCATT ACACCCATTA 400

5 (2) INFORMATION FOR SEQ ID NO: 3082:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3082:

TGAATTTGCT CCAAATAAAA ATACAATTGC CATTAAAATC ACCAGATATT ACAAGTGGCA 60
 ACATGTTAGA AACACCGTTC ATTAAGTGTT TATAGAATGC TTTACCTGGG CTTATTTCTT 120
 20 GACTGTCATT TGAGTTACCT GGCAACAAAA GGTTTACGAC TTGTATCTAA TGAATACCAT 180
 CTGCTACTGG TnCTTCTACG ACATTTTTAC CATCGAnGCG GTCCGTCTCA ACATGTACAT 240
 CAGCAGCA 248

25 (2) INFORMATION FOR SEQ ID NO: 3083:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 368 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3083:

TACTAAAGGT TTAAATCAAA AATGGCTAGG TATCGTATTT GCGATTTTAA TTACAATTAC 60
 ATTTGCATTT GTATTTAACA CAGTGCAATC TAATACAATT GCGGAGTCGT TAAATACGCA 120
 40 ATATAATATT AGTCCAGTAA TCACAGGTAT TATTTTAGCA ATCGTAACAG CTATTATTAT 180
 ATTTGGTGGT GTACGTAGTA TTGCTACGTA TCCTCGTTAA TGTACCGATA TGGCTATCAT 240
 TACATGGTAT GGTTTAGTAA TAATGCTATT AATTAGACC AATTGTCCnA TGATAGGACG 300
 45 ATATAAAAGG CATTGGnACG ACAAGnACTG GTGCGCTGAG GGCTCGGTCT CCAGGACAAC 360
 GGGGTATC 368

50 (2) INFORMATION FOR SEQ ID NO: 3084:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3084:

5 TTGGACTTTA TAAAGTTACT AAGTTGTAGA TTATCCTGGT AAAGAAGATA TTGCGGTTGT 60
 ACAAGTTGAA GAAAAATCAA CACAACCAAA AGGTAGAAAA TTCAAAGATT TCACTAGTAA 120
 ATTTAATATA GCATCAGAAG CTAAAGAAAA TGAACCTATA TCAGTCATTG GTTATCCAAA 180
 10 TCCTAATGGA ATAACTACAA ATGTATGAAT CAACTGGTAA AGTATTATCA GTGAATGGGA 240
 TATAGTGnAT CGGATn 256

(2) INFORMATION FOR SEQ ID NO: 3085:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3085:

25 ATATGCATAT GCTTCTTTAG GTGAACGAAT ATCTGGTTCA GATACGATTT CAATTAGCGG 60
 TGTACCTTGA CGGTTCAAGT CAACTAATGA ATACTCCACC TTTATGTGTT GACTTACCAG 120
 CATCTTCTTC CATGTGAAGA CGAGTAATAC CGATTCGnTT TGTTCACCG TCGACTTCGA 180
 30 TATCGATATA TCCCATTTCA CCAATTGGGT TGATCAATTG AGAATTTGAT AGCTTTGGGA 240
 TATCGGGATA GAATAGTCTA CGGTCAACTA GATCnGGTGC GAnTCCATAT TTAGTGCCAT 300
 GCAGCACGCA T 311

(2) INFORMATION FOR SEQ ID NO: 3086:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 271 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3086:

45 ATGTAAATGA TCATCCTTCA TAATAACAAC GATTACTGAT CTTGATCATG ATTTTGAACA 60
 ATAACAACTG CTTTATTAAT ACCTTGTATA CGCTCGAGnC ATGCCAACCT CTGACAACTC 120
 50 AATCCTAAAC CCTCGAATCT TAACTTGTTT GTCCTTTCGA TATAAATAAT CTATGTTGCC 180
 ATCGGGTAAC AAACGAACGA TATCACCCT TCCTATACAT CAGCTGATTT ATATTTGAAT 240

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(2) INFORMATION FOR SEQ ID NO: 3087:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3087:

GTAAAGATTT CAATTCATCA TCTTTAAATA AACTTAATGG TAATTnGTTA TACChAATAA 60
 AGCCTTCTGG AACTTCCTT TAGACCGACG ACCGTCTTAG CTAATGTCTGA TTTCCCTGAC 120
 CCTGATTCAC CGACAATGCC TAATGTTTTCG CCTTTTCTAA TAGCCAAGTT AATATCATAA 180
 CTGCTCGGTA TGGGCTGCCC CTCGGTGATG TGTAATCCAC GCTCCACGCG ATCGATTTTA 240
 ATAAAAATATC ATGGTT 256

(2) INFORMATION FOR SEQ ID NO: 3088:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3088:

AAGGTTATTT GAATGATCAA GGTATCCACA AAAGAGGTGC TGAAATAGAT CGACTCGTTA 60
 AAGGATGTAC AGGTGTTAAA CGTACAACG GACAGCATCC AGGGGGTATT ATTGTAGTAC 120
 CTGATTACAT GGATATTTAT GATTTTACGC CGATACAATA TCCTGCCGAT GATCAAAATT 180
 CAGCATGGAT GACGACACAT TTGATTTCCC TTCCTnTCAT GATATGTATT AAAACCTGAT 240
 AAACHnTGGAC ACGTGATCCC ACCATGATCG ATGCCTCCAG ATTATCAGGA ATGATCCAAA 300
 ACCATACCTG AGATGTAAGA GTATCAGTAT TAGACnC 337

(2) INFORMATION FOR SEQ ID NO: 3089:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3089:

AAACATTACT TTACGCTATC AATGGTGGTA AAGATGAAAA TCTGGTGCAC AAGTTGGTCC 120
 AAACCTTCGAA GGTATTAACA GCGAAGTATT AGAATATGCC GAnATTCAAG AATTTGATCA 180
 5 AATGATGGAT TGGCCTAGCA GGTGTTTACA TTAACCTATT AAATGTATnA CTACATGCAC 240
 GATAATACAG CTATGACGAT TGAATGGATT ACATGTACAG AATTGTCCGn CCATGGCACA 300
 GGA 303

10 (2) INFORMATION FOR SEQ ID NO: 3090:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3090:

CTTTCGTAA AGGGGCATAT TCATATAATG GATGGTCATT AATAATAATT CCTGCCGCAT 60
 GTGTAGATGT ATGTCTTGGT AAACCTTCTA ACTTTTACA AATACTGAAC CAGCGTTCAT 120
 25 GTCGATGGTT TCGATGTACA AACTCTTTAA AATCGTCAAT TTGATATGCT TCATCAAGTG 180
 TAATTCCTAA TktATGTGGG ATTAACTTG GAAATTCAT TLAATGTAAC TTCATCAAAC 240
 CCCATAATTC TTCCAACATC TCTAGCAACT GCTCTTGCAA GCAGATGACC GAAAGTCACA 300
 30 ATTCCAGATA CATGTAGCTC GCCATATTTT TCTTGGACGT ACTGAATGGA CCCTTTCTCG 360
 GnGTGTATCT GCAAGGTCAA TTTTCATTnT CAGGCATGGT 400

35 (2) INFORMATION FOR SEQ ID NO: 3091:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3091:

TTGTTTTTTC ACGTTCAATn ATTATCTTCA ACTTGTGACT ACAGATTTTA AAATGGAATT 60
 TACAAGTATC TTCTTCAATA TTTTGCATCA TGATATCAAA TAATTCATGA CCTTCATTTT 120
 GATAGTCACG TAATGGATTT TGTGTGTCAT AAGAACGTAA GTGAATACCT TGACGTAATT 180
 50 GGATCCATGT GTCGATATGG ATCAGTCCAA TGGCTATCAA TAGAACGAGG TAAAATCATA 240
 CGCTCAAACC CCATCCATTG GnTCCTCTAA GATACCTTTT GACCTTGGAT AGCnGCTCAA 300

(2) INFORMATION FOR SEQ ID NO: 3092:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3092:

CGACACCTCA ATAATCATAT CGTAATGTTT AACTTTTCCT GATTTAAATG TAATTTTCATT 60
 TCCATTGATA GCATTAATTT CCTCATTTAA ACGGTATGGA ATCTCCCGCT TATCTAATTC 120
 ATCAAGTATA GGTTGATTCA GTCGGCATCC ATAATTTATT TATCTTATCA GATCGATGAA 180
 TAAAGTAGGG TGTAACCAC GTTCATAAA GATTTCAGG AACTCCAATG GAACATAACC 240
 TGCACCTACC ACCAATACTT TATCCACTTG GATTGGCTTG GAGGAATGGT CGGATAGGCA 300
 TCCAGGGCCT CCAAATTCC nAGGGGAAAn GGTAATATCC ACCTTCCAAG GCCAAGGGCC 360
 AATTGGCACC TGGCCACCCA GGGnCTTAAA AAGGGGTAA 400

(2) INFORMATION FOR SEQ ID NO: 3093:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3093:

TTATACCCGn CAAATTCATA AATATAGTn CTTTTCAATA GATTGATATG TATGTCTAAA 60
 TGTATCGATT AACTTTGCTA ATGCTGCTT ATCTAATGGT CGGTCTGCTA ATTTTAAAAA 120
 TGTATTCTTC AATAGGTATT CCCATATAAT GCGTTATTTT TTTAGATGAT GGTTCGGTTA 180
 AGCCACATGC TTAAATGCA CTTTGTGTG CTACTTCACC ACATTTTTTC GTGTCTGCCA 240
 ACGTACCATC AA 252

(2) INFORMATION FOR SEQ ID NO: 3094:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATCTATTAA TAATGAAGAA AAAATTGTAC TAGCACGTAG ACGGTTAATA AAGTTCGATA 60
 AAGATATCAG TATTCCATAT ATTCTAAAGC AAGCATATTC TAAAGAAAAA AACAGTTATA 120
 5 TATTCTTGTT AGAATCACAA GATTCTATAT TCTTTTCACA AACACCTGnn CAATTAATAA 180
 AGGTCAATAA TAAAATCTAT CGACTAAAGC TGTGCAGGTC AATTAAACGG TCACAAGTGA 240
 GGCCGAGGTA CAAAAAATGT TGAGCATTTT AAAGTATAAA CTTATCGACA CGnTTGTGTG 300
 10 CAGTTTTTCAT GTTT 314

(2) INFORMATION FOR SEQ ID NO: 3095:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3095:

GGTGAGGCGG CATTGAGAAA AAATGCTGAA GTAATCGAAG CTGTATCGCA GTCTTGTTTG 60
 25 ACAACAGGAT TTTGTTTATG GTGCCAATTA GCTTTTTCAA CGTATTTAGA AAATGCCACG 120
 CAGCCACATT TAAATAATGA CTTACAACAG CAATTGTTAT CTGGAGAAAT ATTAGGTGCT 180
 ACCGGATTGT CTAATCCCGA TGAAGTCATT TAATGGATTT AGAAnAAGTT GGACCCTTTG 240
 30 AAACACCACC TTAATGTTGG ATGGGACCAA TTGGGTGGTC CAGTGGGAnC GTAATGCCCA 300
 GGTGTAAAGT nATAATCCAA GGAAAGACCC AT 332

35 (2) INFORMATION FOR SEQ ID NO: 3096:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3096:

45 TTTATGCATA CGCGCACTCA TCACACTACC GACAACAACA TCATCTTTTC GAGCATATCT 60
 ACTTAACAAC GTCATGACCA CACTCATAAA GAACATAAAA TCAGTAATTT GATGCTTTTC 120
 TACATACTTT TGAAGTAGCT GTCTCATTTG TTGATTCATG TAAATGACAT CATGCTCCAT 180
 50 TTGTCGGTTT AATAATTGGT CTAACATAnT CTGTCGGGTA AGCCTAAAAT AGGGTACTTC 240
 ATCCTTGAAT TGAGGATACC CATATTGGTC CTAAGGTTTCG GTCCATATCC ACGGATGGCG 300

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ATTTAAGGTT GGATAAAGGT GCCGTTAAGG ATCCAATTCC

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(2) INFORMATION FOR SEQ ID NO: 3097:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3097:

15	ACTCTGGTCC TTCTGCATAA CTGCCGTAAA TAATTCACCT TCATCACACG CTGTACCTAC	60
	CAATAATCCC nCACGATATA CGTGGAATTC GAGGTGTACG GTAGAAATAC TTCACCAATG	120
	ATGCACTTAC AATTTTAAAT AGATTTTAA GACCTGTGTG GTTTTGTACA ATTAATGTGA	180
20	CATGACTAGG TCTTGCACGT TTATATGCAT CTTCACTACT GAGTTTTTTG GTTGATTnC	240
	GTTATGATTT AATACGGCTA ATTCT	265

(2) INFORMATION FOR SEQ ID NO: 3098:

25

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 321 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3098:

35	CTAATGTATC AGTTTGGCAT GAATTCTTTT GCATCTTTCA ATAATTGTTG TGATCTTTTT	60
	TAGTCACATC ATCAATTTTC TTATCTTCGT ATAATGCTTT TTCAATCTTA TGATATCCTG	120
	ACCATCTTTT TTCCTTTTTC TCCTCTTTCA TATCTGCAAG CGGGCATCCA ATTTTAGGAT	180
40	CCTAAATCTC CCAAATGCTT CTGAACTGGT CAGAGCGTCA TAATACATAC GACTTTTGGA	240
	TATACGCTTT TnCTTGGGCA TACATTATTT CAATCGTTTA CAAATTTTTC TGACCTTTTA	300
	AAATCATThA CTGTCAncAG A	321

45

(2) INFORMATION FOR SEQ ID NO: 3099:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 276 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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ATCCGCAATC TGAGAAACAT CATCTTCGAG TTGTTGGAGG GTTCCAATTT TCAAGTCATA 60
 AATCAGATGA TGAATGGCGA GAGTTTGGAC TAAATCATTT TGTATTACCT GAAGTTTAA 120
 5 TTTCAACTGA TAATAATGGG ACATTTTAA CTTATACAGT TAAAAGGGAA AGTTTACTG 180
 TTGAGGCATT GAACGATTTA ATGGATTGTT CAACAATATA TCGGACATAG AGTGGACGAC 240
 CAATGGGGGA ATACCAGAAT GAGATATTAT AAAACA 276
 10

(2) INFORMATION FOR SEQ ID NO: 3100:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3100:

GTCATTTGAT GACAATGGTA TTAGACCAAG TACCAACCGT TCTGTGCCAC nTAAAACGTT 60
 GTTAATAACT TGCCGGGCTT CACACTAATC AATGGTGGCA AAGTAGGGGT GTTTAGTCAT 120
 25 GCAAnGTTAA GAACGAGCAT GTTTGATTCA GGAGATAATA AGAACTATCA AGCACAAGGA 180
 AATGTAATTG CATTAGGTCG TATACATGGA ACTGATACGA ATGACCATGG CGATTTT 237

(2) INFORMATION FOR SEQ ID NO: 3101:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3101:

nCGATATAAC AAGGTTGTTA GACTTAAAGG TGGCGATCCA GCGATATTTG GTCGTGTGCA 60
 AGAAGAAGTC GACATACTAA ATGAACATCA TATTGCGTTT GAAATTGTAC CAGGGGTGAC 120
 ATCAGCGAGC GcNAGTTTGG CTACTATGCA GACAGGTTTG ACAATGCGTA CAGTTGCTAA 180
 45 AAGTGTGGAC ATTTTCTACA GGTCACTTTT AAAGATTGAG AAGAAAATGA AGTGGGATGG 240
 TCCATTCCTT AAGT 254

(2) INFORMATION FOR SEQ ID NO: 3102:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3102:

5 CAATCACTCA TGTAGTAATT GATACCTAAG AAGTCGTTTA AATCTTTGGC TGCATCTAAA 60
 ATGGCATAAT CTTCAThTGT AATGTTTAAT TTACCGCCAn TAACAGATAA GATATGTTGC 120
 ACACCTTCCA TCGTTTCACG AGTAATACTT ACCTAAATAT GTTGCATCTA AGATGAATTT 180
 10 ATTATGGATG GATATCTTCT AAATTCTGCT GCACGGGACA TCTTCAGGAT TTGGATGGTT 240

(2) INFORMATION FOR SEQ ID NO: 3103:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3103:

20 GTTGTAACCT TCAATTGTTT AAATAAATAA CACATATCAT TGGAGGTGAA TTGATATGCC 60
 AGATTCAATC ACAATTATAG ATGAAAACAA AGTGGTTGAT GTTGTATTAA TTGCAGGTAG 120
 25 AATTTTACTT GAATCAGGTG CTGAnACATA TCGAGTTGAA GATACAATGA ACCGTATCGC 180
 ACATAGTTAT GGTCTTCATA ATACATATAG TTTTGTCACT TCAACTGCAA TTATTTTTTC 240
 ATTAAACGAT CGAACAAGTA CAAGATTAAT TCGTTACAAG AGCGTACAAC AGATTTAGGG 300
 30 AAnGTGCGAA TAAGCGGGGn AATTCTTC 328

(2) INFORMATION FOR SEQ ID NO: 3104:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3104:

40 TTTTGCTTTG TGCCTAATA ATCTAATGTT CGTGGAACCG nAACCAGAGA TATTACAAAT 60
 45 ACATCATCGA CTAATCGCAG GTGTCGTTGA TTCTCCAACA ACATGTGCCT GTTTGCCGAG 120
 CTGATTTAAG GCGGCATTGC AAAACTATTC GCCACGAATC CTGAACGTCC TTTGCCAGCT 180
 ACAATATAT GTTCAGCATG TAGTATTTTG GATGCAAAGT TGAAAACTCA TCCGCTTCAA 240
 50 CATGTGACAA AGTCACTTTA ATCnA 265

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3105:

ACTAGTAGAG TATCTAATGG TGATTTAATC ATTATTACTG CTGGTGTACC AACTGGTGAA 60
 ACTGGAAC TAATATGAT GAAAATCCAC CTAnTTGGTG ACGAAATTGC TAATGGTCAA 120
 nGTATTGGAC GTGGATCAGT TGTTGGTACT ACATTATTGC TGAAACTGTT AAAGATTTAG 180
 AAGGTAAAGA TTTATCTGAC AAATTGATCG TTAATACTC AATCGATGAA ACGTTTGTGA 240
 CCT 243

(2) INFORMATION FOR SEQ ID NO: 3106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3106:

CTATTGCGTT TGGGTAAATC TAAAGCAGGC GTAnATTATC AAAGTTTGGG ATATGCAACC 60
 AGCACACTTA TTCTTTATGA TTGCAGCGCC AGAAGTGGnG CCCAAACACA TCTAGATGCT 120
 TTAATAAGTT GTCTGGTATT TTAATGGATG AAAATGTACG TGAGAAATTA TTACATGCTT 180
 CATCACCTGG AAGAAGTACT AGCGATCATA GATGAGGCTG GATGATGAAG TGGA 234

(2) INFORMATION FOR SEQ ID NO: 3107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3107:

TTTTGAAGCG GCATAATCAT GAAGAATAGG ACTAGGATTA TAACCTTGTA CAGATGATGT 60
 CGTTGTAATT GACGCACCCG GTTTTAAATA TTCCAATGAC TTTTGAAC GTCCAAAATA 120
 GCGGnTAGAn ATTGTTTCA AATGTTTCTG TAAATGCCTC AGTTGTAAAT CCATGAATAT 180

(2) INFORMATION FOR SEQ ID NO: 3108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3108:

CTTTAAGTTA CGTTCGGCTT TGATTAAAGT AAAACGTGGT ACTGTTTCCT ATGACAAGAG 60
 TCTAATTGGA TACAATGTAA ACAAATGGT GATTGTAT TATAGATAAT AAACATTTCGn 120
 TATACATTCA ACATATCGAT GACCACTTGG ATTAAGCAAC GTAATATCAT TCGTACTGCT 180
 CAAGAAATGA CAAACGAAAT ACGAGAAAAT TTTGAGTCAT ACACGTCATT TAGAATGAAT 240
 AGTATTATGC AAGTACT 257

(2) INFORMATION FOR SEQ ID NO: 3109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3109:

CTTAAAGCCA AGTCGATCTG CTAATTTTGC AAGTGTCCT GAATCTTGCA ATGCCTTTTG 60
 TGCATCCTTA CCTTCATCTA TTAAGGCATA GTCTAATACG CTTAATTTAA CCAATCCGTC 120
 ATCTCCAAAC TTATCCTGTC ATGTCAAACC GACATAACAT TTGTAGCGTT CTTAATACCA 180
 TTCCCTCTGC ATATACCCAC GTATATGATA ACGTnTTTCA nTTAACT 227

(2) INFORMATION FOR SEQ ID NO: 3110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3110:

TTTCTTCATC GTTTGTGAGA AAGAGGTATT TTAAATGGG AAAnCAGGTA AAAAGGATGG 60
 AAGTACATAA AAAGAGCAAT GCTTGGGCAT TATTCnCTT GTTATTATTT GTGGCGTTGT 120

GATAACGTAA TTGTGCGTTA TTAATGAATC GAAAAGAATC ATTGCTAAAA AGTGAGTCTC 240
 CGAAAGGCGG CCTTCAACTG TTAAGAGTGA TTTATTGCAG GCTTCAATCG CGAAATGGTG 300
 5 CnAAGCGCGT ATTAGCACTA GCCGAA 326

(2) INFORMATION FOR SEQ ID NO: 3111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3111:

CTACGGCGCC TTGCATCTTT CCCAACAATT AACCCCAACT CTATTAGCAC AGATTTATCA 60
 20 ATTGATTCAT AAGCTTCATC AAAGGGTGAA CTAACATGCA TTAACGCTTC TTTAATATCA 120
 ATTAAGTCGG CATGTTCAAC ACCAATTTTC CCTTTTTTAT TTTTAGCTTT TTCTCTATCA 180
 ATATACGCAT GTTTAACACC TTTGACATGT TCAGTAAATT GTGACTTCCT nAATTTTTTA 240
 25 TCCTCCCTTG GTGnnGGGGG GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG GGGGGGGGGG 300

(2) INFORMATION FOR SEQ ID NO: 3112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3112:

TTATTGTTAA CACAAGGnTT CGAACAAAGGT TGGTTTAGTA CATTTTCAAT CATTTGTCTG 60
 40 AGCATTTTTA TCATCACTAC GTTGATATTC ATCATCATCG AACGTCGACA TGAAGTACCT 120
 TTTATTGATT TCTCAGTATT ACGCAACCGT CCGTTCATTG GTGCATTTTT AAATAACTTT 180
 GTTTTAAATA GCGGTCTAGC GTAACAGGGT CTTTCATATA TGCTCAACAC ACCTGGTTTA 240
 45 TCGCGCGCAA TCGGACTGTT ACATGCCAAT GCCATGGGCG TTCGAGATCG TTAGTGAAAG 300
 CACATAGTTC GGGCAATGAG CCACATGGTC GTGTCCGTCA CGCACACATA TAGCAGCT 358

(2) INFORMATION FOR SEQ ID NO: 3113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3113:

TCGGTCTTGA AAACCGACAG GGGACTTAAC GGCTCGCGGG GGTTCGAATC CCTCTTCCTC 60
 5 CGCCATCAAT ATTTATATTA AATTCTATAT ATAATGAAGG TAAGTGCTCA AATTTTGAGT 120
 ATTTACCTTT TTTATTTGTC TTTGAATGGC TCGTAATTTT TGATAATAGA AATGATAAGG 180
 CATTGAGATT GGAAGGGCAT TTGGCTTGTG CAAnATACAT AGCnAAATGT CGTTGTTGTT 240
 10 TTGTGATAGA T 251

(2) INFORMATION FOR SEQ ID NO: 3114:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 6591 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3114:

TTAAAGTGAA TtnCTTTGGG TTACAGAAWt TTCAACAACt TTAAAGCACG TATAATGATG 60
 25 ATTTTCAGCT TGTACAAAGG AGAAAAAAG AAGACAACCA AGCCCAATAA TGGACTGGCC 120
 GCCTAATAAT AAAAActCTA AAAGTTGTAT TTTAAAATA GTTCTTTAAA TTATATACCC 180
 ACCACATTTG GTGGAGaACC GTTAAACAAT GCATAGTTGC TTAActTCCA ATATTGAACT 240
 30 CATCATTACA ATTTGACATA GAGTCTATTA AAGCGTGTGC CATTTGAGTC CACTTTTATT 300
 TGTATTGTAT AGAGAGAAAT AAAAAGAAAC CTtGTTTtAC AAGGTTTCTA ATACGTTATG 360
 TTATGTAAAT AACAGTTAAT TATACCGGTG GTCGGGGTCG AACCGACAct CCACAAGTGG 420
 35 AACGgGATTT TGAGTCCCGC GCGTCTGCCA ATTCCGCCAC ACCGGCTTAA TGGTAAACAA 480
 AAAActTCCC TTTGGAAGCA ATTATGGAGC GGAAGATAGG ATTTACACCT ATACCTCGTT 540
 CCGGAAGGA ACGTGTtCTA AAAGTTGAAC TACTCCCGCA AATATTAAAT TATGGAGCGG 600
 40 AAGATAGGAT TTACACCTAT ACCTCATTCC AGGAAGGAAT GTATTCTAAG AGTTGAAATA 660
 CTCCCGCATT ATTATTAAAT TATGGAGCGG AAGATAGGAT TTGCACCTAT ACCTCGTTCC 720
 45 GGGAAGGAAC GTGTTCTAAA AGTTGAACTA CTCCCGCATA AACCTGGAGG CGGCAACCGG 780
 ATTTGAACCG GTGATAAAGG TTTTGCAGAC CTCTGCCTTA CCACTTGGCT ATGCCGCCAA 840
 TAACTGGGCT AGCTGGATTc GAACCAACGA GTGACGGAGT CAAAGTCCGT TGCCTTACCG 900
 50 CTTGGCTATA GCCCATTAAT AATAAGGGCG GCTGAAGGGG ATCGAACCTT CGAATGTCCG 960

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	CGAACCCACA CCAAAGGTTT TGGAGACCTC TATTCTACCG TTGAACTATG CCCCTATTAA	1080
	AAATAATAAA TGGAGGGGGG CAGATTTCGAA CTGCCGAACC CGAAGGAGCG GATTTACAGT	1140
5	CCGCCGCGTT TAGCCACTTC GCTACCCCTC CATAAATGGT GCCGGCCAGA GGAATTGAAC	1200
	CCCCAACCTA CTGATTACAA GTCAGTTGCT CTACCAATTG AGCTAGGCCG GCTAAGAAAT	1260
	GGTTCAGGAC AGAGTCGAAC TGCCGACACA TGGAGCTTCA ATCCATTGCT CTACCAACTG	1320
10	AGCTACTGAA CCATAATAAA AATGTAATGA TGGCGGTCTC GACGGGAATC GAACCCGCGA	1380
	TCTCCTGCGT GACAGGCAGG CGTGTTAACC GCTACACTAC GAGACCTATA AAATATTGCG	1440
15	GGAGGCGGAT TTGAACCACC GACCTTCGGG TTATGAGCCC GACGAGCTAC CGAACTGCTC	1500
	CATCCCGCGA TAATAAAAAA TAATGGCGGA GGAAGAGGGA TTCGAACCCC CGCGGCCCGT	1560
	TAAGGCCCTG TCGGTTTTCA AGACCGATCC CTTCAGCCGG ACTTGGGTAT TCCTCCATTA	1620
20	TTATAGGTAA ATCGCTATTA ATTATAAAAT TAAATGGCGG TCTCGACGGG AATCGAACCC	1680
	GCGATCTCCT GCGTGACAGG CAGGCGTGTT AACCCTACA CTACGAGACC ATTAGTAAAA	1740
	CGGAGGAAGA GGGATTCGAA CCCCCGCGAG CCGTTAAGCC CCTGTGCGTT TTCAAGACCG	1800
25	ATCCCTTCAG CCGGACTTGG GTATTCTCC AAAATTATAT GGaCtTGCAG GACTCGAACC	1860
	TGCGACCGAA CGGTTATGAG CCGTTAGCTC TAACCAACTG AGCTAAAGGT CCTAAATATA	1920
	ATTTTACAAC TAATAAATAG TGGCGGTGGA GGGGATCGAA CCCCCGACCT CACGGGTATG	1980
30	AACCGTACGC TCTAGCCAGC TGAGCTACAC CGCCTTATAT AGTTTGTAAG TAATATGGTG	2040
	GAGACTAGCG GGATCGAACC GCTGACCTCC TGCGTGCAAA GCAGGCGCTC TCCCAGCTGA	2100
35	GCTAAGCCCC CATAATAATT ACAGTATATC GGAAGACAG GATTCGAACC TGCGACCCCT	2160
	TGGTCCCAA CCAAGTGCTC TACCAAGCTG AGCTACTTCC CGTATAATTA ACGCGCCCGA	2220
	TAGGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG	2280
40	GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAcGgTGATC	2340
	ACTCACGCA GGATTTTAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA	2400
	AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TGTATTCTAC	2460
45	CGCTGAACTA CTTCTGCATA TGCGGGTGAA GGGAGTCGAA CCCCCACgCC GTAAGGCGCT	2520
	aGATCCTAAG TCTAGTGCGT CTGCCAATTC CGCCACACCC GCAAATGGTG AGCCATAGAG	2580
	GATTCGAACC TCTGACCTC TGATTAAAAG TCAGATGCTC TACCAACTGA GCTAATGGCT	2640
50	CTTCCATGGT GCCGGCCAGA GGAATTGAAC CCCCACCTA CTGATTACAA GTCAGTTGCT	2700
	CTACCAATTG AGCTAGGCCG GCAATATGTA AGAATAAATG GTGGAGAATG ACGGGTTCGA	2760
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	AAACTGCCTG	GCAACGTTCT	ACTCTAGCGG	AACGTAAGTT	CGACTACCAT	CGACGCTAAG	2880
	GAGCTTAACT	TCTGTGTTTC	GCATGGGAAC	AGGTGTGACC	TCCTTGCTAT	AGTCACCAGA	2940
5	CATATGAATG	TAATTTATAC	ATTCAAACT	AGATAGTAAG	TAAAAGtGnA	TTTTgctCGC	3000
	AAAACATTTA	TTTTGATTAA	GTCTTCGATC	GATTAGTATT	CGTCAGCTCC	aCATGTCACC	3060
	ATGCTTCCAC	CTCGAACCTA	TTAACCTCAT	CATCTTTGAG	GGATCTTATA	ACCGAAGTTG	3120
10	GGAAATCTCA	TCTTGAGGGG	GGCTTCATGC	TThAgGATtT	TCAGCACTTA	TCCCGTCCAC	3180
	ACATAGCTAC	CCAGCTTATG	CnTTGGCACG	ACAAcTGGTA	CACCAGAGGT	ATGTCCATCC	3240
15	CGGTCTCTC	GTACTAAGGA	CAGCTCCTCT	CAAATTTCTT	ACGCCCACGA	CGGATAGGGA	3300
	cCGAACTTcT	aCGACGTTCT	GAACCCAGnC	sTGTACCGCT	TtAATGGGCG	AACAGCCCAA	3360
	CCCTTGGGAC	CGACTACAGC	CCCAGGATGC	GATGAGCCGA	CATCGAGGTG	CCAAACCTCC	3420
20	CCGTCGATGT	GAACCTCTGG	GGGAGATAAG	CCTGTTATCC	CCGGGGTAGC	TTTTATCCGT	3480
	TGAGCGATGG	CCCTTCCATG	CGGAACCACC	GGATCACTAA	GTCCGTCTTT	CGACCTGCT	3540
	CGACTTGTA	GTCTCGCAGT	CAAGCTCCCT	TATGCCTTTA	CACTCTATGA	ATGATTTCCA	3600
25	ACCATTCTGA	GGGAACCTTT	GAGCGCCTCC	GTTACCTTTT	AGGAGGCGAC	CGCCCCAGTC	3660
	AAACTGCCCC	CCTGACACTG	TCTCCCaCCA	CGATAAGTGG	TGCGGGTTAG	AAAGCCAACA	3720
30	CAGCTAGGGT	AGTATCCAC	CAGCGCCTCC	ACGTAAGcTA	GCGCTCACGT	TTCAAAGGCT	3780
	CCTACCTATC	CTGTACAAGC	TGTGCCGAAT	TTCAATATCA	GGCTACAGTA	AAGCTCCACG	3840
	GGGTCTTTCC	GTCCTGTCGC	GGGTAACCTG	CATCTTCACA	GGTACTATGA	TTTCACCGAG	3900
35	TCTCTCGTTG	AGACAGTGCC	CAAATCGTTA	CGCCTTTTCGT	GCGGGTCGGA	ACTTACCCGA	3960
	CAAGGAATTT	CGCTACCTTA	GGACCGTTAT	AGTTACGGCC	GCCGTTTACT	GGGGCTTCGA	4020
	TTCTAGCTT	CGCAGAAncT	ArCcACTCCT	CTTAACCTTC	CAGCACCGGG	CAGGCGTCag	4080
40	cCctATACAT	CACCTTACGG	TTTAGCAGAG	ACCTGTGTTT	TTGATAAACA	GTCGCTTGGG	4140
	CCTATTCACT	GCGGCTCTTC	TGGGCGTTAA	CCCTAAAGAG	CACCCCTTCT	CCCGAAGTTA	4200
	CGGGGTCATT	TTGCCGAGTT	CCTTAACGAG	AGTTCGCTCG	CTCACCTTAG	AATTCTCATC	4260
45	TTGACTACCT	GTGTCGGTTT	GCGGTACGGG	CACCTATTTT	CTATCTAGAG	GCTTTTCTCG	4320
	GCACTGTGAA	ATCAACGACT	CGAAGACACA	ATGTCTTCTC	CCCATCACAG	CTCAGCCTTA	4380
50	ACGAGTACCG	GATTTGCCTA	ATACTCAGCC	TTACTGCTTA	GACGTGCAAT	CCAATCGCAC	4440
	GCTTCGCCTA	TCCTACTGCG	TCCCCCATC	GATTAACACG	ATTATAGGTG	GTACAGGAAT	4500
55	ATCAACCTGT	TATCCATCGC	CTACGCCTGT	CGGCCTCAGC	TTAGGACCCG	ACTAACCCAG	4560

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	TTCGCTACTC ACACCGGCAT TCTCACTTCT AAGCGCTCCA CATGTCCTTA CGATCATGCT	4680
	TCAACGCCCT TAGAACGCTC TCCTACCATT GTCCAAAGGA CAATcCACAG CTTTCGGTAAT	4740
5	ATGTTTAGCC CCGGTACATT TTCGGCGCag TGTCACTCGA CTAGTGAGCT ATTACGCACT	4800
	CTTTAAATGA TGGCTGCTTC TAAGCCAACA TCCTAGTTGT CTGGGCAACG CCACATCCTT	4860
	TTCCACTTAA CATATATTTT GGGACCTTAG CTGGTGGTCT GGGCTGTTTC CCTTTCGAAC	4920
10	ACGGACCTTA TCACCCATGT TCTGACTCCC AAGTTAAATT AATTGGCATT CGGAGTTTGT	4980
	CTGAATTTCG TAACCCGAGA GGGGCCCCCTC GTCCAAACAG TGCTCTACCT CCAATAATCA	5040
15	TCACTTGAGG CTAGCCCTAA AGCTATTTTCG GAGAGAACCA GCTATyTCCA GGTTCGATTG	5100
	GAATTTCTCC GCTACCCTCA GTTCATCCGC TCACTTTTCA ACGTAAGTCG GTTCGGTCTT	5160
	CCATTCACTG TTACCTGAAC TTCAACCTGA CCAAGGGTAG ATCACCTGGT TTCGGGTCTA	5220
20	CGACCAAATA CTAAACGCCC TATTCAGACT CGCTTTTCGCT ACGGCTCCAC ATTTACTGCT	5280
	TAACCTTGCA TCAAATCGTA ACTCGCCGGT TCATTCTACA AAAGGCACGC CATCACCCAT	5340
	TAACGGGCTC TGACTACTTG TAAGCACACG GTTTCAGGTT CTATTTCACT CCCCTTCCGG	5400
25	GGTGCTTTTC ACCTTTCCT CACGGTACTG GTTCACTATC GGTCACTAGA GAGTATTTAG	5460
	CCTTAGGAGA TGGTCTCCC AGATTCCGAC GGAATTTTAC GTGCTCCGTC GTACTIONGGA	5520
	TCCACTCAAG AGAGACAACA TTTTCGACTA CAGGATTATT ACCTTCTTTG ATTCATCTTT	5580
30	CCAGATGATT CGTCTAATGT CGTCCTTTGT AACTCCGTAT AGAGTGTCTT ACAACCCCAA	5640
	CAAGCAAGCT TGTGTTTTG GGCTCTTCCC GTTTCGCTCG CCGCTACTAA GGGAATCGAA	5700
35	TTTTCTTTCT CTTCTCCGG GTACTAAGAT GTTTCAGTTC TCCGGGTGTG CCTTCTGATA	5760
	TGCTATGTAT TCACATATCG ATAACATGAC ATAACATCATG CTGGGTTTCC CCATTTCGGAA	5820
	ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCTT	5880
40	CATCGGCTTC TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATAACCTAAT CTATGTTTCC	5940
	ATCCTACAGG AAACGCGTTA TTAATCTTGT gaGTGTTCTT TCGAACACTA GCGATTATTT	6000
	CTTATGAATT CAAGCTTATT TAAACTCTT TATTCACTCG GTTTTGCTTG GTAAAACTA	6060
45	TATTTTACTT ACTTATCTAG TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA	6120
	AGCAATATCA CTTTAACCAA AAAATATTTG AATGTTAAAT AAACATTCAA AACTGAATAC	6180
50	AATATGTCAC ATTATTCGC ATCTTCTGAA GAAGATGTTT CGAATATATC CTTAGAAAGG	6240
	AGGTGATCCA GCCGCACCTT CCGATACGGC TACCTTGTTA CGACTTCACC CCAATCATT	6300
	GTCCACCTT CGACGGCTAG CTCCTAAAAG GTTACTCCAC CGGCTTCGGG TGTTACAAAC	6360
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ATCTACGATT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT TGCAGACTAC AATCCGAACT 6480
 GAGAACAACCT TTATGGGATT TGCTTGaCCT CGCgGGTTCG cTkGCCTTTG TAATGTCCAA 6540
 5 TGTAGCACGT GTGTAGCCAA ATCCATAAGG GGCATTATGA TTTGACGCAT C 6591

(2) INFORMATION FOR SEQ ID NO: 3115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3115:

GGTGCCAAGC AATAAATATG ACTATGCTCA AACTGAATTA ATGGTGGGTG TGTCGCCATC 60
 20 GTAATTGGAT CGTCTGAAGG CGCATATAAA TGATAGTGCT CTTCGAATAA AGGTAGCATA 120
 TGTAATTGTT TGTGTTTACG TATTTCTGGT GTAAGTTCOG TGAAACCAAT GTCTATATTC 180
 CCATTAATAC GCTATTATAA TGTGTCAGGT CCAATAAGCC CCGGATGACA TGTGTATCCA 240
 25 TTTGGAAATG GAACCGTTGG GAAAGTGGGA ATAACATGGG GGAACGTCAa TCCCCnCCAA 300
 GCCCATnGAG GTACCTTTAA TTTTA 325

(2) INFORMATION FOR SEQ ID NO: 3116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3116:

CCGnTTGAGT TCGGTGGCGA CATGATTGAT TTTGTAAGTA AGTATGATGC AACATGGGCT 60
 GnTTTACCTA CTAAATTTGA GGCGGGTACT CCATTAATTG CTCAAGCATT GGGCTTGTCa 120
 GAAGCTATTC GCTATTTAGA ACGCATAGGT TTTGATGCAA TTCATAAATA TGAACAAGAA 180
 45 TTAACGATAT ATGCTTATGA GCAAATGTCT G 211

(2) INFORMATION FOR SEQ ID NO: 3117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3117:

AACGThTTTT GAAATGATTG CGGCGATGTT GGCGACAGTT AAAGTAGGTG GCATCTTATA 60
 5 TACCTATCGA TATTGATTTT CCGAATAAAC GACAAGGTGC AATTTTGGAG GATGCTAAAG 120
 TAACTGCAGT CATGTCTTAC GGCCTTgNAA TTGAAACGAC ATTACCAGTC ATTCAATTGG 180
 AAAATGCTAA AGGCTTTGTT GAATCAAAGG 210

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(2) INFORMATION FOR SEQ ID NO: 3118:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3118:

TTAATTGATC CTAGCTTGGT TTGCCTCTGT CACTTTATCA TTGATATTTT GGACAGTTGG 60
 GTTGCCATTC AACACTTGAT TAATTTCACT TAACTTTTGA CGCGCTGCTT GTAATTTTTG 120
 25 GGTGTACGCA TTTAACGAAC GgNCGTCATA CCTGTTGTAT CCGTTGGTTG ATTAATGCTT 180
 GTTCTAAATT GCGTTTCCAA GTTThAAGCG GCGCTTATCT GGTGT 225

(2) INFORMATION FOR SEQ ID NO: 3119:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3119:

CCAACATGAT GCTAGTTTGA TTAAGTTTCT TCTAAACAGA CTTCAAACGG CATGGTTTGA 60
 CATATCCTAT TAAGGTTGAA TCGCGTTAAC AGCACATAGG AAATGCTGTT AGGCGATGCA 120
 GAGTGCGATT AGGCAGCTAC TGGAAAATTA TTGTTTGATT TGCCAGTTAT TATAAACTGT 180
 45 GTGTGTTGAT GNCGANcACA ACCCCTCCGA ACACGCTTAA TG 222

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(2) INFORMATION FOR SEQ ID NO: 3120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3120:

CGGCGATTAT ATTAAAAAGC CAATTACAGA ATGTAGTGGT AATGAAATAT GCCAAGAATG 60
 5 GCTGTATCAC TTAGGTGTAT CAACTGACAA AATTGAAGAC TTAGCAAAAC ATGCATCTAA 120
 TACGATTTCCT GTTTATATGC CATATATCAC ATCTTATTTC ATGGACGCGT GCTATCGGCG 180
 nACAGACCTT TTAGTCGTGC CCGGCATGCA ATCTnCAGGA ACTTAGGCAT TTATTGGTGA 240
 10 ACTTTG 246

(2) INFORMATION FOR SEQ ID NO: 3121:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3121:

CAAATACCTT CTCAACnTTG TACTTTTTGTC CTAATTGAGC TGCACGAATT GCTGCAACGT 60
 25 ATCCACCAGG ACCTGCTCCG ATTACTATAG aTCTGTTTCA ATTGGGAAAT CTCCAACTAC 120
 CATGTTTTAC CCTCCATTA ATAATAATTC TGGATTATTT AATAAACGTT TAATGTGATT 180
 CATTGCATTT TGGCCAGTTG CACCATCAAT TTGTCTGTGG TCAAAGCTTA ATGakrtGct 240
 30 AATACTGGTG CTGCAACAAT TTCTCCATCT TTAACGATAG GTTTTTGAGC AATACGGCCA 300
 ATTCCCTAAGA TTGCTACTTC TGGGGTGATT GATAACTGGA GTGAACCATT GTCCACCAGC 360
 35 TGAACCGATA TTACTGATTG TGCATnnGCA CCTTnCATT 399

(2) INFORMATION FOR SEQ ID NO: 3122:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3122:

CAGACAAACC TTGAATTATT CTACCTATAA TTAAAAATGC TGGCAAAGGT GTAATGATGA 60
 TGAGTAATGA ACCTACAACA TTTAATATCA ATCCTACATA AGTAATTTTG ACGCGACCAA 120
 50 ATTTATCAGC AACATCACCA GCACCTACGT AAACCAACCA GCCAATAAGG CAGATAAGCT 180
 AACAGCGTAT TATCGTTCCC ACGTCACTAC TATATGTGGA TGTATGGGAC ACAGTTTACC 240

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301

(2) INFORMATION FOR SEQ ID NO: 3123:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3123:

15 GGAGCAAATT TATCATCTGC AACTAGACAC AACATCACTG TTATTAGTAC CGGGTTATAT 60
 AGTAGCAGTC ATTGTTGGTG CACTAAGTGG TAAAATCGGC GAATATCTGA ATTCAAAACC 120
 AGCGATTATC ACAGCAATTA TTTAATAGCA CTGAGCTTGA TTTACCTGCA TTGCAGTAGG 180
 20 TAATCACATT CAATCTCGTC ATTCTATGAT ATCTTGCACT AGCTTGCTTA ATGATGCACT 240
 TACTACGAGC ATAAACATGT CTATATGCAG GTGCATGTTA TATTATATAT GGCGACGAGA 300
 TCGTnGGCCn ACGTTAACTA ATTnGCATG TCTAGCCTCG AATTATATAG TAGGAGCGTA 360
 25 GTACGCCAAC TGCCACGA 378

(2) INFORMATION FOR SEQ ID NO: 3124:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3124:

TATTGCAAGA AATGAACTGC TGATTTTTAT AGTTTTAGTG GTCATAAAAT GCTTGGACCA 60
 40 ACAGGTATTG GCGTATTATT TGGTAAACGT GAGTTACTAC AAAAAATGGA ACCGATTGAG 120
 TTCGGTGGCG ACATGATTGA TTTTGTAAGT AAGTATGATG CAACATGGGn CTGATTTACC 180
 TACTAAATTT GCAGGTCGGG TTA CTCCCAT TGAATTGGCT CCAAGCCAAT TGGGGCTTGG 240
 45 CnAGGAAGCC T 251

(2) INFORMATION FOR SEQ ID NO: 3125:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3125:

CGGTTAAGTA ATACAGGATG TTCTCTAATT ACTTCTTCCA ATACGTCCCA AACTTCATCA 60
 5 TCCATACGTT CGATTTTACT CTTCGCATTT TTAATGTTAG TTGCAATTC ACGTTGAACT 120
 AATTCTTTCA TTACGAATGG TTAAATAGT TCAAGTGCCA TTTCTTTTGG TAAACCACAT 180
 TGGTACCATT TCCAnGCTTG GACCCnACGG CAATTACCTG AACGGTCCCG GAA 233

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(2) INFORMATION FOR SEQ ID NO: 3126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 413 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3126:

AATAGATTCC CGGGATTCAA AAGCATGGAT GTTGTAACCTT GTTGTACTCC ATTGGCAATG 60
 TACTACCTGA TGTCAAGATG AATTATCCAT CACTTTGTTG ACGTGCTTTA TTTTACAGCA 120
 25 TCAATTTGAT CCAATCGAAA TACCAGATAA CTTAGACTGT GTCCCAGTAA AATAACGATC 180
 AATCACATCA TGAGACAAGC CAATCGCTTC AAATATTTGT GCCCCTTGAT AACTTTGCAC 240
 TGTCGAAATT CCCATCTTAG CCATTACTTT AATGACACCT TCTGACAATA CATCCGTATA 300
 30 TGTCTTAACA TTATCGACAA CGGTGCCTTG TAACCTTCT GTCAATGTCA GTTGTTCAAC 360
 TGTACGTTGC GCTAGGTATG GCACAATTGa TTCGCGCCAT ATGCGAGTAA ACA 413

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(2) INFORMATION FOR SEQ ID NO: 3127:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3127:

GTCGTAAATA CTGAACAAAA ATCACGGCAT ACTGTGCAAA TTTnTGAAGA AGCTCAAAAA 60
 CTATTACAAG CACATCATGC GATTGTAGAA GGATATATCG AATCAGCTTT AGAGCGTGCG 120
 45 TAnATCATCT TCTACATACA TAGGTAATTT TATGGCGATT CCTCATGGAG CATCCTGTAA 180
 50 AAAGTTTTAC AATCACATGT GCTTATTTT 209

(2) INFORMATION FOR SEQ ID NO: 3128:

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(A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3128:

10 TAAATTAATG GAGTTTGGTA CACGTCGTCG CAAGAAATTG ATGCAGTGGG GCGCTAGAGC 60
 TGCTTACATC GGGGGCTTTG ATTCTACAAG TAATGTTAGG GCGGGGAAAT TATTTGGTAT 120
 ACCTGTGTCT GGTACACATG CACATGCATT TGTCCAAACT TATGGAGACC AATATGTTTG 180
 15 CCTTChAAAA ATATGCTGAA AGnC 204

(2) INFORMATION FOR SEQ ID NO: 3129:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3129:

GAAATACCAT TAATATAATA GTCGGTAAAT TAAGAAACGT GGTGCGCGAT TCACAACAGA 60
 30 AATCTTAACT TATCGAAGTA TCCTGTTTTT TCTGCAACAC CAATACCAAT CATCACTGCT 120
 AGTACTAAGC CTAATGCGGG AACTCTGAGA AATTTTAAAT CGTATTCTTC TTATCATCGT 180
 AAATCCATCT GGCTATTATA TTTTAATATA AnGGTTTGAG CTACCGGATG CTAACGnAC 239

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(2) INFORMATION FOR SEQ ID NO: 3130:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 259 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3130:

45 ATCACAATAA ACATTTTAAA ATTCTTGTTA TCATAATCAT TAAAAGGTAT TAACCTTAAT 60
 AATATATTCT CThGTCTCAA CCTTAATCGT ATACTTCAGA CGTCTGTTTG TAGACAATAA 120
 50 AGTCATTAC GTCTTCATAT GTCATCanAT GTTTATCATG ATATGATGAT ATATAATCGG 180
 TATATACTGT AGATATTACA CATAAGAGAG GATATAATAT GAAAAGGTCA TTAAGATGTG 240
 CTGAGAGCTG TGTATCAGT 259

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3131:

TGTGCCTGCC ATTTTGCAAT ATCTTCATCT TCACGTGGTA ATGCACAAAA ATGTTTACCA 60
 TGTGCATTCA CAACTTCAAA AATATGTTGA CATGTGATGT TACTTGATCA TCACGCGTTG 120
 CCATGGTATG CAAGTGCTGC GATAAATCTG CGGCACCTTC GACTATCATG CTAACCTTCG 180
 CTTGTnnATA TCGCAATGGC ATACCCCTTC AACATCTTCT ATCATGG 227

(2) INFORMATION FOR SEQ ID NO: 3132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3132:

ATCGCAGTGA TGTnATCATC TGCTGCTGTA GCnTAGCAGG TTCAATTTCA TTTATCGGAT 60
 TAATGGGTCC GCATATTGCC AAACGTATCG TTGGACCACG TCACCAGTTG TATTAACCAA 120
 TTGCCATTTT AGTAGGGGCA TGTATACTTG TAATAGCTGA TACAATTGGC CAAAATTGTA 180
 TTACAACCAG GTGGGGTTCC AGC 203

(2) INFORMATION FOR SEQ ID NO: 3133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3133:

AGCATTTAGT TTAGCGGCAG TAGCTGCAGA TGCACCGGTA GCTGGCACAG ATATTACGAA 60
 TCAnTTGACG AATGTCACAG TTGGTATTGA CTCTGGTACG ACTGTGTATC CGGACCAAGC 120
 AGGTTATGTC AAACTGAATT ATGGTTTTCh AGTGCTAATT CTGCTGTAA GGTGACACAT 180
 TCAAAATACT GTACCTAAGG A 201

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3134:

CATTTGTAAC TGTTATTGTT TATAACTTCT GTGTGAAGCG CAATATTACA ATTAAAATGC 60
 CGAAAGAGGT ACCGnCGAAT ATTTCAACAAG TATTTAGGAC TTAATTCCAT TTTCAGCGGT 120
 AATCATCATT CTTTATGCAT TAGGATTnG TCAATCGCAA CCAGCTTTAA ATCAAAATGT 180
 AGCGGAGGTA TTTTAAAATT ATTCGGT 207

(2) INFORMATION FOR SEQ ID NO: 3135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3135:

AACACCTTTA GGTCGTGCAG GTCAACCTGT TGAGTTATGT GGTACTTATG TGCTATTAGC 60
 GTCAGAAGGA ATCAAGTTAT ACAACCGGAC AAGTnTTCGG TGTTAGCGGT GGAGTGCAAn 120
 TAGGTTAGGT TTGTATGAGC TTTTAATTGA GCACCATAAT GTTAATTTAG TTACTTCAAT 180
 CCATTAAATT AAATGAATTG GTG 203

(2) INFORMATION FOR SEQ ID NO: 3136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3136:

CACATCCAAT GCAnTCTACT AAATCAGACA CACCACAATC TCCAACCATA AnACAAGCAC 60
 AAACAGATAT GACTCCTAAA TATGAGGTTT AAGAGCGTAT TATACAAAAC CGAGTTTGA 120
 ATTTGAAAGC AGTTTGGATT TATGCTCAAA CCATGGACGA CGGTTAGGTT TATGATGTTA 180
 TTCCAATAGG TTCACTATAA ATAGCTTAGT T 211

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3137:

```

10  ATTGGGAAAT GTTCCCCAC CACCTACAAT TTGTGAATAC AAACAATACG TATTGCAATG      60
    GACTTTACCT GGGCTTACCA AGTGAATGTA TACGTCACGT ATGATACGAT TGTAGTTGnA    120
15  AAATAATGCG AACAGAAAAT CGTTATAAGT ACAAATAATA CAGGTGACTC AACTCCTGCT    180
    TTTAGATTAA CAAATCTCCA ACCGATACAA TGAGTGCTTG CAACATACCA AGCATTATAA    240
    AGAATCCTGC CTTACCTAAG                                          260
  
```

(2) INFORMATION FOR SEQ ID NO: 3138:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3138:

```

30  CATAAGCAAT TAATGACTTC GTTAATTGCG AAAGTGTATC TTTTGTATTA TCATTGCGTT      60
    TTGCATCTTC AAGCTTTCTC ACATCTGATT TGACAGCAAT ACTTTCATA TTATCTTCAA    120
35  GCGATAATTT CTTAACTGCA CTTACCACTT GCTCAATTGC TTCTGCTAT TGTCATTCGA    180
    TATCGGAGTA GTAGGAAGTG CnGAATTCCG CA                                  212
  
```

(2) INFORMATION FOR SEQ ID NO: 3139:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3139:

```

50  TATTGGTTTT TATGCGAATA TGGATAATAA AAGGTCTCAC GACATCATTG ATAAATCGCT      60
    TGAATGTTG CGACGCTTAG ATCACAGGGG CGGGGTCGGC GCAGATGGCA TCACTGGTGA    120
    TGGCGCAGGT ATTATGACTG AAATACCTTT TGCATTTTTC AAACAACATG TAACGGAGGA    180
  
```

GCACCTGTTA GAAAAGAAGG GAAATTACCT CGTGAAGTCA TTCGTTATGA GTATGACCTA 300
 GAATATGGTA CAAATGTTTT AACAAATGGCA CAAAGATGCA ATTGAAACCA GGThCAACGT 360
 5 GTGTTAnTAC AGG 373

(2) INFORMATION FOR SEQ ID NO: 3140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3140:

AGCCTTATAA TAAAGTGCCT TTCATAGCAA TAAGTTGTGT CCATTGACCT ATTACATTTT 60
 20 TCGTTTTGTA CATTAAATAT AAGAAATACG GTGCACCAAT AATTGCTACG ACAATACCTG 120
 CTGGAACCCC CACCTGGTTG TAATACCATT TTGGCCATTT GTATCAGCTA TAACCAAGTA 180
 ACChTGCCCC AACTAAATG GCATTGGGTA AAACCACnTG 220

(2) INFORMATION FOR SEQ ID NO: 3141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3141:

GAGGAGCAGC ACAACCAAAT ACACAACCAG CTGGACAAGG TGATCAAGCT GATCCGAATA 60
 ACGCTGCACA ACACAACCTG GAAATCAAGC AACACCGGCA AACCAAGCAG GTCAAGGnAA 120
 40 TAACCAAGCA ACACCTAATA ATAATGCAAC ACCGGCAAAT CAAACACAGC CAGCGAT 177

(2) INFORMATION FOR SEQ ID NO: 3142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3142:

CTTTTTIAGC ATTTGGTTTA ACAACChGGT GTTGCAGTAT CCCCACTTAA GGTCTGTATA 60

ATTTTCATTTT TATGTTCTCTC GATAACTTGT ATTGCTGCTT GTTTTCTCTCC ATCTGTCAAT 180
CCATCATTTG ATTGAGAGAA nCAG 204

(2) INFORMATION FOR SEQ ID NO: 3143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3143:

GTGATGCCAT ATAAATTGGC AATAATGGCA CAAGTACTGT CAGTCCAGCA ATCGCTATAA 60
ACTGACTGAG CCATAAAATG CGAAAGTTAC TCGCCCATAT AGACTGATTA ATCATATGTC 120
ACCATTTGGAT TTGGTACGGT AGTTAAACCT GAAGGCATAC TACCCTCCAC CCACTTATTC 180
AACGTTGGAT nATAGGCAAT GGGTAATTAA AAATTTTGT TTTGAAATGG GCCCACGGGC 240
TTGTTTTAAT CAAAATTAAA AAATTGTGGT nCTTGGACC 279

(2) INFORMATION FOR SEQ ID NO: 3144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 514 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3144:

TGACTTAATC AAAGCATTTG ATCAAAACAC CAGAATACCA TTATTCTTTA ATATGTTGTA 60
CAGTAAACTC TnTATTATTT GTTGCTGTTG GATCCATTGT TCGTCTTTCA ACAAAAACnT 120
GACCCAGAAT GAAGTCCGAT AGAGTCAACA AAGCtATAGT ATTTGTAACC ATCTTTTAGT 180
TGATaAATGC CACGCGCATC TGTTATTGCG TCATTTTTAG GTAcAAATG AATTTkGAGA 240
TTTCTCaCaT TATCAGGTAC TTAAATAAA CGCAAAGTTG GACCGnCTTC AACAGTCTTT 300
TCAGCAATCG TATCATTAGT ATCAGCATTT TTGATAATAA CATTTGTTGC GCCTTGACCG 360
TTTTTAGTAG TCATTGTATT AAATCAAGGT TAATTCAGAA TTCGGATTTA CTGTTAATGC 420
TTTCTCGATA CCATTAAAAT CGCCATGGTC ATTCTGATCA GTTCCAGTAT ACGGCCTAAT 480
GCAATACATT TGCCTGTGCh TGATAGTnCT TATT 514

(2) INFORMATION FOR SEQ ID NO: 3145:

(A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3145:

10 ATTCAGACTT TGCATGTGGA ATGGCCACGT TCATGCCAAT AGCTGTCGTA CTCCCATTTC 60
 ACGTTCTAGT ATTGCATTTT TTAAATGCGA TGTGTGCTCT ACATAACGGC AAATTTTAAG 120
 TTTTATGAAT CAACATATCC AATGGCTTCG GTTTCGAGAC ATGTCCGTGG ATTCAGTAAT 180
 15 TAACCATAGT TTGGTTGGAT CCAAACCAT GAGnAGGGTT TAATGGAGGA TGTnGAATGG 240
 TTCnCCGGTG GTTAATCCTA CATGGTCCAC CCTCTGGTA ACCATGGTGG TGGTAATAAC 300
 CC 302

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(2) INFORMATION FOR SEQ ID NO: 3146:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3146:

30 CAGGAATAGG ATCATTTGCA TCCATAGCTT CACTTATTTT TTCAGAAGCT AGCGTACAAT 60
 CATTTAAATC TACGCCACCT TCTTTATCAA TAGAGATTCT AAGAAAATGA TCTCTACCCT 120
 35 CTTTGACCAT ATTCAACGTC TACAAGTTCC AAAATTCAAG GTCTTCCCAT AATTGGGTTT 180
 AACCAATCCA CTTTCTACCT GGTTCGCGT AAATTTTAC CTCCATACCA GGGnCCCTCCC 240
 CCTTTTTTGG GCCAAAATAG GAAAAAnGAG GCGGGGGAAA TCCTCCCCC AATTCCnTTC 300
 40 CTGGCCCTGG AGGTTTCCAC CTAAATTTT TT 332

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(2) INFORMATION FOR SEQ ID NO: 3147:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3147:

GAGAGTGGTT AACAAGCAAA TAGAAATAAT TAAAAATGCA GATGCAGATG CATCGGCGAA 60

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5 CnCCAACAAA TGCAGAAGTT GCTGAATTCC AAATGTAACG ATACCTGCCC ATGAGCGATG 180
 TGCTCAGAAT GATCAGAGCT AATG 204

(2) INFORMATION FOR SEQ ID NO: 3148:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 217 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3148:

15 CAACCGGGAC AGGTGGGGTT ATTGGACGTT ATTTTGGCC TTTGGATTTT AAGATATTGG 60
 TCGAAAAGAG ATTACATAAA ATTGTGGCCA AATGCGGATT GCATATTATT GTAACGCCGn 120
 20 CTATTGCATT GTTGATTGTT AGGnCTATTA ACTATCTGGA TCTGTATGCC ATTAGCCAGG 180
 TTTTGTTCa GACAGTTTAG TTTCAGTAGT TAACGGA 217

(2) INFORMATION FOR SEQ ID NO: 3149:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3149:

35 CTATTATTAT ATTCCGCGGT GTACGTATAT GTGCTACGTT ATCTTCGTTA ATTGTACCGA 60
 TTATGGCTAT CATTACATT GGTATGGTTT TAGTAATATT GCTATTTAAT TTAGATCAAA 120
 TTGTTCTAT GATAGGTCAC GATTATTAAn AGTGCAATTG GTCATCGAAC AAGT 174

(2) INFORMATION FOR SEQ ID NO: 3150:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 181 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3150:

50 GGGACCGAAT TGACTTCAGC ATTACCAGCA AATTGATTAA TnTTGTGGGC TGGTATTGGC 60
 TCTGGCGGTA CCATTTACAG GTACCGCACG TTATTAAAGC AACATCACGG GCAATGTTAT 120

A

181

(2) INFORMATION FOR SEQ ID NO: 3151:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 172 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3151:

GTTTTAATTG AGCGACATAC TCTTCTGTTA GCTCTGCTAC TTTTAAAAT AGAGCGATTG 60
 ACATCAAACA TAACTGCTAA ACGCTCAACG TCTGCCTTCG TAATGGCTTT TGTAGAAATT 120
 CTAATAAAT AATTTGGAAT GCTATCATTG GTTGTTTCAA CAGCTTGATG CT 172

(2) INFORMATION FOR SEQ ID NO: 3152:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3152:

ATGGACGTTG AGACATTAT AAGCGATATA GATTTCGCAT GTTGCAATTA TTAAACCTAA 60
 TAATGGTAAA CGACAAGTGT GACTGTTACT GGACTTTAAT GAAGGTAGTA ATCAGAATGG 120
 AAATCAACCA AAAGTAGGTA TTTGAATnTT GGAATAATG AGACATAGCG AGAGTGTATA 180
 TGCAATACGA CAGTACTnTA AATTAAGAG 209

(2) INFORMATION FOR SEQ ID NO: 3153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3153:

TTCTCACAAA GCGCTCAGTT GAAGTAAATC CACCTGGACA ATCCAAATGT ACCTGCTTCA 60
 TTGCCTAAAG GTTCAATCGT TAnACCTTCC AATAAATTTG CTGTTGCTGG ATAAGGAGAA 120
 ATTATTGGTA TATTGTCTTA AATTACTATG ATGCCAATTT AAGGTCTGGA TGAT 174

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3154:

GGATCACATC GTTCATTTAC ACAATCTATT AATATTCAAT GGCACAATAT AGTGTTTATG 60
 GCATTACGGA TATGATTTAG TAGCnCACCA TTATTAACCG ATCTCTATCT GTTAAAAGGA 120
 ACTTAAGAGC AATGTTTGCG CATCATCATT TTATGTTGCG TCTTTGCACG AGTTTTCGCA 180
 AACTTTACAA TATTTGTTGC GGATGATTAT TTAACTTTTC GAGAATGTTG ATGGCACAGT 240
 CCACTATAnC AATCAGTATC GCAATGG 267

(2) INFORMATION FOR SEQ ID NO: 3155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3155:

AATTAAAAAT CAAGCAACTG CTGCAAAAAT GCAAGATCAA ACTGTTCTCTC AAGAAGCAAA 60
 TTCTCAAGTA GATAATAAAA CAACGAATGA TGCTAATAGC ATAGCAACAA ACAGTGAGCT 120
 TAAAAATTCT CAAACATTAG ATTTACCACA ATCATCACCA CAAACGATTT CCAATGCGCA 180
 AGGAACTAGT AAACCAAGTG TTAGAACGAG AGCTGTACGT GTTtAGCTGT TGCTGAACCG 240
 GTAGTAAATG CTGCTGATGC TAAAGGTACA AATGTAAATG ATAAAGTTAC GGCAAGTAAT 300
 TTCAAGTTAG AAAAGACTAC ATTTGACCCT AATCAAAGTG GTAACACATT TATGGCGGCA 360
 AATTTTACAG TGACAGATAA gTGAAAYCAG GGgATTATTT TmCacGAgTT ACCAGATatT 420
 TAcTGgTAAT GGAGACGTGG GATTATTCTA ATTCAAnATAA TACGATGCCA ATTGCAGACA 480
 TTAAAAGTAC 490

(2) INFORMATION FOR SEQ ID NO: 3156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3156:

CCTTCAGTAC CTTGTAATAG TTAnTTAAAT GTTCCGATCA TCGTGTAGTG TGATTCATCA 60
 5 TACCGGCCTT TTCAATTGAA TACGATCTAA ACCGTTTCGT CAGGTGCTAG TAAGTTACCT 120
 TCGCCACCTA AATAAGAAGT TCACTCGTTA CGATTTTTTC AGATAGCATC ATTGGTGGAT 180
 TCGTAACTTG TGCAACAGCT GTTTAAGTAT TAATAGTGAT TCGGTCGTCT TCACATGCAT 240
 10 TGGCGCACAA TCCnTGCAACC GT 262

(2) INFORMATION FOR SEQ ID NO: 3157:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 170 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3157:

ATGGTAAAAA TTGCACTATC TGCTCGGGAA ACGATTTTGC ATAACCTATT GTTAATTTTT 60
 25 TACCTGTTGA TTTAGCTGTA TCTGnCCATT TTTGAGCTT CTGCTGTCGT TTTAGCCATT 120
 GGGTTTTTCAC ACATCACATG TTTACCAGCA TGCAACCCTG GCTACAGTAA 170

(2) INFORMATION FOR SEQ ID NO: 3158:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3158:

CCAGGCAGAG GAGCAGCACA CCAATACACA ACCAGCTGGA CAAGTGATCA GCTGATCCGA 60
 40 ATAACGTGCA CAAGACAACC TGGAATCAAG CAACACCGGC AACCAAGCAG GTCAAGGAAT 120
 ACCAAGCAAC ACTAATATAA TGCACACCGG CAAATCAACA CAGCAGCGAA TGTCCAGCAG 180
 45 CAGCGAACCA GCAGCACTGT AGCAGCAACG ACAACTCAGn CCAATGTAGC ATATGGTGAG 240
 GCAGTTTATA GACATACATT GTGnCCCTGCA TTCACAGTGG ATAGCAGGTC CACTGTACTG 300
 TACAGTAAGT An 312

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(2) INFORMATION FOR SEQ ID NO: 3159:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3159:

AATCACATCA AAAACTTCAA TTGTTTACGT TGGCAACTAA CTTTATGTTA GAACGCACAC 60
AATATCTAAT GTTTAAATC TATCGTCGCA AGATGCTTCC TGnTAATTAT CAGTGCCATT 120
TTCGATTGGG TTATACAATC TAGTAATCGC ATGATAATTT AATGCTACAA G 171

(2) INFORMATION FOR SEQ ID NO: 3160:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 211 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3160:

CTTGTTCAAT TAATCCATAT AGTATACGAC GATGTACTGG TTTTAAACCG TCACGAACAT 60
CTGGCAATGC ACGAGCAACG ATAACACTCA TCGCATAATC TAAAAATGAT TCACGCATT 120
CACTGGTAAT ATTTCTGTTCA TTAATCnTGA TTGAGGGAAT TCCGCCCATC CAGAnGTCCC 180
CCCTCCAAAG TTCAGTTCCA CAGGGGCTAG A 211

30

(2) INFORMATION FOR SEQ ID NO: 3161:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 321 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3161:

GCACAGGTAG CGGTAGTGGC GGTCTGTATGA TGACTTTGGT AATCTAAAGC AAAATGTACG 60
ATAATAATAA ACGTCGTTTC GTTCTCTGTA TGTCAGAGG GCAGTGAAGA AACAAGATTA 120
TTGAATTGTT GATTTCTTGA AGATATAAAA ATTCAAGAAT GGGCTAGGA TTCCTAAGGT 180
GTCTTCTTTT GGGCTCAGTA CGTAAACATA TTGTAGAGCG TGCAGTGAGT GGCGCACCAT 240
CTCTTTTGGG TCAGnTTTGG AGTTTTGTTT GTCGGCTGTC GGATnTCGT ATGTAGGAAC 300
GGCTGTTTAC TnCGTGGAT G 321

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(2) INFORMATION FOR SEQ ID NO: 3162:

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- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3162:

10 AACATTTGAG CAATATCAAG AACATTAGA GTATATTTTA TCCCATCATG TAACTCGTAA 60
 TACAGCAATT ATTGCTTTGG GTGGTGGTGC ACTGGTGATT TTGCTGGGTT TATTGCGGCG 120
 ACACITTTTAC GAGGCGTGCA CTTTATACAA GTGCCAnCG 159

15 (2) INFORMATION FOR SEQ ID NO: 3163:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3163:

25 GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGAC AAGTCTTACG GCATCTTCTA 60
 TTTTAAAGCT TGAAATTTAA CAAATCATAA GCCGTATGAA TATTAAATA TGCCACCATG 120
 ATTGAATGGC CCCTTTCTAT TAGTTAnGTT TTGTGCG 157

30

(2) INFORMATION FOR SEQ ID NO: 3164:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 216 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3164:

TATAAAAATA TAACGCGGAC AAAAAAGTGA GTTATTACTG ACAAAGTATn TGAGATTGTA 60
 ACAGGATATA TGAAGCAATA TCAGTTGATC CAACTGTCAT AGGTATTTCa TCAGCAGGnG 120
 45 TTGTTGATGA ACAAAAAGCG AAATTGTATA GCAGGCCAAC ATTCCGATTA TAAAGGTATA 180
 ATTTAAAGGA TTATTAAAAT CATGTCTCTT ATGTCA 216

(2) INFORMATION FOR SEQ ID NO: 3165:

50

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3165:

5 AGAAACACTT CTATTGAATC GTCTTACTGC TGTTCCTAT TTATAACACT TCGTATTGAA 60
TGAATTCATT ATGCCTATTT GACACATTAT TGAAGTTTTC CTAATGCCTG GATCCTTTAT 120
ACGTTACGGC TTCGTGCTAT GTTTTGGTAC ATAAAGCTTT GACATATCGA nATTC 175

10 (2) INFORMATION FOR SEQ ID NO: 3166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 160 base pairs
(B) TYPE: nucleic acid
15 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3166:

ACTGTTACAA CAAATTAAAA ATACAACAAG CGAGATATAG TTATTGTTGC TGGAnTGTAC 60
CAAGTAGTAT TCCAAGCGAT GCTATGGCAA ATTGCACAAA TTACAGCACA GACAGGTGCT 120
25 AAATTAGTAG TCGACGCTGA AAAAGAATTG GGCTGAAAGT 160

(2) INFORMATION FOR SEQ ID NO: 3167:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3167:

TGTGGGGGAA ACCTGCACAG CAAAACTAA AGCTTATCGA TACATCTAAA CATTGTATTA 60
40 TAAATCAGT GCATCCTAGT CCACTGTCTG CATATAGAGG ATTCTTTGGA TCAAAACCGT 120
ATTCCAAAGC GAATGCCTAT TTAGCGTCAG TAGGnA 156

(2) INFORMATION FOR SEQ ID NO: 3168:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 174 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3168:

55

GTGGCGAGAA ATACCGCAAG CATAAAGATA TCTTTGATCC AACTTACCAA CAGATCAACG 120
 GAAAAGTACC AGGTAACCAG GAATCAAGAT CCAGACACAG GAAAAGTGAT CGAG 174

5 (2) INFORMATION FOR SEQ ID NO: 3169:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3169:

TCAAACGGGG TCAATTTCAA ATGGAAAAAT TATACCGCAT CTTCTCCTGA TAACTACGTG 60
 ACCTTATCTT CTTTATATTT GCAGACCACG AACATTCAAA CTGCATGCTT GCTCGATTGG 120
 20 CAATGTCATA TAACTAGTAA CATGATCATC nCATCAAAT TAGTATGTCA AATGTCCCAA 180
 TCAnTAATTT GATCGGTGTT GCTCAATTGA TTA 213

(2) INFORMATION FOR SEQ ID NO: 3170:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3170:

35 AAAGCACCTT TTCCTAATGA AAGTTGTGCT ACTGGTATCT GTGTTTGATT TACAAAATCT 60
 TCTAATTCTT GATGGAGGTG AAAACTGTTA ATTTTCATGTC CAGTAATGAT GATAGGCTGC 120
 TTCGCTTGAT GCAGTTTAGT TGCTAATAAC TCTATATATG TTGATGCATC CGTATATTTA 180
 40 GTTGCCGTCA CTTCAAATGG TGTCGGTATC TCAATTTTCAAG AGATTGCGAC ATCGATTGGT 240
 AAATGTAAAt GAACTGGGCG TCTTTCGGCG ATTGCTGTAT TAATTAAACG TGGTATTTTCG 300
 GTTGTTCAT TTTCAGGTGT GATATAACCT GTGCACGnTT ATATGTGCAA ACATTTTTTCG 360
 45 ATAGTCGTCA AATGTACCnn 380

(2) INFORMATION FOR SEQ ID NO: 3171:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 401 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3171:

5 TAGAAGGTAA GAAGGATCCT ATCGGTGCAA TGGGATATGA TCGGCCAATT GCAGTGTGTA 60
 ACGAGCGACC AGAATCACTA TTTAATTACT TTAAACAGCT GTTTGCACAA GTTACGAATC 120
 CACCAATTGA TCGGTATCGT GAAAAAATCG TAACGwGTGA ACTTTCTTAT TTAGGTGGCG 180
 10 AAGGTAAC TT ACTAGCACCT GACGAAACGG TTTTAGATCG TATTCAATTG AAAAGGCCCG 240
 TATTGAATGA ATCACACTTA GCAGCGATTG ATCAGGAACA TTTTAAATT AACTTATTTA 300
 TCAACGGTAT ATGAAGGGGG ATTTGGGAAG ATGCGTTAGA AGCATTAGGC CGAGAAGCAG 360
 15 TGAATGCTG TTAAGCAAGG GCGCTCCAAA TTCCTAGTGG T 401

(2) INFORMATION FOR SEQ ID NO: 3172:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3172:

ACATAATTTA AAATAATATT ACATTTGTAA TGGnCACCAA GTAACGTTTC GGTTGCTTGG 60
 30 TGTTTTTTGG TATGAATTAC TTCTGTAC AAAACAATCT AAAGCGTTCT GTTATGTTTT 120
 ATTAAGATTT AATTACAAAC GGAACTAAA TGTAATAGAA TAAACT 166

(2) INFORMATION FOR SEQ ID NO: 3173:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3173:

45 ATAATGAGAn TGTTGTACGT TATGGTGGTG GAAGTGCTGA TGGTGATTCA GCAGTAAATC 60
 CGAAAGACCC AACTCCAGGG ACCGCCGGTT GACCCAGAAC CAAGTCCAGA CCCAGAACCA 120
 GAACCAACGA CCAGATACCA GAACCAAGTA CCAGACCCAG 160

(2) INFORMATION FOR SEQ ID NO: 3174:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 158 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3174:

5 CTTTATATAA AGAAGGAATT ACTAAACATA CAGTTAGATT ACTTCATGCA ATCGAATTAG 60
 AACGTTTGAA TTAAAGCCGT AGATTAGGTT TTGAATTATC AACAGCnAAA GAATCACGTA 120
 TTGAACGGGG GTTATTTAGA ACGTGATAAA GAAGGATG 158

10 (2) INFORMATION FOR SEQ ID NO: 3175:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3175:

20 TATTTGAAGA TGGCTGTGTA CAAAAATCGG TGTTACGTGA TCATGATACT GTCAGAATTT 60
 ATAAACCATG GCTAACAGCA CATCAGCTTT CATTGCCnA GTATGTCGTC AGAGAAGATA 120
 CACCTAATCG CTAATTAATG AGGTTTGGAA ACAT 154

25 (2) INFORMATION FOR SEQ ID NO: 3176:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 472 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3176:

AGAAGGTATT TTAGCTCAAT CTCCAGGTCT AAAGGTTGTT ATTCCTTCAG CCCATACGnT 60
 GCGAAAGGTT TATTAATTTT TCTATTAGA AGTAATGACC CAGTCGTATA CTTAGAGCAT 120
 40 ATGAAATTGT ATCGTTCATT CCGTGAAGAA GTACCTGAAG AAGAATATAC AATTGACATT 180
 GGTAAGGCTA ATGTGAAAAA AGAAGGTAAT GACATTTCAA TCATCACATA CGGTGCAATG 240
 GTTCAAGAAT CAATGAAAGC TGCAGAAGAA CTTGAAAAAG ATGGTTATTC TGTTGAAGTA 300
 45 ATTGACTTAC GTACTGTTCA ACCAATCGAT GTTGACACAA TTGTAGCTTC AGTTGAAAAA 360
 CTGGTCGTGC AGTTGTAGTC AAGAAGCACA CGTCAAGCTG GTGTTGGTGC ACAGTTGTAG 420
 50 CTGAATTAGT GACGTGCATC CCTTCATTAG AAnnCCTATG GAAGAGTGCA CA 472

(2) INFORMATION FOR SEQ ID NO: 3177:

55

(A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3177:

10 TGAAAGCTGG CGAATACAGT GATTGTCATG ATGCGGATCT AnTTGTCATC TGTGCTGGTG 60
 CTGCACAAAA ACCTGAGAGA AACACGTTTA GATTAGTAT CTAAAACTT GAAAATATTC 120
 AAATCAATTG TTGGTGAAGT AATGGCATCA 150

15 (2) INFORMATION FOR SEQ ID NO: 3178:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3178:

25 TTACTCTATC TTGATTGAC GAAATACTAT TanGCTAATA TCGATATTTT AAAAACGAGA 60
 TGATGTTCCA AAGCAAGCCA TTTGATGGA CTGCTAATAT TCTTCAGCCA AACGTATCAT 120
 30 TTTACTCGCA TTTGGTGAAA AGAAACGGCT GCTATTACAC ATTTAT 166

(2) INFORMATION FOR SEQ ID NO: 3179:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3179:

CTTCGACTCT AGAGGATCCC CGCGCTCAAA TTCTAGTGTT AGATGATAGT GGATTAGTTG 60
 ATAGCAATGG CTTTGCAATG CCGATGTTAC TCGCAATAAG TCATGTGCAT CAATTACTTA 120
 45 TTAAAGCAGA TTTACGTATG TCTACAAGTT TanTTGCTA AATCTGGTGA 170

(2) INFORMATION FOR SEQ ID NO: 3180:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3180:

AGCTAAGGTT GCCnTGGGCG TTGCCCCAnT TGGTTAGTCC AGGTGGTCGC GGTGGCCATC 60
 5 GGTGTATTTCG CCAGGTCCTT CAGCCAGGGT TTTTACTATT ATATCCAGTT GTAGCAITCA 120
 TGATTGGGGC GATTTCGAGAT AGATTCATCA ATGAAATTAA TTTCTGGATT TTATTCGTTG 180
 GTATTTATTT GGGTATACAT AAGTATGGTA CATGATAGGC AGATATACAA CATTACAACA 240
 10 TTCATTCTAC TATGCTGGAA ATAACATGAC AGTGATGACA CTACTATCCC CGTCGCA 297

(2) INFORMATION FOR SEQ ID NO: 3181:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3181:

CACTAGGTAC CCCAAAACGC CAGAGGAACT TGGTTAAATC GCACTTACTT GGTGGCTCCA 60
 25 ATCAACTGGT ACTTCATAAC GTTTGGCATC TTCGCCACTT CACCACTATT ACTCTTTCCA 120
 CCTAATTGGT TCATGGCTTG TGCTAACGTT TCATGTGCTT CCGCTGAAAT CGATCCATAA 180
 CTCATCGCCC CTGTATTAAA GCGTTTGACA ATGTCACTTA CCGGTTCAAC TTGGTCGATG 240
 30 TCAATCGgTG TACATGCTTT AAATTCAAGT AAATGTCTAA TGTGaTCTGT TCTATTTTTG 300
 TTnCACCGnT TnCAGAGTAT GCTTTAAATT GCGCCATAGT CCATTTTCT 349

(2) INFORMATION FOR SEQ ID NO: 3182:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3182:

45 TACCAACACG TACACCTTCT AAAATAACTG CATTTGCACC GTnTTAATAC ATCATCCTCG 60
 TTTATAACCG GTGTAAGCAC TAGGGGGTTC AATCACACCT GCTAATACTG CGCCAGCCCT 120
 ACATGTACAT TTTTACCACT TGTAGCACG 149

(2) INFORMATION FOR SEQ ID NO: 3183:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 147 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3183:

GCGGTGCCGG TGTTCGAATT GCGCAGTGG TGTGGTAGC ATGTGGTCTT TCAATCAATG 60
TTCAATACAC CAGGAGATCC GGAAAAGATG CGTATGAATT TTATGGTAAG TGCACCAGGC 120
ATTACCACAC CACGCAAnAA CATGCAT 147

(2) INFORMATION FOR SEQ ID NO: 3184:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 180 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3184:

CAGCGATATG TTGGCGTTGA AAATCTGCAA TTGTTCATA ATTCTCTGTT AAAGAACGAC 60
TTAAATTGAT AAAAATGGAT ACGATCTCTT GGTAAACAGT GACATTTTCT CAATCGGCGT 120
ATGATGTTTG TGGCACCGAC CATCGAGAAC ATGAAAATCT CATGTCCAC GCTAGTCGnC 180

30

(2) INFORMATION FOR SEQ ID NO: 3185:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3185:

GGTAAATACG TATTAATCAG ATTAAGATCT GGTGAAGTTC GTATGATCTT ATCTACTTGG 60
CCGTGCTACA ATCGGGnCAA GTTGTAACC TACAACACGG GTTAGTTAAC GTTGGTAAAG 120
CCGGCACGTT CAAGATGGGA AAGGTATCCG 150

45

(2) INFORMATION FOR SEQ ID NO: 3186:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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GAATTTnAGG TGAATCAGAA GATTAAACGCT GTTGCCTCCT AAGCTAACAG ATACTGGTTC 60
 GTCAGTTGTC GTTGAAAAAG CGAATGAACA ATTAAATAAA ACCGTAATC GAGCATTATT 120
 5 AGAGGAAGCT AACCAAAGCA GGTTTA 146

(2) INFORMATION FOR SEQ ID NO: 3187:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3187:

AAATTGGCGA GTATGTTGTT ATTGGGTCAG TACTCTGAAA TTAACAATAG nTACGATTGA 60
 20 AAATGGTGTC ATGTATTCAA CAGTCTGTTG TTAATGTATG CTAGTCGTGG TGCGAATACT 120
 AAGGTCGGAC CGTTTGCGCA ATTGAGACCA GCGCGCAAT TAGGG 165

(2) INFORMATION FOR SEQ ID NO: 3188:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3188:

CAGTTTAGTG GAGACGAATC TAAACGAAAC AAAGCGATTG GACGTGCATC AGTTGTACCA 60
 35 ACATTCTTTG GTGTAAACGn AACCAATTTT ATTGGTGCC ACCACTAGTT ATTGGAATCC 120
 TGTGTTCTTT ATTCCATTG TATTAGCACC AATTGTAAAC GTATGG 166

40

(2) INFORMATION FOR SEQ ID NO: 3189:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 146 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3189:

50 AACCCCTTTAT CTAATCCATT TTCAGTTAAG CGATGACCGC CTGCTAAAAT TTGTGCATCT 60
 GATTCTTTTG CTGCATCAAT ATATGATTGA ATTTATCTA ATTGATCCTT ACCAGTTTGA 120

55

(2) INFORMATION FOR SEQ ID NO: 3190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3190:

TCCCCCAAAG GGTTTAAGGG GTTAACCCGG GTTGGGAAA AATTTTAA CCCCCCTTAA 60
 AATTCCCGG AAAAAGGAAA CCCGGGTTTT TAAAAAAAC CCGGGTTCC CAAAAATTTT 120
 TTGGGAAAGG GAAAGGAAA AAGGGTTAAA AAATTTTGG GAAAAACCG GGCCTTAAA 180
 AAAGGGTTTT TTTCCCTTA AAAAAATTT AA 212

(2) INFORMATION FOR SEQ ID NO: 3191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3191:

CTTCACTGAC TTTAGCAATT TCATCACCTT TTGCCCTAC AACGATAGCT AATGATTAT 60
 ATTGTAACT CAAATGACCT TGTGAATAC CTCTGACAC AAGCGCGCA CATGCTGCA 120
 AGTTTTGCGC TAAACCAACG GCAGCAAC 148

(2) INFORMATION FOR SEQ ID NO: 3192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3192:

CTGCTAATCC GAAATCTTTT TGGAGTTTA TTAAACCAGC TGCTTCTAAT AGTTTAAGTG 60
 CACGTGCTTG GTTTGACACA TCATTTGGAA TGACAACTTT AGCnCCATCT TTAACCTTTT 120
 TGACATCTTT AATTTTATCT GCAGAAATAA ATCCATCAG GATGGCTCTT AAATATATGT 180
 TACGTGATAA TTTCTCGAA AATGGCTTCC CT 212

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3193:

TCGTGCAGTG GTCTTCTGTT AATTGGTGAA TTTGGATACT GGTATATTC AGCTGCACCG 60
 CAAGCAACTT CTATTGATGG CCnAACTGCC TTTTACCTC AAGCAATGGG TATGGTAGTT 120
 GTTGCACTCA TTTATGGCTT T 141

(2) INFORMATION FOR SEQ ID NO: 3194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1290 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3194:

AATAACGTTT TGAAAAACGA AGATGTTTTA AATGCCTATA TCCGCGGTCG TGGCGGAATG 60
 GCAGACGCGC TAGGTTGAGG GCCTAGTGGG AGAAATCCCG TGGAGGTTCA AGTCCTCTCG 120
 GCCGCATCAA AATTCTTAAT TTAAATAAGC GGGTGTAGTT TAATGGCAA ACCTCAGCCT 180
 TCCAAGCTGA TGTGTGGGT TCGATTCCCA TCACCCGCTC CATAGATAAT TTTAATGAAC 240
 ATTGAAAAC GAATGACAAT ATGTCAACGT TAATTCCAAA AACGTAAC TAAGTTACAA 300
 ACATTATTTA GTATTTATGA GCTAATCAAA CATCATAATT TTTATGGAGA GTTTGATCCT 360
 GGCTCAGGAT GAACGCTGGC GGCGTGCCTA ATACATGCAA GTCGAGCGAA CGGACGAGAA 420
 GCTTGCTTCT CTGaTGTTAG CGGCGGACGG GTGAGTAACA CGTGGAaTAAC CTACCTATAA 480
 GACTGGGATA ACTTCGGGAA ACCGGAGCTA ATACCGGATA ATATTTTGAA CCGCATGGTT 540
 CAAAAGTGAA AGACGGTCTT GCTGTCACTT ATAGATGGAT CCGCGCTGCA TTAGCTAGTT 600
 GGTAAGGTAA CGGCTTACCA AGGCAACGAT GCATAGCCGA CCTGAGAGGG TGATCGGCCA 660
 CACTGGAAC GAGACACGGT CCAGACTCct ACCGGAGGCA GCAGTAGGGA ATCTTCCGCA 720
 ATGGGCGAAA GCcTGACGGA GCAACGCCGC GTGAGTGATG AAGGTCTTCG GATCGTAAAA 780
 CTCTGTTATT AGGGAAGAAC ATATGTGTAA GTAAGTGTGC ACATCTTGAC GGTACCTAAT 840
 CAGAAAGCCA CGGCTAAtAC GTGCCAGCAG CCGCGGTAAT ACGTAGGTGG CAAGCGTTAT 900

CGGCTCAACC GTGGAGGGTC ATTGGAACT GGAAACTTG AGTGCAGAAG AGGAAAGTGG 1020
 AATTCCATGT GTAGCGGTGA AATGCGCAGA GATATGGAGG AACACCAGTG GCGAAGGCGA 1080
 5 CTTTCTGGTC TGTAAC TGAC GCTGATGTGC GAAAGCGTGG GGATCAAACA GGATTAGATA 1140
 CCCTGGTAGT CCACGCCGTA AACGATGAGT GCTAAGTGTT AGGGGGTTTC CGCCCCTTAG 1200
 TGCTgGCAtA ACGCATTAAAG CACTCCGCCT GGGGAGTACG ACCGCAAGGT TGAAACTCAA 1260
 10 AGGAATTGAC GGGGACCCGC ACAAGCGGTG 1290

(2) INFORMATION FOR SEQ ID NO: 3195:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3195:

TGGTACAGAG TTATCGCTGG TGGTCCTGTT CGTGCCGTAC TTGAATTATC AGGTATCACT 60
 25 GATATCTTAA GTAAATCATT AGGATCAAAC ACACCAATCA ACATGGTTTCG TGCTAACAAT 120
 CGATGGTTTA ChAAACCTTA 140

(2) INFORMATION FOR SEQ ID NO: 3196:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3196:

40 CTATTGGATC AGGAGGCAAC TACGCTTAAG CGCAGACTGC CCATTGAAAC GCCATGCATC 60
 GCATTTGTCTG CCTGAAGAAA TGGCATATGA GAGCTTGAAA GTAGCGGCTG ATATTTGTGT 120
 CTTTACCAAC GntAATATTG TTGTC 145

45

(2) INFORMATION FOR SEQ ID NO: 3197:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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TGTCGAGTTG GAATTGGACG ATTGAATATC CCATCTCCAT CACTATCAAA GTATGGGAAT 60
 TGAATTGTTT CTAATTCGTA TCCACCTTCT GTCATTGATA ATGTAGGGTT AATTTTAGAA 120
 5 CCATCTkCTG TTTCTAGTTT TAAGTTCCAC TTCCTACCTT CTTCCCAACG TTGACCCATT 180
 GTGCCATTAG GTACTACTAA ACTATCGCTG ATTGCATCAT GAATAACTGG CTTCCATTCh 240
 CTTGCTCTG TTGTTTGACC TAAGTCACTC GCGCTnAAAA ATCGACCCGC TTTATATCCA 300
 10 TnTTCAGCTG 310

(2) INFORMATION FOR SEQ ID NO: 3198:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3198:

25 TGCTTTATTA ATGCATTGGC TAATAATCCA CTGTACCAC CACCGGCACA AAGTACTAAG 60
 AGGTTTGTTT TGTGATATTT GAAGCTTTAG TGCATCGTCT GATACACCAC TGCCGCTAA 120
 AATTGAATCA GCTTTTnTCG 140

(2) INFORMATION FOR SEQ ID NO: 3199:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 184 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3199:

40 TGGTGATTTT AAATCATGAG ACTGGGACAA AATGATGTTT TCATAAAAAT TATTTGTTG 60
 TTCCAATCTC ATGATTTTTT TGATGAACAT AATTACATGA TTGATTGCAT CATTGTGTTAA 120
 AACCAGTGAT TGCAACCTGC CATTCAcAnG GAAAATTACC TAATAAGTGG CGTATTTACC 180
 45 AGTC 184

(2) INFORMATION FOR SEQ ID NO: 3200:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3200:

TTGAGAAGCG TTTAGGAAGT AACGTTTAAAC GACGACAGTC GTTCAATGCG ATCAAAATGT 60
 5 TTTAACACAT GAATCGCTCT CGTACTATTC GTGTGTGACA CATGTTCTTC CAGCATTTC 120
 TTAATGAATG CTTTTTCTTC TTGGTnTTTA ATCTTTGTAA ACG 163

(2) INFORMATION FOR SEQ ID NO: 3201:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3201:

20 GTTATGTTTG AGACTATAAT GAATAAATAT TTAGAAATAT GACTCCGATT GTTCGATGCT 60
 TAATTCAGTT AGAAGCATCA TAAGAATGCA TGATTACTGG TGTAAGATA CGTAATGTnT 120
 TGTATTGACT GGATGTCTTT GGATAGAGT 149

(2) INFORMATION FOR SEQ ID NO: 3202:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 192 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3202:

35 CAAGTGACTG AGATTACTGA AGTAAACCCG TTACCGCCAC ACTATATTTG TCCGAAGTGT 60
 AAAACGAGTG AATTTTTTCAA TGATGGTTCA GTAGGATCAG ATTGATTTAC CTGATAAACG 120
 40 TGTGAAnTTG TGGAGGCCAC TATTAAAGAA GACAGAATCC GTTGAACATT TAGATAAGGG 180
 AAAGTCCGAT TC 192

(2) INFORMATION FOR SEQ ID NO: 3203:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3203:

CGCCATCTAA CGTTTTTTGT ATTGTTGTT GCTGAGCTAG TTGTAAGTGC CnCATTAAAGC 120
 ATCTTATAGC GTGATAGCCA TCGGCCAACG TACAAATCTG CTCCGTATTG TACGCACCAC 180
 5 TAAGCAGTAC ACACCAGTAA CATTGATAG CGTTATAGCG CAATATACAG TACA 234

(2) INFORMATION FOR SEQ ID NO: 3204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3204:

AACGCCATAA GCTACATGTA TGCTTCTTGC ATGGTTATCA TCCTCTCTTA ATGACTATCT 60
 20 TTAAATTACG NAATGGCTTA CCAGTTTTTA ACATATGTGC AATTCTTTCA TATGATTTTT 120
 AGATTTAGTA GCATAAGCAA TTTCTCCACG TTGATGTACG TGATGTAATG ATTCTGGG 178

(2) INFORMATION FOR SEQ ID NO: 3205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3205:

TATTAATCAC GTTGTTGTGC GTTCGTGTTT TCGCAGTATT GATTTGTTGT TCGCATTAT 60
 GCATTGCATT ATTGTACTGC GTAATTGTAC CTGGCTTTTT ACCTTCAGTG CTTACTGGnT 120
 CATCTAAATG ATTTTTAGCT GTGATTA 147

(2) INFORMATION FOR SEQ ID NO: 3206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3206:

CAGCTGTACT AGTTGAGCGT ATTATCCAAA ACATTTTACG TGATGGCATT GATGTCGATC 60
 GACTTTTCAGT CGTAACGTTT ACAAACCTAA GCGCACGTCA nATGAAGCAT CGTGTAGACC 120

(2) INFORMATION FOR SEQ ID NO: 3207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3207:

TAGGGACTTT GAAGCGGAGA GTCTAATGCA TATGGGCAGC ATTATGATCA GCAACTGCTG 60
 AGAAAAATCC AGTTCTAGCT TGGGATTTAA ATGTGGAGTG GntTAATGAA TGCATTAAAGA 120
 AGCTGCAAGA ACTTATAAGT GTGCA 145

(2) INFORMATION FOR SEQ ID NO: 3208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3208:

AAACGGTTTT AGATCGTATT CAATTGAAAA GGACCGGTAT TGAATGnAAT CACACTTAGC 60
 AGCGATTGAT CAGaACATTT TAAATTAAC TATTTATCAA CGGTATATGA AGGGGATTTG 120
 GAAGATGCGT T 131

(2) INFORMATION FOR SEQ ID NO: 3209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3209:

ATAAATTAT CTATAATCTG TTGCTTGTTT TnCTGTTCTA CAAGTATTTT CACATTAGGT 60
 CCCGCATCCA TTGTAAAATA ACACGGATAC CCCGCTTCTC GGCATTTCGTG AACAGCGCCA 120
 TGACATCATA ACTTTCTGCA CAGTAGGAAC GGGGGTG 157

(2) INFORMATION FOR SEQ ID NO: 3210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3210:

AACGTAATAG ATATGGTACT TACTACATGG GAGAGAGTGC TAGATTCACA AACGGCAATC 60
10 AACCAATCAC AGTAAGAGAA GTGGGGCCAT TCTTATCTnG TCCAGTGGGT TATCAGTTCC 120
AACCTGGTGG GTATTGTGAT TAT 143

(2) INFORMATION FOR SEQ ID NO: 3211:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3211:

ATGCATACTG TATGTGTTCC AGCATATACA ATTTTGnCCA TCTTTAATGA CAACTGTACC 60
25 ATTTTTCACA ACATTTAATT CATCTAATTC CTTACCCTTC AAAGTTTATC TGTTGATCTC 120
GGTAAAATTA ATTCTGC 137

30 (2) INFORMATION FOR SEQ ID NO: 3212:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 239 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3212:

40 ATTCACGCTT TAAAGGACGT AAATACACGA CTAGGCTGTT TACCTTTAGA TCTAAATCAG 60
AACAATTTTT TTACCATGGT GTTCCCCTTG AATTAGGAAT TTTATATAAA AATAAGCGGG 120
45 AAGCGTTGTG CCCCCTTAC TCATAAGCTT TAATTAATGC TAAATAGTCT GACACTAGCG 180
ATTTGATAAA ACTATACTAA AATTATTTAG AAGTCACTAA GATGCTAATG ACGACnAnT 239

(2) INFORMATION FOR SEQ ID NO: 3213:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3213:

CATCCTCAGA GTAGGAATAG CCATACCATC GAATAATTCA CGTACTGTTT CGAATTGAGG 60
 5 TTCAAATTCT TGAGTTGTAT AGAGCTCGAA AATnTTTGCC CATTAGCATA ATCAGACTTT 120
 TCAAAAGTCT TGATATTTGA TACCCACGCT 150

(2) INFORMATION FOR SEQ ID NO: 3214:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3214:

20 CTAAGCATTG GTTTAAACTA ATGTTTCAGAG CTTnTGTGG TTTGTAAAnA CAAGTATATT 60
 nCGAGAACAC GTTTTGTAT AGAGTCTCAA TTATAAAAGT TAGAATAGTT GACAACAGTG 120
 TTACGATATT ATTAAACAAC TGTcTATCAT TAACGAAAGC AATTAAACAAG AGTACTtGTT 180
 25 GTGAAATCAT CGTTTAATAG TCAAAGATGA TCATCGTAGG gTAGACAACA TATCaTTGAC 240
 TtAAGGAAGG GGAATGACCG ATGGGATTAA AAGATCAAGC TGTTACCTGG AGAAGGTATT 300
 TTCATCAATT TCCAGAACTA TCCGATAAAG AATTTAAGAC TACACAAAAA ATTAAAGATA 360
 30 TTTTAACAGA ACATCATATT AGAATATTAG ACTTACCAC 399

(2) INFORMATION FOR SEQ ID NO: 3215:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3215:

CAGGTGAAAG CACAAGAGGA TTTGCTGTTT ATTTCTCTCC TGAAATTAAG AAATTCATTG 60
 45 CAGATAATTT AGATAAATAA TTAAACTTA GACATTCACC CAATCCTGAC AAAATATACT 120
 ATAAC TAACA TTTATTAATA TATATTGCAT TATTTAATAT GCATCAAAGC CAATCAACGr 180
 50 TTGATTTTCA CCAACTCAAT TGTGATTGG TTTTATTTAT GTATGAATGA ACAACTTTTT 240
 GACATCATTA AGAATATAAA TGC GTTTGAA AGCATTTGAA AGChACAACA TTTCTATAAA 300
 ATTTTTCAAT AACAAATGCG CCACTAAAAC TCAAAATTTc CACCACCAAC ATCCAAATTA 360

55

(2) INFORMATION FOR SEQ ID NO: 3216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3216:

AGTTGCATCA ACTGAATCCA ACGCTACGCA ATACGAATTA TTCCAATCTG GCATGCGTGT 60
 TGGTAGAGAA ATTTTAGCGA CATCTCGAGC ACGGTTTACC TTGCCTTTnT TGGTGGCCAA 120
 CTTGCTTTAT GCTATGGGTT TTTCAAACCTT AAA 153

(2) INFORMATION FOR SEQ ID NO: 3217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3217:

CTTTGCATAT TCTGGTTTGT AGTATTCATG GTCCGTCAAT TG TAGACCCA TCAATTGCAG 60
 CCATTACATA TGCGGAATAT CGAAGCGAAC TTCAAGTTGC TTCAAGCTGG TAGAACACGC 120
 AnATAAAATT ATTACATC 138

(2) INFORMATION FOR SEQ ID NO: 3218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3218:

CACTCCAAAC CAAGGATTTA CGTGCTTTAT ATnGAGGTAA AGCACATCAT GTkGTTaATT 60
 TTATGCMTTT TaTTGCMcMa GraTTAaGAG AAATTTTAGC nTCTTTAGGT TTGAAACGTG 120
 TAGAAGACTT AGTTGGAAGA ACTGATTTAT TACAACGATC aTCAACATTA AAAGCGAATA 180
 GCAAAGCGGC TAGTATTGAT GTTGAAAAAC TGTTATGTCC TTTTCGATGGG CCAAACACAA 240
 AAGAAATTCA ACAAATCAT AATCTTGAGC ATGGATTGA TTTAACAAAT TTATATGAAG 300

AACAACGTGA TGTAGGGGTT ATTACAGGTA GTGAGATTTC GAAACAATAT GGAGAAGCAG 420
 GACTTCCTGA AAATACAATT AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTTGACAG 480
 5 ATATGCA 487

(2) INFORMATION FOR SEQ ID NO: 3219:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 176 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3219:

ACCAACTCGG AATCATGCAA TGAACACCAT GGTGAAATA AGTGAATTGC ATAAGTATCC 60
 20 TGGCCTGGCA ATGCTGGTAT AACCTAAAAC CTTGTTGCAC GAAATGTATT CGCTACAATT 120
 AATGTACCTG CAAAACCGTT TAATAAGAAG TTCGAAATCG TTGCACCTGT ATATGG 176

(2) INFORMATION FOR SEQ ID NO: 3220:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3220:

35 CTGATTTAGG TAATCTTTC GCAATTGTTT TTTTACAGTT TCGGCAAATG GGTGCCCnGG 60
 CAAATAAATA TTGGCTATGC TCAAACCTGA ATTAATGGTG GGTGTGTCCG CCATCGTAAT 120
 TGGGnCCGCC TGAAGGGCCG CATATAAATG ATAGTGCTCT TCCGAATAAA AGGTAGGCCA 180
 40 TATGTAATTG TTTTGTGGTT ACG 203

(2) INFORMATION FOR SEQ ID NO: 3221:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3221:

AGCTAAATCT TGCCAATATG GTATCAACTT TTCATTCCAC TGATAATCAT AAATTTTCAGA 60
 55

GCAATGCCAG AAATGTATTA ACAACTGGCA CGTCTAATAG ATTGCTAACG GATTGTTTAC 180
 GTACGTTTCAT CGGCTTCTTT CGCTTCTATC GGATCTGGAG AATTGGGATG TTATGACCAC 240
 5 TGAACCACTT ATTTGTAAGC TCTGTCGTGA TTGACTTCAT AATGCTTGCG CTTGnCCTCA 300
 TTTCTAACAA CTCATCCTAC TTACnAAATT ACCCCnGGGG TACACCTGGT CCACTTCATC 360
 A 361

10 (2) INFORMATION FOR SEQ ID NO: 3222:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 152 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3222:

GGGGCTCCGn GGAGGCAAGG GTAGAAAATG ATGTAAACGC TGCATTACTA GGCGAATTGA 60
 AATTACATCA ATATCAAGCA GAACGGATCT TTTGTATGAC GCTTGGTACA GGCATTGGGG 120
 25 GTGCGTACAA GAATTAATCA AGGTTTCATGT TG 152

(2) INFORMATION FOR SEQ ID NO: 3223:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3223:

TTTGTTAAAT ATAGGCCCTG CAATGAGTGT ACTGGAATGG CAATAATCAT ACCATACAGT 60
 40 AATACATCTC CAACATTTGC CTTnAATTCT TTTCCCATGA CTACCGGTCC TGGGATGTGG 120
 TGG 123

(2) INFORMATION FOR SEQ ID NO: 3224:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3224:

55

TGGTTGGTAA CCGTAAATTA ATGCCTGACA ATGATATTAG CTnCTAAGC ATATTTCTGA 120

TGATTTAACA CATTATGAAA CGAGA 145

5

(2) INFORMATION FOR SEQ ID NO: 3225:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 129 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3225:

GGTATTGTCT AGTCAATTAC TAACACCATT TAATTGTGGn AAGCAAAGC TAAAGGTTAT 60

CGTGCGCTAT TGCAGGCATT GATGCTTCCA ACAAAGTCGA GTATTCAGTT GCATCAAAAG 120

20

TTTGCTTTT 129

(2) INFORMATION FOR SEQ ID NO: 3226:

(i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 170 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3226:

GACACTACCG TTCCACGTA GCATCAATCG TCTCAGTCGC ATCGTAGTCA TCTGTATGTG 60

35

TTCCAGCATA TACAATTTTG CCATCTTTAA TGACAACGTA CCATTTTCAC AACATTTATT 120

CATCTAnTCC TACCCTCAAA GTTATCGTTG ATCTCGTAAA TAGTCGGCAA 170

(2) INFORMATION FOR SEQ ID NO: 3227:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3227:

TTACTGCTTT ACGTTTATCA TTTTCTAATT CAnAAATTCG TCATTCAGTT TCAACTTTAT 60

50

CGACAGCTGG ACTTTGCGCA GATAAATGTG CTGCTGTAAT ATCTAACACA TCGATTGCTC 120

TTATCTGGCA ATAATCGTTG 140

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3228:

GCGCCTATAA TTGCGCTACT TGATTTAATT GAGTAGATAA ATCTAATCCG AATAAATCCG 60
 TGACTTGCTT GATAAATAGC AACAATGCTn CAACTAAACC AGTTAGTACT GCTTTGTTTT 120

(2) INFORMATION FOR SEQ ID NO: 3229:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3229:

GGCTATACAC CGACTACAGT AACATCTGGT AGCGACATTG AAAAAGACTC TAATGGTTTA 60
 ACAACAACAG GTGTTATTAA TGGTGCTGAT AACATGTACA TTAGATAGTG GntTCTACA 119

(2) INFORMATION FOR SEQ ID NO: 3230:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3230:

TGGGAATAGC AACCAACAAT GCGACAACAA AGCCCGCTAC AAATCTCCAT nAACTAATTG 60
 CTAAATGTTG GAAAAATTTC TCCAGTCAAC AATGAAAGGC CATATGACTT TTTCTACAA 120
 GAGCAGGG 128

(2) INFORMATION FOR SEQ ID NO: 3231:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATGCAGCTA TTACTTTTCA CAGATTCCAT ATCGTTCAAC ATTTAAATAG AGAACTTAAT 60
 AAGTATCGTG TACAAGTTAT GAATGAnTAC CGTAATAAAA AAGGACCTGA TTATACAATT 120
 5 TTC 123

(2) INFORMATION FOR SEQ ID NO: 3232:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1656 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3232:

GCCTCAAAGA ACATGCTGAA CAGTCATCGC aTTCATATAG TTTGAAGTCT CGTTTAAAAC 60
 20 CATATCTATC ATTACGGTAT GCATATCTTT TAAAACCTAT TCTTTTGTTA TTAGGACATA 120
 TAAATTCATC ATTAAGTTTCG TCATATTTCC AATTTTGAGT GTCGAAAATG TCACTTTTAA 180
 ACTTTCTAGT TTTATCTTTA ATAAACATGC CATACGTAAT AAGTGGCGTT TTATTAAAAT 240
 25 CATCTATAAT GGCCATATAG TTTTGCTCAC TACCATAACC TGCATCAGCT ACAAATAACC 300
 GAAGtATTTT GAATCATTGT TAAAAATGGA ATTAAAGTTC TAGTATCTGT CGGGTTTTGA 360
 30 AATAGGTCAT AGGATAAAAC AAATTGAGAA TTTGTCGCTA TTTGTAAAT GTATCCTGGC 420
 TTAAGTTGGC CATTTTTTCAT ATGGTCTTCC TTCATTCTCA TAAAAGTTGC ATCATGATCA 480
 GTTTTAGAAA AaCTATTTCT ATCTTTAAGA ATCGATTTTT GTTCTTCATA TTTATTTTTT 540
 35 CTTTCGGAAT AATCATCAA TTTmTTTTTG AACTTCTTAA TCTTAGTTCT TTTTtaCGGG 600
 TCTGTTTTCT AATTGAGTA CTATCTTCGT TCTCAATAGA ATGATTTAAA yCTTCGATTT 660
 CTTTATCTAA ATGACTACCA ATTAAATCTA TTTCTTCTAT TGTTAAATCG CTATCTCCAT 720
 40 CTTCTTTTAT CTCTGGTATT ATTTTTTCTT CAACTAAGTC ACGATATAAT GTTTTTGAAT 780
 TTTCTGTTCAA TTTGATTTCG TGATTTTGAA TACTTTTCTT CCACACAAAT GTATACCTAT 840
 TGGCATTAGC TTCTACTTTT GTACCATCAA TAAGATTTTG CTTTAAACAT TGAATATGAA 900
 45 ACTGGATAAA TAAAGATTCA ATTAACGCAT CAGTATTAGG ATTCACTCTA ATACGATTAA 960
 TAGTTTTATA AGAAGGTGTT TGATTTTGAG CTAACCACAT CATTGGAATA CTGTCATGAA 1020
 50 GTAATTTCTC TATTCTACGA CCAGAAAATA CAGATTGAGT ATATGCATAT AAGGTGATTT 1080
 TTAACATCAT TTTTGGATGA TAGGATGTTG CGCCACGATG ATGTCTGAAT TTATCGAATT 1140
 CGCTATCAGG TATCGTTTCA ACAATTTTCAT TAACATATCG CGAAATATCA ATTTGAGGAA 1200

55

GGCACTTCAT TAATTTAGTT TAGTGGTATT TATTAAATTA TACGAAGGGA CCCAACACAG 1320
 AAAATTCAAA TTATTGAATT AAACATTTAT GTGCAAGTTT GGCAAAGTGT CTTATTTTTT 1380
 5 AAAAGTATGT AAAAGTAAAA TTACATGTTA ATACGTAGTA TTAATGGCGA GACTCCTGAG 1440
 GGAGCAGTGC CAGTCGAAGc CGAGGCTGAG ACGGCACCCT AGGAAAGCGA rCCATTCAAT 1500
 ACGAaGTATT GTATAAATAG AGAACAGCAG TAAGATATTT tCTAATTGAA AATTATCTTA 1560
 10 CTGCTGTTTT TTTAGGGATT TATGTCCCAG CCTGTTTTTT GTGATTTTTA ATAATTTGAA 1620
 TATGGrAAAT GTATTAWTct CTCATTTGTA TAGATT 1656

(2) INFORMATION FOR SEQ ID NO: 3233:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3233:

25 TTGCTCATAA ATCTTTTCTT GGCGCTCTGA ACACTATCTT CTATTCTGTC GGAATTTTTC 60
 AAACATAGTC TTATCATTTn CTTCTAATCG CGTTAAACGC CAATCTTGTT CATGTCGTTT 120
 GGTAAATCCA 130

(2) INFORMATION FOR SEQ ID NO: 3234:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3234:

40 GCCACGATAA AGAAGTAAGA ACAACACATG GTGTTACTGG TACAGGCTCA TGTTCTTGGG 60
 AAAGTTATTT GTGnAAAATG GTGTGAATTA CCTGGGGAAA AATCAACAAA CTGACTATCC 120
 45 AA 122

(2) INFORMATION FOR SEQ ID NO: 3235:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3235:

5 AACCAGGATA TGAAATCTGT GACTTATTGC GTTAGATCGT TTTGTAAGTCT ACTATTGA 60
 AGAAGCAGAC CAATATAAAG GTACCATTCA TTGCAAAAGC ATTACATGCA TGAACCCAGT 120
 TGACATTTAG TTAGAGATGG AAGATAGTAT TGTGCATTTG CAGnTTCCAC ATG 173

10 (2) INFORMATION FOR SEQ ID NO: 3236:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3236:

20 GCGGTGTGCA TTTGAAAATG TTATCAAGAA TATTGAGTTA ATTCGCAACG ACATTATACC 60
 AGCGATTAnA AAGCATTTAT CAAAATACGA GGGGCGTCAT CATGAATATT GTATTATTGT 120
 CA 122

25 (2) INFORMATION FOR SEQ ID NO: 3237:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3237:

TTTTTTGCCC AAAATTTTTG GGTTTTTTTT GGGTTAAAGG AAAAAAAATT TTAAAGGGG 60
 GGGGGGGGTC CCCCAAAAT TTTTTCCCT TCCCTTTGGT TTGGTTTTTT GGGGGGGGGG 120
 40 CCCCCCCCCT TTGAAAACC CCTTAAAAA ATTTAAngGT TAAATTGGAA AAAAAAATT 180
 AA 182

45 (2) INFORMATION FOR SEQ ID NO: 3238:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3238:

55

GATGAnGTTTC GACAACGTAT TGTGGCAGAT GTTGCA GTTG ACTTTGAAGA A

111

(2) INFORMATION FOR SEQ ID NO: 3239:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3239:

15

AGTTGATCGT ATTTTCCAGA AGAGACAGAA TTAATTGATT ATCGTGTTAG TTCTGTCACT

60

GAAGGTACTG ATGCCCAAGC AGnAGTACAT GTAAGTTTAT TGATTGAGGT AAGACTGTCA

120

(2) INFORMATION FOR SEQ ID NO: 3240:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 127 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3240:

30

TACACATCTn TCTACGATTG TAGTTTATCG ATAGGTTTCG CATCATGAAA CGTGATAAAC

60

AACCAACATG ATGCTAGTTT GATTAAAGTTT CTTCTAAACA GACTTCAAAC GGCAGTGTTT

120

AGCATAT

127

35

(2) INFORMATION FOR SEQ ID NO: 3241:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 124 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3241:

45

GACTAAAATA CATGTTGGAA TACTTGGTCC CATGGGAAAA TATTGGACTG GGTAACCCAA

60

TCACGGCTTC TGAAGTAGTT CTTTnTCTTC TATTAAAATA GCGACGGAAT CACACCTTCT

120

GCGG

124

50

(2) INFORMATION FOR SEQ ID NO: 3242:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 122 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3242:

TACGTGTATA CACCGTTATC TTTATGGCTT TGAATTTCCA TAATAAATAC ATACGGnTTT 60
TGTGCAGAGC TCAGCACATA ATCATCTTTA ACTATAGTTT CTGGGAATCA CTTCATAGTT 120
TT 122

(2) INFORMATION FOR SEQ ID NO: 3243:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3243:

AACCTTTTCT GCAACCATAC GCCATAGgTA TGtTTTCTTT TTACAATTAA AGaGCCAACC 60
GTTGTTATAG TCTAACAATG GTTGGCTCCT CTTtTTTtTAT GTGCTAAAAA TTTATAGGCA 120
ATTTTATTAC AACAAATGTAC ATTTAAGGTG ACCTTCATGC CAAAATCGCA TCACTCATTT 180
AATGGAAGCA GCACGTCTTC ATACAAAGTC ACGATCCTAA T 221

(2) INFORMATION FOR SEQ ID NO: 3244:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3244:

TTGCATTTTG ATTGTCTGGT GACCTTGGCA ATGACAATTC CCGCTTGCAA TCGGTATCTT 60
CAATATTATA ATCAGGTCTT GCCTTAGATT TTCGCTAAGT ACCGGTGATT CTCTACCATC 120
ATACTCACCT CATGnGCTAT TTTTCTAGAG TGCTTCTTTT CACACTTTAT CTTATAAAAG 180
GCTAGCTACT ATTACCGATT TATCATTATT AGTGGTTTTT ACCn 224

50

(2) INFORMATION FOR SEQ ID NO: 3245:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3245:

GAAAGAGATT AGTGACAAGT TGGTTGTACT ATTACGTTAA AATTGGAGA TTATGTGTGG 60
 TGTTCAGTA TCGGTTCAAT AATTGATATT GCGCACCCT ATAACCATGT CAAAGTA 117

(2) INFORMATION FOR SEQ ID NO: 3246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3246:

CTACAGGCTT TCGTACCACA GGATCAAAAC TACGCACTGT GCCTGTGACA TACGCATGAT 60
 CAGCAATGAC ATTCCAAGTA TTACCACATG ATATTGnCC AATTGTTACT ACCGTTC 117

(2) INFORMATION FOR SEQ ID NO: 3247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3247:

TACACAnCTT TCTACGTGTG TAGTTTATCG ATAGGTTTCG CATCATGAAA AGTGATAAAC 60
 AGCCAACATG ATGCTAGTTT GATTAAAGTTT CTTCTAAACA GACTTCAAAC GGCATGT 117

(2) INFORMATION FOR SEQ ID NO: 3248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3248:

CCCGTCCTTT GGTGGAACCG TTTTGTAGAA TTAAATAATA TTACAGAGCC GCTAGCAGTA 60
 ACGATCCAAA CGAATTTACC ACCATCACGT GGATTAGGAT CGAGTGCACT GTCGCGGTTG 120
 CnTTTGGTCC TGCCA 135

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3249:

AAAAGCCAAC CCATGnAATG TTGGATTGGC TTTTTCATG CCATCTGAAT CTCTAATTTT 60
 AAAAAAATAT GGAATATAAA TAAGACAGTA AAAATTAAAT TTCAGT 106

(2) INFORMATION FOR SEQ ID NO: 3250:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3250:

AACGCTGAAG CAGATAAAAA ACGTCGTGAT AGAAGTAGAC TTAAGAAACG AGTCTGACAn 60
 TCTAGTATTC CAAGTTGAAA AACTTTTAA CTGTATTTAG GCGAAAATAT CGGTGAAGAA 120
 GA 122

(2) INFORMATION FOR SEQ ID NO: 3251:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3251:

GAACGTTGAG ATGTCACAAA CTGGTGAAAG TGCACGTTCA ATGCCAATGA CTGATAAAAC 60
 CAAATTCATC AATCACAATT ACTCCGAAAG CnGGTACAGG TCACTCAGTA AGTAGTAATC 120
 CCAGTACATT AA 132

(2) INFORMATION FOR SEQ ID NO: 3252:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3252:

GGAAAACTCTT CAAATTCTGC AAATTGCCAA TTTACCTAAT AACCAAACAT CTAAGGCATG 60
 5 TGTAATGCTG CTACnTCCGC TTCGTCATCA GCTACAATGA CAAATACAGG TGCCA 115

(2) INFORMATION FOR SEQ ID NO: 3253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3253:

TTTCGTCAAA TTATGGGAAT AAAATAATCA TATTTAAGAT AGTAAATATT GAATAAGTTG 60
 20 CTTTGAAATT TATAAAATGA AAGTATAGTG TCATGGGnAG TATAATAGTC AGATATATAT 120
 GTAACGGCAC TATATTGAAA 140

(2) INFORMATION FOR SEQ ID NO: 3254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3254:

AAATCTCCTA CTTTTTCTAC CCATAAATAA TTGGCTAACT TTTTCATCTT ATCTTCATCC 60
 35 TTTCTCTTCT ATTTAAATG CTACAAATAA ATTTCCGCGA GTAATTTTAA TGTTTTACAA 120
 CGCTGTTCAA TACCTGGAAT AAGCGGTGCT ACTAACACCT CATCAACTTC ArACGTAGCA 180
 40 ATGAAATCAT CTAATTGTGC TTAACTTWT TCTTGTGTAC CTGcAATGAT GCGTGCTTGg 240
 ATGTGCTTGA ATCATCTCTT TGTCTCGATC ATTAAGCTTA TACTTTTGTG CTGTGTCTAC 300
 TGAAGGAAAA TCTTCAAATT CTGCAAATGT AATTTACCnA ATAACCAAAC ATCTAAGGCA 360
 45 GTTGTAAGCG GCnACTTCCG CTTCGTTATC AGCnACAAG 399

(2) INFORMATION FOR SEQ ID NO: 3255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3255:

ACCATTCGTC AAAATATTCC AACACGCATT TAGGTGTGCA AGGTATCGGT ACCTAACAAAC 60

5 GAAGCTATCG TCTCACTAnC CTTAAAAGAT TTTAGAACAA CAGCTGCACT CATCAT 116

(2) INFORMATION FOR SEQ ID NO: 3256:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3256:

AAAGACCTAA GGTTATGTAA TTGGCCTAAA TTTATTAATC GTTTAAAnTC AGTTAGTAAA 60

20 AAGTCTGTGA GTAAGGGTGT ATGGAAACTG GTTAAATATT ATAGAG 106

(2) INFORMATION FOR SEQ ID NO: 3257:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 114 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3257:

AACGTCCATC GTAATACCTT TTGTGTCTAA TGTAACCTGT ACATCGTCTA ATAATAAGTT 60

35 GACGATATCT TGACAAATGCA TCTTTATCTA GATGTAAGAn TTCAACGGAT GCCG 114

(2) INFORMATION FOR SEQ ID NO: 3258:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3258:

TTAAAGCAGT TAATCCACAG GGAAAGTGGT TAATACAGTT GGGCTCTGGT GGATAGTACA 60

GTTGCAGGCA TGGTGGGCTG GGAATTGCTT CAGGGTTTAA CGAnTGGGAA AAGCCTT 117

50

(2) INFORMATION FOR SEQ ID NO: 3259:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 124 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3259:

GGACCGCCAT ATCGTTGGCA ATCATCGCAC CTATAATCAT CGCAAGTATA ATAATATTAG 60
CACCTTGCAT ACTTTTTTAAC CAGGTTGTTA ATGCCTCAAA AATATTAGAA ATTGGTGCCC 120
GnTT 124

(2) INFORMATION FOR SEQ ID NO: 3260:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3260:

TACCAATGTA TATCCATATA CTTTTATCAT AATCATTTCA GCCGACTTTA GTTTGATGTT 60
TTTGCTTGAT TAAAATCTTT CGGCGATCTT CAGCTTGATG TTTTCGTTTG ATTAAATTGG 120
TACAATAnAT 130

30

(2) INFORMATION FOR SEQ ID NO: 3261:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3261:

GGCCTTTTTG GGCCGGGGTT GGAAATTGGG GTTGCCTTAA TTTTTTAATT AAATTTTGGG 60
ATTAAAAAAG GAAAAAnTCC AAAGGTTAAT TTTAAAAAAA GCCCAAGGTT TTAAAAATTC 120
CCCCAACCAA AAAGGGGGGG AAAAAGGTT GGGGGTTTTA AAAATTAnCC AAGGTTTTTG 180
GGGCCCTCCC TTGGGGGTG GGAATTAAAG GTTAACCAAG GTTTTTGGCC AAGGGGCCCA 240
ATTGGGGGTT GGGGCCCTGG GGGAAAATTT TTGCCCTTTC CCAAGGGGTT TTTTAAAACC 300
CGGATTTTTG GAAAAAAnAA AGCCCATTTT CCCCCCAACC CnAAAGCCCA GTTCCCGCCC 360
ATTTCCCGG GGTAAACCCTG CCCCCACCGG GGCCATTTTT 400

50

(2) INFORMATION FOR SEQ ID NO: 3262:

55

(A) LENGTH: 134 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3262:

10 TGGTTCAATG GAAACGTGTA CCGCAAATnC CGTTAAATGT TGTTGGATGT TGAGAGACGT 60
 GGCTGAACTG GCACATTG GCAATGACCA ATGGAACAAG CTAATGGGCA AGCGATTATT 120
 GCGACGGCTG ATGG 134

15

(2) INFORMATION FOR SEQ ID NO: 3263:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3263:

25 TTTTTTCTG TTGGTACTTG TTTTGTGGTT GGCGATTGTG GTGTGTCTGA nTTAGTAGAT 60
 TGCATTGGTT GTGGCGTGTG TGCTTGATGG AGGTGTTGTC ACTTT 105

30

(2) INFORMATION FOR SEQ ID NO: 3264:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3264:

40 GTTCCATCAT TCCCACnAT ATCCAACATG TGGGCTACTG CAATGCTTTA GCGTCAATG 60
 CCTCATCATC ATCACAGCGC CAGTAAATGC GTATAATTAA ATTAATT 107

45

(2) INFORMATION FOR SEQ ID NO: 3265:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3265:

55

GTCGTAACAA TGGTTCGTTA CCAAAGCATA NTTGCGCTTC TTGGCATCG

109

(2) INFORMATION FOR SEQ ID NO: 3266:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3266:

15

TTACCTTTAA AATAAaGTTT TCCACTAGTT GGGCTAAACA AATTACATAT TTTGCTTTTG

60

GAAATGTACT TTTTACCACT ACCTGATGGA CCTATAATGG GCAA

104

(2) INFORMATION FOR SEQ ID NO: 3267:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 117 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3267:

30

TAAGCCATCA GAAACAAATG CATATAACGn AACAACACAT GCAAATGGTT CAAGTATCAT

60

ACGGTGCTCG TCCGACATAC AAGAAGCCAA GCGAGAACGA ATGCATACAA TGTAACA

117

(2) INFORMATION FOR SEQ ID NO: 3268:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3268:

45

GCTGCACAAG CACAACCTGG AATCAGCAAC ACCGGCAAAC CAnCAGGTCA AGGAATAACC

60

AAGCAGCACC TCATAATAAT GCAACACCGG CAATCAAACA C

101

(2) INFORMATION FOR SEQ ID NO: 3269:

50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3269:

5 CATACCCTAT TTTAGATATT ACCTTATTAC AAAATATTTT TACATTAATG TCAGCTGCAG 60
 GTTAGTATTG TTTTCCAAAA TTTACCGGTC ATCTTTGCCA ATTGGGTGTC GCCAATCGGG 120
 ATTTATCCTA GGAAGCCGAT TAAAAGGGTA CTGCCAGGT TTTAGCCTGC nGCTGCCTCG 180
 GGGTTTTCTT TAAATTAATG nAACCGC 207

10 (2) INFORMATION FOR SEQ ID NO: 3270:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3270:

ATATTGCGAC CACCATAAAC ATAGATGGTG TTTTGTCTT CTGCATTCAC AGTGATAAAA 60
 GGGCTTGGnC CCGTTTTTGC TTCAGCTGTT TTGAATAATA TATGATG 107

25 (2) INFORMATION FOR SEQ ID NO: 3271:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 122 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3271:

TTGGTTACAC TTCTGCTAGT TTTAGTAACG ATGGTCCAAG ATTGTATGAG CCTATTCATG 60
 GATCAGCACC AGATATTGCA GGTAAAAACG TTGCCAATCC ATTTGGGATG GTTCTnATGC 120
 TT 122

40 (2) INFORMATION FOR SEQ ID NO: 3272:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3272:

GAAGGATGAT GATTCGGAGC AnCTTCTTGC AGAAGAnGCG GnAATAACGT GACATATTGT 60

55

TGCGAGCGCT TGACAATCTA TTCTTTTAA AGAAAGCGGT TGTTAGACAA TGCATTAAGA 180
 GAAATTAAAG CGGmGTTTAC TTTTGTAAT GAGCATTTGA TTTTtTGAAA ATAAAGCAGT 240
 5 ATGCAGGCGC TTGACTAAAA AGAAATTGTA CATTGACAAC TAGATAAGTA AAGTGAAAAT 300
 ATAGATTTTA CCCAAGCAAA ACCGAGTGAA TAAAGAGTTT TAAATAAGCT TGGATTCATA 360

(2) INFORMATION FOR SEQ ID NO: 3273:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3273:

20 TCAATTTTAA CTGCAAATAA TAAAGCTGCA TGATTACTT TGTACATTAT TGTAATTTCA 60
 GTAATACGAG GCAATGTCAG TnGCAGTGTT TAATAAATTT TGTTGCTAT TT 112

(2) INFORMATION FOR SEQ ID NO: 3274:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3274:

35 TACATTTATG CAATCAACGT TACATTCAAT CGTTGGAGAA AATTGGCTTT ATTGACTTAC 60
 TAAATCTAA AAAATCATAT GAAAGAATTG CACATATGTT AAAAActGGT AAGCCATTAC 120
 GTAATTAAAA GATAGTCATT AAGAGAGGAT GATAACCATG CAAGAAAGCA TACATTGTAG 180
 40 CTTATGGGCG TTCAGCGCAG CGAAAGCAAA GCAAGGCGCA TTATTCCACG AAAAGACCTG 240
 nTGATGTCGC AGCCAAAGTA ATTACAAGGC GTATTTGAAA ACGTATTGAC GGGAnAAATT 300
 CCAATAAGGA TTATGGATTG nAAGATGGTC CATTTG 336

(2) INFORMATION FOR SEQ ID NO: 3275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

CAAATGCTTT TGCCACCCCA GATGCAATGG TACCAACACC TGTTTTCGAA ACTAATTTTA 60
 CCGGCGATAT CTGGCATCTT TTATTTTCGGC ATTTTTCGAA ATCATGGTTA TTCCAGTTTG 120
 5 GCGGCTTAAA AATTChTT 138

(2) INFORMATION FOR SEQ ID NO: 3276:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3276:

CATTATACGA GnATAAGTAA AATTGATGAT GTGACTAAAA AAGATGCACA ACAATTATTG 60
 20 AAGATGCAAA AGAATTGCAT GCCAAGCTGA TACATTAGAT A 101

(2) INFORMATION FOR SEQ ID NO: 3277:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3277:

TGGTTATTCG TTCCTGATCG TTGTTGGTAT CTCACTATTC AAnATTATC GTGTGGCATT 60
 35 ACTTTAGTTA CACCAGGTAC ATTTGAACCT GGCACTTGTT GCGAGTATTT CCGGTCTCGT 120
 CATT 124

(2) INFORMATION FOR SEQ ID NO: 3278:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3278:

GACTTTTTGA CCAGTTGTAG CACGACCACC GAGAGTAGCA TTGCATATGC AATCATTGTA 60
 50 CCTTCGCCAA CGACTGnGCC AATATTAATT GTTGCGCCCA TCATAACGAC 110

(2) INFORMATION FOR SEQ ID NO: 3279:

(A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3279:

10 TTGGTATATA GAGGGCAACC GCACCTGATA AAATGTGnCA CAGTTTTTAC AAGAGGTTAA 60
 GGAATGAGTT TGGAGGCATA CGAGCATCAA GATACCATTC GATGTTAGTA ATT 113

(2) INFORMATION FOR SEQ ID NO: 3280:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3280:

25 TTACCGTCAC CGTAATCAGT CCATACTTTA TCAGCTATAC CGGCTTTAAC AGCATAAATG 60
 TTCGTTCTCG TAGGCATACC AAAGnCGATA CCATAGTGAC G 101

(2) INFORMATION FOR SEQ ID NO: 3281:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3281:

40 ACTATGTTTG AnAAATTCGA CAGAATCAGA AGCACAGTCT GAGAACGCAA GAAAAAATTT 60
 ATGACAAGTT AGATAGAAAT TTCGACGAAC TAAGGGCGTG ACCAAGAAGA AGATGA 116

(2) INFORMATION FOR SEQ ID NO: 3282:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 148 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3282:

55 ACTTGGTTAG ATAATATAGC GTCGATTGTA TCACGAGTGT CTGTTCCAGT CATTATAAAA 60

CGTCGTTCTG ATGCTTTTCC TGAATCAT

148

(2) INFORMATION FOR SEQ ID NO: 3283:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3283:

15 AAATGACGAT AGAGTCAGGT ATTAATCAT TTTnCAATAG TATCAGGAAG ACTACCAAGC 60
 TTATGTTGAA GGGCATCTTT TGGCGTTACC GGGTTGGGCA 100

(2) INFORMATION FOR SEQ ID NO: 3284:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3284:

30 TTAAGAAACC GAGCAGCGCA TAAnCCTGCA GTACCTTATC GCTTCTAGAT AATCCGATTG 60
 CGACACCATT GCAAGATGAC CGGTAATTTT GGAACATATA C 101

(2) INFORMATION FOR SEQ ID NO: 3285:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3285:

45 TAAATATTT CGCATCCCTA CACGCTAAAA TAATACATTA CACTTAAAC GGCTGTTTTA 60
 AAGCATCCTC CCATAACAT CATCTAGTTG ATAATAGGGG GGGGGn 106

(2) INFORMATION FOR SEQ ID NO: 3286:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3286:

TTTAACAATA CCTCAGAACA TACTATGGAA ATTGCTGCAA AGTTAATTGG GCATGCATAT 60
 5 TGATCATAAT GCGCTTTTAA ATAAAATGGT GGAGA 95

(2) INFORMATION FOR SEQ ID NO: 3287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3287:

TCGAAATAAT ATCTACGCAC ACTGATAACA TAAAAATGCC TGGTAGAATA CTAATGAAAT 60
 20 AAGTGCATAC ATGACCACAT GAATGCTAAT AACATGCnAG AACCCATTTT TTGAATATTT 120
 CACCACTCGA ATCATCAATA C 141

(2) INFORMATION FOR SEQ ID NO: 3288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3288:

TAGCTGGACC AGAACACGGT TCGACGTTGC AGGAAGTCTT GAACAGTCGC TGAACGCCAA 60
 35 GGCGATACTT GGGTTATCCA TGGTGAAAGn AATGGATTGG TGGTGCA 107

(2) INFORMATION FOR SEQ ID NO: 3289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3289:

GCTTTGCAAT GCCGATGTTA CTCGCAATAA TCATGTCGCA TCAATTACTT ATGGAAAGCA 60
 50 GATTTACGTA TGTCTACAAG TTTAGGCGC 89

(2) INFORMATION FOR SEQ ID NO: 3290:

(A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3290:

10 TGTTACGCCA ACAACAAATC CTACGTCGAC AACTATTTTT AAGCGATGAT TGCAATTAGA 60
CAGAAATCCA ATCATTTTTTG CATTCCATCC AGTGCACAGA ATnTCGAG 108

(2) INFORMATION FOR SEQ ID NO: 3291:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3291:

25 GATCAAGnCC TGAGAATTTA ATTTAATTTA TTTTATATT GGAGATGGTT AAAATGCTAA 60
AACTCAACAT GAGTAACCAA AATATTGCCC TTAAAAATGC TGATCATTG 109

(2) INFORMATION FOR SEQ ID NO: 3292:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 121 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3292:

TTGATAATTT TGATATAGAA AGTTATTTAA AATTCGAATA AAAATAATAA CTCATCGACG 60
40 TTTAATGGCT AGGTTCCAAT CAACTATGnG ACATAAATTC AAATTCGATC ACGTAACGAA 120
A 121

(2) INFORMATION FOR SEQ ID NO: 3293:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3293:

55

GCGCGTAATA CCTGCAGTAC CTCTATCGCT TCTAGATAAT GCGGTTG

107

(2) INFORMATION FOR SEQ ID NO: 3294:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3294:

15 AAAATGTTAA ACCAAAAAGT TTGGTGAGTT ATAATATGGA ATATTAAATC TGTAGAAGAT 60

AAAGCGAATA TAAAGTGATT AACTTTGGTA ATAAAGAATT AACAGCGAAA n 111

(2) INFORMATION FOR SEQ ID NO: 3295:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3295:

30 CCCCCACTAA ATCGAACGCT TTAATGTAAT GATTTGTCCG AATCCCCATC CTGCACCTGA 60

TAATAAGGCG AATAGCAAGT TGGTTCCCGT nGGGAAGCCA CTTGA 105

(2) INFORMATION FOR SEQ ID NO: 3296:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 201 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3296:

ATTTATTCAA AACCCGCCAC ATGGGGCAAC GGTGCCATG GCATGATAGT CCAGATACAT 60

45 GGAAAGGAAT ACAGTCCGGT TAACACTCCA TTA AAAACCT GCGGGTTGGT TAAACCATTT 120

AACCTAAATG GGTTC CAAGG GTTAACGCGG TTAAATGTT TGGAAAGGTT TnCCCAGTTT 180

CCAAAAAGTT TTTnATTCCC C 201

50

(2) INFORMATION FOR SEQ ID NO: 3297:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 415 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3297:

TTTAGACTTT CATCAGTGTT GAATATTTCT CCTTTAACGG TTATAGGTAA TATTCCTGA 60
10 GAAATATTTC CATTCTTTAC ATTTTCGGCT GTCAATTGAT GACTTCGATA AGCAAATTCA 120
TCTTGTAATT CTCTTGAAAC ATCATAATC TKGGCCACAT TTTCAGCACC TkGAATCATT 180
GATGGGTCGC TCATTTCAGG TGCAAATGAT GCACGCTCAT AAAACTCAGG TAATGCTGTT 240
15 TCGTACACAG AATGCGGTCG TTTGATTTTC CAAGGTGCTC GACTTGTAAT TTCAACACCA 300
CCTGCAATAT ATACCTTGCC AGCTCCGGCT TGGATCATGC GACATGCATA TTGAACACTT 360
TCAAGTCCAG ACCCACATTG cCGATCGrTT GTGaCGCCAG TATTGAAGCT TAAGC 415

20

(2) INFORMATION FOR SEQ ID NO: 3298:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 164 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3298:

TTAATTGCAG CAGAGCGACT AGCTGATTCA GAGGTGTTAG TTTGTACGGT AATAGGATTC 60
CCATTTAGGT GCATCGACCA ACTGCCCCGAC GAAAAGCCAT TTTGAAAACC AGAAnGATGC 120
35 CGATTCAAAA ATGGGTGCCA AGATTGAAAA TTTGGACCAA TGGG 164

(2) INFORMATION FOR SEQ ID NO: 3299:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3299:

GTAGATGCCA TTTTCACGTT TCTTAGTTAT TGGCATTTTT TAAATGCGAT GTGTGGCTTC 60
TACATAACGG GAAATTTTAA GTTTTATGAA TChACATATC AATTGC 106

50

(2) INFORMATION FOR SEQ ID NO: 3300:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3300:

AAAAGGTGTT ATGAGATTAG TAAATCANTA GACAAGCAGG TAAATTAAGT GATGTCGCGT 60

10 CATTTAAGGA AGCGATTAC AATCGAGAAC ACAAAGTACA AC 102

(2) INFORMATION FOR SEQ ID NO: 3301:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3301:

TTAAAAGTTT GGAGATTATC GTGTCGTCTT CAAGTATGCG TTCATTAATT GATATTGGCG 60

25 CACCGTATAA CCATGTCAAA GTACCATTG NAATCAGTCA TTGGCGCATT GGCTGCCCTA 120

GCGTTCA 127

(2) INFORMATION FOR SEQ ID NO: 3302:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3302:

CCAGCTAGAC GATTGCTAAG GTATTGGATG TTTGAAACGT CCATGGACCC AATTGATTAA 60

40 TTGGnTGTA CTGGTCAAT GGGTATATCC TAAATGCACT GGCTGCTGG TGTTCTTCTG 120

GGCGTTGCTT CGGAAAT 137

(2) INFORMATION FOR SEQ ID NO: 3303:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3303:

55

ATATAAATTA ACGACGCGTT AATGCAGGCT GATGTGATTT TTATTGGTTT CCCAATTTTC 120
 AAGCTTCCAT CCCTGGTGCT TTGAAAAATG TGTTTGATCT ACTTCCAGTC AATGCGTTTC 180
 5 GTGACAAGGT AATAGGACTT GTAGCGACAG CAGGTTCTAG TAAACATTAT TTAATTCCTG 240
 AAATGCATTT AAAACCAATA TTGAGTTACA TGAAAGCACA TACGATGCAA ACGTATtATT 300
 TATTGAAGAG AAAGATTTT CAAATCAACA AATTGTCAAT GATGATGTTG TATTTCGGTT 360
 10 AAAAGCGTTG GCACAATCCA CAATGCGAAC TGCCAAAGT 399

(2) INFORMATION FOR SEQ ID NO: 3304:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3304:

CACCATTATT TACAGGACCT nCGATGACGT GTGGTCCTGT GTTAAGACAT AACATAATAT 60
 25 TCTACCTTTG TAATCAGTAC GGGTTTATCT ATCACAGTAC GG 102

(2) INFORMATION FOR SEQ ID NO: 3305:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 202 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3305:

TCAGCGTTAT CAATGAnTGA CTCTAATGCC TTTTtACCCA TTTTtGTAAA TGGAACATGG 60
 AAGCATAGAG ATGCGrAGTC AGCTAGCGAC TTACCTTGAC GTTTTtGCGTA TTCATTCCAG 120
 40 CTTTGTGGr ATGAGCGGAT ATAAGCATCT TTAGATAATG CACCATCAAC TAATGGATAT 180
 TTATGTCCAG TTGGACGCCA GA 202

45

(2) INFORMATION FOR SEQ ID NO: 3306:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

AAGATAGGGA TTTACACCTA TACCTCGTTC CGGGGAAGGG TCGGTGTTCT GAAAAGTTGG 60
 AACTACTCCC GnC AAATATT AAATTATGGG AGCGGGAAGG ATCAGGGATT TGACACCTAT 120
 5 GACCTCCATT CCCAGGGAAG GGAATGTGAT T 151

(2) INFORMATION FOR SEQ ID NO: 3307:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3307:

AATTTTCGTTA CCTGCGCCTT CTTTTTGC GG TTTTAAATA AGCGAAAATT TCAGGCGGTA 60
 20 AGACATAACG TCCCAGAATA GCTAGGG 87

(2) INFORMATION FOR SEQ ID NO: 3308:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3308:

ATGATGGCAA AGTCACCAA CTGATTGTGC ACACCAATCC ATCCATCTGC GCTGTAAATA 60
 35 ATGGTTCGCA ATAATTTTAA AATACCTTCC GCTACATTTG ATTTAAAGCT GGTTGCGCAn 120
 TGGACTAGA 129

(2) INFORMATION FOR SEQ ID NO: 3309:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3309:

GTTCCCTTTTA TCGTAGTTGG TGGGACTCCT TATCGGCATC GCGGCTGGAC TCTAGGCGGT 60
 50 GGAnACGGAC ATTCAAAGG GATTTAGTTC ATCCAGATG GATTTCAATT TGGGGAATTC 120
 CATTTGGA 128

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 83 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3310:

GTACGATTCA GCATAAAGTA CACCACATTG GTCACCTACGA CATCTGTAGC TGGTATTGAT 60
 CATGCAATCA TGAATAACGC TAA 83

(2) INFORMATION FOR SEQ ID NO: 3311:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3311:

CTGAGGATAA AGCGTCTCCA AGATAAGTCT AAAGATCATC ATAATGGGCA AAAAAGGTGG 60
 CAGCGATTCT GTGGCTGGGA ACAAG 85

(2) INFORMATION FOR SEQ ID NO: 3312:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3312:

ATTTTATGTC TAAATGCTGG ACCAACAGTA TTGGCTATTA TTTGGTAACG TGATTACTAC 60
 AAAAAATGGA CCGTTGAGTT CGTGGCACAT GATTGATTTT GTAAGTAAGT ATGATGCACA 120
 TGGGCTnTT 129

(2) INFORMATION FOR SEQ ID NO: 3313:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 82 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TCACCTAAAA TTAATCAAGG GACTTAACAT TGGCGAGTCA AGGTATTGAT CAAGCTAATG 60
GCACAGTTAA ATGATGCCAA AG 82

5 (2) INFORMATION FOR SEQ ID NO: 3314:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3314:

15 ATGTTATGGA AGAATATTGA GTTAATTGGC AACGACATTA TACCGGCGAT TAAAAAGCCT 60
TTATCAAAAT AGTGAGGGGC GTCATCA 87

20 (2) INFORMATION FOR SEQ ID NO: 3315:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3315:

30 TGAACCCGTC GTTGCCCAT TGCCGGTTCC CGAAAGCCGG CGCCnACGGT TCTCCCTGCC 60
TAAATAGGGG ATGGAATATT AAACCATCTG CACCTGGTTT AACACGCTTT GCAATTTGAG 120
35 TTAAGACATC ATAAGG 136

(2) INFORMATION FOR SEQ ID NO: 3316:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 base pairs
40 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3316:

45 CATTTGGCTGT GTCCATTTTT AATCGTTGCG AGTACGThTA TTAGCAACTT GGAAGTGCCA 60
TTGTTAATTT CAGCTGTCTG TTACATTTCA ACCATAGTCT TTCACAAT 108

50 (2) INFORMATION FOR SEQ ID NO: 3317:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 142 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3317:

10

ATCTGAAGCT GGGTTTACTA GAGAAGGTAT GTACGTGACA TGAATTACTA ATGGATTTAT 60
TCATCGAGTT ACATCTATAG TTTATTAAAT CAGATACGCC AAAATGCnAA TTAGCTTACA 120
AAGATGATGC ATTAAATGCA CG 142

(2) INFORMATION FOR SEQ ID NO: 3318:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 386 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3318:

25

30

35

AACATTATGT TAATCAACCT AATGAACGtC TTTATAAATT ACGCTAAACA ATATACAGAT 60
ATGCCGTTTC TTATCATGCT GGATGAAGAT GAAAATGGAT ATAAAGCGGG TCGATTTTTA 120
AGAGCGAGTG ACTTAGGTCA AACACAGAG CAAGGCGAAT GGAAGCCAGT TATTCATGAT 180
GCAATCAGCG ATAGTTTAGT AGTACCTAAT GGCACAATGG GTCAACGTTG GGAAGAAGGT 240
AAGAAGTGGA ACTTAAAACT AGAAACAGAA GATGGTTnTA AAATTAnCCC TACATTATCA 300
ATGACAGAAG GTGGATACGA ATTAGAAACA ATTCAATTCC CATACTTTGA TAGTGATGGA 360
GATGGGATAT CATCGTCCAA TCcnAC 386

(2) INFORMATION FOR SEQ ID NO: 3319:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3319:

50

ACAATGAATG ACATGATTCTG AGGTGGACGA CCCCTCCTAT TTTCATAAA TGCTTTTTGA 60
ATCGCCGGTC ATAATGTTCTG TTGnCCAATT AACTCAATAT TCTTCATGAC ATTTTCAAAT 120
GGC 123

(2) INFORMATION FOR SEQ ID NO: 3320:

55

(A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3320:

10 GCGGAAGTGT CAATTGCCGG TATACAACTG ATTTTAAGAG CTGCAGAACA TnCGGGTGTG 60
 AAACGTGTGG TCAATGACTG CCAACTTTGG TGCAGTTGGT TTTA 104

(2) INFORMATION FOR SEQ ID NO: 3321:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3321:

25 GCGCCGGTTT TAACAGGTAA TTAAAACCA AATACTGATA GTAATGCATT AATAGTCAGC 60
 AAAATACAAG TATT 74

(2) INFORMATION FOR SEQ ID NO: 3322:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3322:

35 TCACTCAGGG GGAGATGTCA ATGGGTCAAC ATTATTTGAC AAGGTGTGGA CAGACATGTG 60
 40 TTATACGGGA AATTGGGCGA CCGCACT 87

(2) INFORMATION FOR SEQ ID NO: 3323:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3323:

50 TGCCAAATGT TCCCATTAATT TCATTACGAG TCTTAAGTAG GTGGCTATCA TTACGATGCG 60
 55

AATGCGGTCG GAAAGATAAA TAGCTTCATC AATGTCATGC GTCACATAAA TAATAGTTGA 180
 TTGCGTTTTA TGTTTTAGTT GCACTAGTTG ATCCTGAAGT TTATAACGTG TAAATGCATC 240
 5 TAATGCACCT AATGGCTCAT CCATCAATAT AACGTTAGGC TTATGCACAT GCGCTCGACA 300
 TAGTGCCAAA CGTTGTTTCA TACCCCGGA CAGTTGCTCG GGAAAATGCT TTCCCCTGTC 360
 TTCTAAATCA ACTAATTAA GCTGTGCGTT AATCTCTTCA 400

10 (2) INFORMATION FOR SEQ ID NO: 3324:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3324:

GAAACCATCG ATTGTAGCAC GAACCATGTT GGATTGGTGT GTTTGnATCC TAATGTATTT 60
 ACTTAAGATA TCAGTGATAC CTGTCTAATT GCAAGTACGG TCAGGA 106

25 (2) INFORMATION FOR SEQ ID NO: 3325:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3325:

35 TCTGAAnTCG CTGTCTGAAT CTGGAATCAC TGTCTGAAAT CCGAAATCGC TAATCTGAAA 60
 TCCTGAAATC CGCTAATCTG AAACCTGGAA GTCGCTGGTC TGGAAGCCCT GAA 113

40 (2) INFORMATION FOR SEQ ID NO: 3326:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3326:

50 TGTCACGTAC TTGCTGTTCA ACAAATACGT CTTACTGGAC GTGCACCTCA TTCTTCATCA 60
 TAGCCTTCTT CATTAACC 78

55

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3327:

AATTGAAAAT TATCTTACTG CGGTTTTTAG GGGTTTATGT CCCAGCCTCT TACTCnAATT 60
ATATTCACTA TCCATTAGAC CAAATGGGCC ATTTCCAATA ATCCGCGGT GGTTCCTGA 119

(2) INFORMATION FOR SEQ ID NO: 3328:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3328:

GTGTTAAAAC GTCACGACCT TTGTTTAAAA TGATGCGTCA TAATGTCTAC ACTTTGCTTG 60
CGATCATTCA T 71

(2) INFORMATION FOR SEQ ID NO: 3329:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3329:

CTGACGAACC TTGCATCATT TAACTGTCCA TTAGCTTGAT CAATACCTTG ACTCGCAATG 60
TTAAGTCCTT 70

(2) INFORMATION FOR SEQ ID NO: 3330:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3330:

CCAATCTCG

69

(2) INFORMATION FOR SEQ ID NO: 3331:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3331:

15

GGACACTAAC ATTAATATGG ACTGGTAATG TTGCTGTAA TAAACTCATA CCAAATCCTG

60

GGCATCTCTT

70

(2) INFORMATION FOR SEQ ID NO: 3332:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 82 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3332:

30

CCTTGGGCAC CTTCAATTG CATATTACGA CGTTTTCAG CTGGTTCAA TTGGCAATAA

60

CTACACCTAG TGCAGTTGGA TC

82

(2) INFORMATION FOR SEQ ID NO: 3333:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 76 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3333:

45

ATAAAATAAT TAGAACTCTA ACATTGGTTT AACTAATGTT TAGACTTTTT GTGGTTTGTA

60

AAAACAAGTA TATTGA

76

(2) INFORMATION FOR SEQ ID NO: 3334:

50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3334:

TGGAAGTTG AATAAAGTAT TGAAATCGTT GCCAATATCT TTATACCGTT GGTCCTGGC 60
 5 ATTTATTGGG AGGC 74

(2) INFORMATION FOR SEQ ID NO: 3335:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3335:

AGATAGTTAT GCGCAGTTAA AAACGGTGAA ATGTATTTGC AATAATATGC ATATAGGCAC 60
 20 CATACGAGTA AGGG 74

(2) INFORMATION FOR SEQ ID NO: 3336:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 76 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3336:

TTGAATCATT GTTAAAAATG GAATTAAAGT TGCTAGTATC TGTCGGGTTT TGAAATAGGT 60
 35 CATAGGAGAA AACAGG 76

(2) INFORMATION FOR SEQ ID NO: 3337:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3337:

CCAAAGAGGC GTTATTAAGC TATTGATAAA AGTTATGTGA CTAAAAAATG TATTTAAATA 60
 50 AGTAGTACCT AA 72

(2) INFORMATION FOR SEQ ID NO: 3338:

(i) SEQUENCE CHARACTERISTICS:

- 55 (A) LENGTH: 75 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3338:

ATAAGTCGTT CTACCGTATA GCCGTCATTA TTAATCACAA ATAATACCGG TTTAATATGC 60

10 TGTCTGGTCA TAGTT 75

(2) INFORMATION FOR SEQ ID NO: 3339:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3339:

TTCATCAAAG TATTCCAATG GGAGAAAAG CACAATAACA TTATCACTGG ATGCTAAATC 60

25 TAAAGGAACC TC 72

(2) INFORMATION FOR SEQ ID NO: 3340:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3340:

GTAAAAATAT TTAAATGAAT GTCTTCACTG GAGAACCATT GACAACCTGG TACAAGTGGG 60

40 ATTATTGGCG TTATTTT 77

(2) INFORMATION FOR SEQ ID NO: 3341:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3341:

AACCAAGGAT GGATTGCTAT TTAAATCCTT GGTGCTCTT TATTTTATTT AAATTGTAGA 60

55 ACCTAGA 67

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3342:

CTGGCAAAAG CACGTTTAC AAGCATCAAT CCATTAATTA ATAATTCCAT TAAATGTAGA 60
 TTCACAGGGA TATG 74

(2) INFORMATION FOR SEQ ID NO: 3343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3343:

GTTTGATCAT TAGAGAGATA TAGATATGCC GTAGAAAATA ATATGTCATT TCGGATATC 60
 ATGGTTAAAG AAGAAATGGA ATTAAGCGGT AAATCACGTG ATGAAGTGCG AGCGaATGA 120
 AACAAAATTT AGATGTCATG CGAGACGCAT AATCAAAGGG ACGACAGGTG ATGGGGTTGA 180
 AAGTGTAcGG TCTACACTGG TCATGATGCT GCTAAACTAC GTGATTATAA TGAAACACAT 240
 CATGCTTTGT CTGGGATATG AAATGATTGA CGCACAAGGG TGCCATTGCA ACAAATGAAG 300
 TCAATGCTGC CGATGGGTAT TATTTGTGCA CGCCAACAGC TGGTTCCTCG GGTACCATTG 360
 CCGGTGGCAC TTTTAAATTA GAAAAACAC TGGATnGAAC CAGAAGAGCC AATGn 415

(2) INFORMATION FOR SEQ ID NO: 3344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3344:

TCCTATACCA CCACGTCAA CAGCTCCTGC CATCGATCGT ACTTTCATA AGTCCAATAA 60
 TCGCAGTGGT AATTCTAAT ACTA 84

(2) INFORMATION FOR SEQ ID NO: 3345:

(A) LENGTH: 474 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3345:

10	CGGGAGGTGT TAAATCTTCA CAAATGCCG TACTATTCTT TGATGnAATC CATCAAATTA	60
	TCGGTTCAGG TGCCACAGGA AGTGATTGAG GTAGCnAAGG GTTATCTGAT ATTTTGAAAC	120
	CTGCATTAAG TCGTGGTGAG ATTTCTATTA TTGGTGCaAC AACACAAGAT GAATATCGAA	180
15	ACAATATTCT TAAAGATGCT GCATTAACGC GCAGATTTAA TGAAGTGCTT GTTAATGAAC	240
	CAAGCGCTAA AGATACTGTT GAAATTTTAA AAGGTATTCG CGAAAAATTC GAAGAACACC	300
	ATCAAGTAAA ATTACCAGAT GACGTATTAA AAGCATGTGT TGAATTATCA ATTCAATATA	360
20	TTCCACAACG ATTATTACCA GATAAAGCAA TCGATGTGTT AGATATTACA GCAGCACATT	420
	TATCnGCGCA AAGnCCAGCT GTCGATAAAG TTGAACTGG AGAACGAATT TCTG	474

(2) INFORMATION FOR SEQ ID NO: 3346:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3346:

35	AAAATTAATA ACTCCTTGGT TATTGATATG CCTAAAGAAG AAGGTACAAT ACAACTAACA	60
	TTAG	64

(2) INFORMATION FOR SEQ ID NO: 3347:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3347:

50	AGGAATAACT TGATATTGAT GATAAAATCG TCAAACGGCA CTAATATTTA AAAACAAAT	60
	GTTTTAAGTT GTTGATTAA AATATTAAT	89

(2) INFORMATION FOR SEQ ID NO: 3348:

55

(A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3348:

10 ATAACTTGTA CTGCTTCCCA TTAATCACTG TGTCTCTTCA CCAGGAGCTG GCATTTCTTT 60
AAAGAACAAT TCTGATAAAG GTACAATTC ACCGGGCATA ACTTCAT 107

(2) INFORMATION FOR SEQ ID NO: 3349:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3349:

25 CAACGCATCC TGCACTTTTA CCTATTCCTG AATCACCGGT AATTAGTACA CCAACACCGT 60
AAACATCTAC TAAA 74

(2) INFORMATION FOR SEQ ID NO: 3350:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3350:

40 AGATGCACCT ACTTCTAACT GTCGCAACA TCGCCGCAAT CATTTCAAAA CTACGTTCTG 60
TA 62

(2) INFORMATION FOR SEQ ID NO: 3351:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3351:

55 GCTGCAAACA ACAAATATT TTGATTAA TTGTGGATAT GATGGTAACC AACCAAGTCT 60

(2) INFORMATION FOR SEQ ID NO: 3352:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3352:

ATTGAACGCA AGATTTCGAT ATAGAACATC TAGCGACGTC GATTCGCAAG GTTGAACCAT 60
15 CTACATTAGG TGAGGAA 77

(2) INFORMATION FOR SEQ ID NO: 3353:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3353:

TAATCAACAC GAGGAGATGC TATTTAATGT CATCTGACAC AACAGTTTA GCACATACA 59

30 (2) INFORMATION FOR SEQ ID NO: 3354:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3354:

TTATGTAACC GACGAATGCT GCGATAGTGC TACGCCATCA CCGCCAGCTA ATCCGATTG 59

(2) INFORMATION FOR SEQ ID NO: 3355:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3355:

TAACTATACC TTTAGGGTTA CTACCACGCT TAGGTAGGTC ATAACCTTTA ACCACATCT 59

55

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3356:
 AATAACGCTA AACCTAAAAT GCTAAATAAT CCGCCGAACA ACATGCCGTT GTTTGTTGA 59

(2) INFORMATION FOR SEQ ID NO: 3357:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3357:
 CCAGAACCAC CCACGCCCTT TGAATATGGG AACTCAAAC GATCTACTGG CTGATGTAAT 60
 25 TACCCCTGTT TTGATTG 77

(2) INFORMATION FOR SEQ ID NO: 3358:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3358:
 AAGTTAGGTC TAGGGAACAT CGATAAATTA CCAGTAGTAA ATGCAGTTGA ACAACCAGA 59

40 (2) INFORMATION FOR SEQ ID NO: 3359:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3359:
 CATGACCTTT AAATTGCATA TCTTCTGCAT CAGGTGCATC GCTTTTAACA ATAACGTCA 59

(2) INFORMATION FOR SEQ ID NO: 3360:

55

(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3360:

10 ACGCGACAAC ACCGCCCTCA ACTAAAGTAG AAGCACCGCA ACAAACAGCA AATGCGACA 59

(2) INFORMATION FOR SEQ ID NO: 3361:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3361:

GATTTGATCG AATTGAACGA ACATTGCTT CTCAAACGAT TGCATCTATT AAAGAAGTAT 60

25 GTCTAG 66

(2) INFORMATION FOR SEQ ID NO: 3362:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3362:

GGTTGCACAT CTTTACTAC AAATTCGCT GGTAAAGATG TTGCAAAAGT ATGTCCGT 58

(2) INFORMATION FOR SEQ ID NO: 3363:

40

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3363:

50 CCTTGAAACG GCAACATTTT TGGGTCCTTC TCCATCATTT TATTTAAAAG CGCATTAT 58

(2) INFORMATION FOR SEQ ID NO: 3364:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 58 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3364:

TTGAGAATTT AGGAGGTTAA TCGGTTGATT AAAAGTGGCA AAGCACGTGC ACATACGA 58

10

(2) INFORMATION FOR SEQ ID NO: 3365:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3365:

20

GTTTTTTTAT TTTGGATAAA AGGAGCAAAC AAATGGATAT TAACTGGAAA TTGAGATT 58

(2) INFORMATION FOR SEQ ID NO: 3366:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3366:

ATTCATCGGT AATGACATTATTTTTACTTT GTAATTTTCAG TAACAGTTGA TCATCATG 58

35

(2) INFORMATION FOR SEQ ID NO: 3367:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3367:

45

TAAATTAACA GCCGGATGAA ATGAAAGGTG CTACATGCAC AATCAGTAAT ATCGGTTC 58

(2) INFORMATION FOR SEQ ID NO: 3368:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3368:

5 TACCTACTGG TGAGATTGGC GAACTTGCAA TTAAGGCTAA AAATGTCACG CCAGGATA 58

(2) INFORMATION FOR SEQ ID NO: 3369:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3369:

TTAAACGGAG AAGGCTTTAC TTTACATGTT GAGGAAGGTC AAGAAGTTAA ACAAGGTG 58

(2) INFORMATION FOR SEQ ID NO: 3370:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3370:

30 CTGCTAAACT ACGTGATTAT AATGAAACAC ATCATGTCTT TGTCTGGTAT ATGTAAATGA 60

TTGACGGC 68

(2) INFORMATION FOR SEQ ID NO: 3371:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3371:

45 ATTACCAACA GCGAAAATAT TGAAAAGCTG TAAAAAAGCT GGTGCAsmCm TACTTGGATT 60

GAGAATTTAG GAGGTTAATG CGTTGATTAA AAGTGGCAAA GCACGTGCAC ATACGAATAT 120

TGCAC TTATA AAATATTGGG GTAAAAAAGA TGAAGCACTA ATCATTCCAA TGAATAATAG 180

50 CATATCTGTT ACATTAGAAA AATTTTACAC TGAAACGAAA kCACTTTTAA CGACCAGTTA 240

ACACAGGATC AATTTTGGTT GAATGGTGAA AAGGTTAGTG GCAAAGAATT AGAGAAAATT 300

TCAAAATATA TGGATATTGT CAGAAaTAGA GCTGGCATCG ATTGGTATGC AGAAATTGAA 360

55

(2) INFORMATION FOR SEQ ID NO: 3372:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3372:

ATTTCACAA CTTTAAAGCA CGTATAATGA TGATTTTCAG ACTTGTACAA AGGAGAAA 58

(2) INFORMATION FOR SEQ ID NO: 3373:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3373:

AAACCGAGCA GCGCAGTAAA CCTGCAGTAC CTTTATCGCT TCTAGATAAT CCGATTG 57

(2) INFORMATION FOR SEQ ID NO: 3374:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3374:

AGTACGAATA TTACCTTTAT TTAATGGGTG AGCTAAGTTA CTTTTCATTI CTCGTG 57

(2) INFORMATION FOR SEQ ID NO: 3375:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3375:

GGTGAAGTAT AACTTTGTAA TGGCAGCGCA CTTAATGACT GCCAATAATT GTGACCAACA 60
ACTAACAGAC 70

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3376:
TTCCAAACTT CATTAGGTGA TAGCTTTAAT TTCAAGGCTG GCAATCGCCA TAACAAG 57

(2) INFORMATION FOR SEQ ID NO: 3377:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3377:
TCCTTCAAAG TCAATGGATT TGATCCTCAG AGGACTCAGT GTATCCTCCA AGTGACCTGG 60
25 CTCGCATCCA 70

(2) INFORMATION FOR SEQ ID NO: 3378:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3378:
ATGAATCATT AAGCCTTTTCG GTGCATATGC TGCAAGACTT TGACCAGCAT GACCAT 56

40 (2) INFORMATION FOR SEQ ID NO: 3379:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3379:
CCAACGACTG CGCCAATATT AATTGTTGCG CCCATCATAA CGACAGCACC ATCTTC 56

(2) INFORMATION FOR SEQ ID NO: 3380:

55

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3380:

10 ACAAAAGCAT CAAGCTGTTG AAACAATCAA TGATAGCATT CGAGATTATT TAGTTAG 57

(2) INFORMATION FOR SEQ ID NO: 3381:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3381:

CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA AATAACCGAA GTATTT 56

(2) INFORMATION FOR SEQ ID NO: 3382:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3382:

35 GAACACACAG GCAACCCAAA GCAGTGACGG CGAAAnTTGG ATTGATCTTG CAGCATTGAA 60

GAAGATCGCG ATGACTATAC AATCAATATC GAGTAGAAGA CCGAT 105

(2) INFORMATION FOR SEQ ID NO: 3383:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3383:

50 nGTATGTGAA AACTATTTTG CGATATTTTA GTGATGAGCC TCAGTGATCC TGGTTCCTGG 60

TTATCACCTC TGCTAGTTTA GTACCGATGG TCCAAGATTG ATGAGC 106

(2) INFORMATION FOR SEQ ID NO: 3384:

55

- (A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3384:

10 TTCTTCGTCA AGATCAATCT CTTCAAGTAC AATCTTTAAT ACCTTCTGCA CCCATTT 57

(2) INFORMATION FOR SEQ ID NO: 3385:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3385:

CGGGCATCTT AAAGCCGATG TTTATCCTGT AATCCTCCAA AAGGAAACAT GTACCTCAAT 60

25 TAGAG 65

(2) INFORMATION FOR SEQ ID NO: 3386:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3386:

CATTTTTAAT TATTTCTATT TGCTTTTAA CCACTTCTCT GACTGCTTCC GAATCATTTT 60

TCTTAACTGC A 71

40

(2) INFORMATION FOR SEQ ID NO: 3387:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3387:

TTAGAAAATG ATAAACGTAA AGCAGTAAGT GCTGAAGAAT ATAAAAAAGC TGACG 55

(2) INFORMATION FOR SEQ ID NO: 3388:

55

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3388:

10 TCTTCGACAA CTTTAATAAT ATTAGCCAAC GCAGTGTCCTCC CGCCAACCTTT TGTTGC 56

(2) INFORMATION FOR SEQ ID NO: 3389:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3389:

ATTTATTAAC GATTAATGAC GCTGGCATGC CAATTCCAGA TGATCATCGT CGTATC 56

(2) INFORMATION FOR SEQ ID NO: 3390:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3390:

35 AAATGCTATG TACCCACTTT AGATGAAATT TTAGTAACGT TATGGCCCGA AATGCCAACT 60

ATTATATTGA 70

(2) INFORMATION FOR SEQ ID NO: 3391:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3391:

50 CAAACGCAAT AGCTGGTGAC TTAAGTGGCG GCACTTGGCA TGTGGATGGC AATACTTCG 59

(2) INFORMATION FOR SEQ ID NO: 3392:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3392:

GCATCTACTG GGAAACGATT ACAAATTGGT GATTTATTAC AAAAGCCAAC TGTAT 55

10

(2) INFORMATION FOR SEQ ID NO: 3393:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3393:

20

TTTATAAATA TCCAGTCTG AACGCGATT CCATAACGGA TCAATGGCAG GATTG 55

(2) INFORMATION FOR SEQ ID NO: 3394:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3394:

TGCTTACGCT CAGTGACATA ATCTAATGTG GCACGTAAAG CGCCACCATA CCACC 55

35

(2) INFORMATION FOR SEQ ID NO: 3395:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3395:

45

AGTCACCATT TGTTGGTACA GGTATGGAA CACGTTGCAG CACGTGATTC TGGTGCGG 58

(2) INFORMATION FOR SEQ ID NO: 3396:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3396:

CAAATGCATT TAAACCAAT ATTGAGTTAC ATGAAAGCAC ATACGATGCA AACGT

55

5

(2) INFORMATION FOR SEQ ID NO: 3397:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3397:

15

TGTTGATGAG TCGTGTTTTA TCTCAAGATG TGTTACTCAA AAAGTTATAG AAGA

54

(2) INFORMATION FOR SEQ ID NO: 3398:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

20

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3398:

CTTCGTCAAG ATCAATCTCT TCAAGTAAAT CTTTAATACC TTCTGCACCC ATTT

54

30

(2) INFORMATION FOR SEQ ID NO: 3399:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

35

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3399:

40

AATGAAAAGC TAGCTGTAGT TGCAAGAAAA ACTGGCTTAG CGATGGCAGT TGGAT

55

(2) INFORMATION FOR SEQ ID NO: 3400:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

45

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3400:

55

(2) INFORMATION FOR SEQ ID NO: 3401:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3401:

TAAAAATCGC GCACTTAAAC CGCTTATGAC AATCATTATT ACCGCAATAT GCTTG 55

(2) INFORMATION FOR SEQ ID NO: 3402:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3402:

GGCACCTCCT TGGATTATTT TTCTTCTACT GTTACTAAGT GCTTAACTTT GTTG 54

(2) INFORMATION FOR SEQ ID NO: 3403:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3403:

GATAAGTCTA ACAAGTGGCA CCCATAATCG ATTAACTAC CGCCACCTTG CAACGTTT 58

(2) INFORMATION FOR SEQ ID NO: 3404:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3404:

TCGTTTTTCGT CCCCAAATTC TGCCAACTTA TTCATGAACT TATCTAGCGC TATTGTTCTT 60

TGTCT 65

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3405:
AAATTTTCAGC ACCAATTGTT ATTGGACGAC ACCATTTAGA TGCTGGTTCA GTTGC

(2) INFORMATION FOR SEQ ID NO: 3406:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3406:
TCGATTTTCAG CGGAACACAT GTAACGTTAG CACAAGCCAT GAACCAATTA GGTGGC

(2) INFORMATION FOR SEQ ID NO: 3407:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 74 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3407:
AATTGCTAAT GGTCAAGTAT GGACGTGATC ATTGTTGGTA CTACTTATTG CTGAAACTGT
TAAAGATTAG AAGG

(2) INFORMATION FOR SEQ ID NO: 3408:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3408:
TGATTTTACA CTTGATAACG GATACITTCGA AGAGATACAT CAGCAGCGTT CAGCTCAGAT
AGTGCTCA

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3409:

TATGATTAGA AAAAGGGGAA TTTTATGGA GTATAAGAGT TACTATGATT CGCC

54

(2) INFORMATION FOR SEQ ID NO: 3410:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3410:

TATCTTTCAT CATTGAAGAA GATCGCGATG ACTATACAAT CAATATCGAG TATA

54

(2) INFORMATION FOR SEQ ID NO: 3411:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3411:

TTGAAGTGCA CGAATCGAAT TATTGTAAGC AGTAATACTT GCCGGCTTCT TAC

53

(2) INFORMATION FOR SEQ ID NO: 3412:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3412:

TAGCCGATGG AACCCCATAA CGGTTGCCCT ATAAAAGTAT TGT'TTTTGTA TAGTGCTAAA

60

TCA

63

(2) INFORMATION FOR SEQ ID NO: 3413:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3413:

10 ACTACCATTG CTTGTTCCGG TTTCACAACT GGTTCAGTAT CATTTACAAC TGC 53

(2) INFORMATION FOR SEQ ID NO: 3414:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3414:

ATGCTGTTGT AAACGGTAAT ACAACATACC TGCCCAACCC GGTAACGCCA AAAAATGTCC 60

TT 62

25

(2) INFORMATION FOR SEQ ID NO: 3415:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3415:

ACTTAGATCA ATCACATGAT GCCTCACGGA ATCCATTATT TGAAGGTCAT GTTAG 55

(2) INFORMATION FOR SEQ ID NO: 3416:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3416:

TTAGTTCCAG CAATACCTGC TACAGTTGCT GCAGATGCTT CTTTCACCCA TGG 53

50

(2) INFORMATION FOR SEQ ID NO: 3417:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3417:

TGATTTAGGT GCAAAAATTG TAGGTATCGC TGAGGCTTAC GGTGCATTAC ACGATCCAA 59

10

(2) INFORMATION FOR SEQ ID NO: 3418:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3418:

20

CGTGGTCACC ATCACCAATT GCTCGATCTA ATTCAGTAAT TCAGATTCAT GTT 53

(2) INFORMATION FOR SEQ ID NO: 3419:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 55 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3419:

TGGACCTACT GCAATAACTG AACGTCCTGA ATAGTCAACA CGTTTACCAG TAAGT 55

35

(2) INFORMATION FOR SEQ ID NO: 3420:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3420:

45

TGTCTCCGGT ACCGTTTGCA CCAGGAATAA AGATGAGCAC GGGTCCTTGT CCG 53

(2) INFORMATION FOR SEQ ID NO: 3421:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

50

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3421:

AAATTAAGAA AATTCATTGC CAGATAATTT AGATAAATAA TTAAAACTTA GACCATTCAC 60

5 CCCAATCCCT GA 72

(2) INFORMATION FOR SEQ ID NO: 3422:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3422:

CATATGTTAA ATGGACTCGC TAGATTAAAG TCGCAATAGT AGCGGCCGTT TCTT 54

20 (2) INFORMATION FOR SEQ ID NO: 3423:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3423:

30 CACGTTTCAA ACCTAAAAGA TGCTAAAAAT TTCTCTTAAT TCTTGTGCAA TA 52

(2) INFORMATION FOR SEQ ID NO: 3424:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3424:

45 ATCGCCTAAC CAAGATGCAC CATCGGTGAT TTTATCGCCT GCCGCTTCAA CCAT 54

(2) INFORMATION FOR SEQ ID NO: 3425:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

AATAGAAAAT GTACGTAGCG GTATGATGAG GATTTCGCAG ACTAGTTTAG GGTCAAGTG

59

(2) INFORMATION FOR SEQ ID NO: 3426:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3426:

15

CCAACGCCAG ATCCAGAACC AAGTCCAGAC CCAGAACCGG AACCAAGCCC AG

52

(2) INFORMATION FOR SEQ ID NO: 3427:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3427:

CCATATTAAT GGTTATGTTT ATGTGAATGC TTGCTTGCTG GACTTGTCTT TT

52

(2) INFORMATION FOR SEQ ID NO: 3428:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3428:

40

TAAACAGAG ATTGATACTG CAGAAGATAA CTGTATCTCT CCATCTACTG TA

52

(2) INFORMATION FOR SEQ ID NO: 3429:

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3429:

TGAAAATCCA CAAGTCGCAC GTACAGTGTT TGAAAAAGGT ATTATGGCGG CA

52

55

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3430:

10

ATAATTCTTC CAAATATATG AAAATGGATT TGTCTTTTTT TTATAAAAAT CTTATGCTTT

60

TTAACTAATT GTAAGA

76

15

- (2) INFORMATION FOR SEQ ID NO: 3431:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3431:

25

CTGCGGGGGA TAACTGTATC TCTCCATCTA CTGGTAAGTC GTATTAGAAC TAAAGCGGCT

60

- (2) INFORMATION FOR SEQ ID NO: 3432:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

35

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3432:

GGCTTCAGGC TCATTGATAG GTAAAAGTTG CAAAGCCTGC AAAGCGATTG GG

52

40

- (2) INFORMATION FOR SEQ ID NO: 3433:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3433:

50

TCGCACGATA CGCCTCCGAA TGAAGAAGGT TTATTGTGCG ATTCTTTTAT TGTTAAATTT

60

TAAATTTTTT

69

55

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3434:
 GATCGCTATC CATTAGCTAA ATTTAAACGT TCAAACCTCAG GTACATGTTA C

(2) INFORMATION FOR SEQ ID NO: 3435:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3435:
 TATAGCTACT GCTGCAGCTG CGGCCATTGC AGATGCTGAA CCAACTTCAG C

(2) INFORMATION FOR SEQ ID NO: 3436:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3436:
 ATTAAAGCCA ACATTAAATT ATCCACTATT AACATAACG GCTACAGGCT TATTAATGAT
 TTATACCTTT

(2) INFORMATION FOR SEQ ID NO: 3437:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3437:
 TTTGTTTGTT GATTCTTCTC CACCTGTTTC AGGTAGTTCA GATTTCTTAG A

(2) INFORMATION FOR SEQ ID NO: 3438:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3438:

10 GTGAATTCCG TAATTACATT TTAGGCTTGA TTTTCTATCG CTTCTTATCT G 51

(2) INFORMATION FOR SEQ ID NO: 3439:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3439:

TTAAGACAGG TTCCTTATGG GACTCTAACA ACGTATGGTG CTATTGCCAA A 51

(2) INFORMATION FOR SEQ ID NO: 3440:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3440:

35 CACTAGAAGA AACGGATTCA TCAGCTATTG GTATCGATTA CCATACTGCT GTGGA 55

(2) INFORMATION FOR SEQ ID NO: 3441:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3441:

CTTCTGGCAA TAGACCGCGA GTTACTGGGG GCAAAACCAG TGTGTAAAAC CGGAACTACT 60

50 ATGAGGGGCA TGAAAGT 77

(2) INFORMATION FOR SEQ ID NO: 3442:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3442:

GTTCGGTTGT GACAGTCAGT GGACGCGTTA CCAAATGGGC GGGAATTAAA GCAAA

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(2) INFORMATION FOR SEQ ID NO: 3443:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3443:

20

ATGAACTTTG GGATAAAGGT GATGCCCAA CTTTCCGTAA CTCATGATGA T

51

(2) INFORMATION FOR SEQ ID NO: 3444:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3444:

CAACGCAGCA AAGCGGAGTG GCCCTTTACC TTCACAGAAT AATGGTCTAA T

51

35

(2) INFORMATION FOR SEQ ID NO: 3445:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3445:

45

ACCGAGCAGC GCACTAAACC TGCACTACCT TTATCGCTTC TAGATAATCC

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(2) INFORMATION FOR SEQ ID NO: 3446:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3446:

CCAATGCAAC GATCCAGTTA TTGTGTTGGC GCAATTGATT AATAGTATTC

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(2) INFORMATION FOR SEQ ID NO: 3447:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3447:

GCGCATCATA TCCCATGCA CCGATAAGAT CCTTCTTACC TTCTACAAGT

50

(2) INFORMATION FOR SEQ ID NO: 3448:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3448:

GTTCTTACTT CTTTATCGTG GCTCCAACGT GCTCTGTACA TTTTITCCCA TCTCTCTACT

60

(2) INFORMATION FOR SEQ ID NO: 3449:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3449:

CAACACCACC GACACCAGAA GTACCAAGCG AGCCGGAAAC ACCAACACCG

50

(2) INFORMATION FOR SEQ ID NO: 3450:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3450:

TTATCACGGT ATATGAGGGG ATTTGAGG

88

(2) INFORMATION FOR SEQ ID NO: 3451:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3451:

15

TGCAAAACGT TATGAAGTAC AAGTTGATGG AAGCAACAAA GTAAGTGCGn

50

(2) INFORMATION FOR SEQ ID NO: 3452:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3452:

CAGTTAAGTC ACCAGCTATT GCGTTTGGTG ATCTTAAGCA GCGGTGGATT ATCAAGTTTG

60

GGTA

64

30

(2) INFORMATION FOR SEQ ID NO: 3453:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3453:

TCGTAAACAA TATACTATCT CAACATTTAT TCATCCAATG GAGATAACGT ATTGCGCGGT

60

TTAACAGGTA ATTTAAACCA AATACGGTAG TAATnATTAA TAGATAGCAA ATCAAGTATA

120

45

AAGAATAAGT A

131

(2) INFORMATION FOR SEQ ID NO: 3454:

50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3454:

TTAAAAATGC AGTTATGGCC TCTAAATCG TATTAAGCAT ATTAGCGCCC

50

(2) INFORMATION FOR SEQ ID NO: 3455:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3455:

TGCTACATGG CGTTACGGTC AAGATCGTCA ACGATTGATG GGTACAATTG A

51

(2) INFORMATION FOR SEQ ID NO: 3456:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3456:

ACAAACTGCC AACGATTGGT CGTGTGAATC ATCCAGTGA AGAAGCGCAn

50

(2) INFORMATION FOR SEQ ID NO: 3457:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3457:

AATCACGTGA GAAGGATACA GCTATTAGTA TCGGTATCAT CGCATTGATT

50

(2) INFORMATION FOR SEQ ID NO: 3458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3458:

(2) INFORMATION FOR SEQ ID NO: 3459:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3459:

GGGCCAACAA ATCGGAAACT GCCAATTGGA CGTTGCCGT CATCAAACCC

50

(2) INFORMATION FOR SEQ ID NO: 3460:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3460:

TGCTTCGCT AGAGGATCCG GTATTGCTAG TCAATTACTA CACCATTAA ATTGTGGAAG
 CAAAAGCT

60

68

(2) INFORMATION FOR SEQ ID NO: 3461:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3461:

TGGTCTTCGC AATCCACGGA TATACCTTAG TACCAGGTAA TTGACCACCT T

51

(2) INFORMATION FOR SEQ ID NO: 3462:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3462:

AAGCTATTAA TGTAATTTAT CAATTGATTG TGCAACGGAC ATCATCTACA AGACCG

56

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3463:
 ATACCAAATG TGAGAAACTG GAGCAGCAAn TTCAATGTGA CCCATTCTTT

(2) INFORMATION FOR SEQ ID NO: 3464:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3464:
 TCTTTACGGC GTGGTTCTAA TCGCATCTTT TTCAATCTAA GTGCGTTTnT

(2) INFORMATION FOR SEQ ID NO: 3465:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3465:
 AAAGAAGATT GGAACGTGTA TTGACGACTG CACCCAGGTA TGGGTGTTTCG CCCGACA

(2) INFORMATION FOR SEQ ID NO: 3466:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3466:
 ACATCCGAAA GATGACTTGT TTA AAAAAGC AGAGCATGAT TTGCTTACTA TGATTACACG
 CGG

(2) INFORMATION FOR SEQ ID NO: 3467:

(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3467:

10 TACCGATGAT TTCCGAGACA TAGACCGGCC TGCTGGGGG TCAACTGGAA CTTGGTC 57

(2) INFORMATION FOR SEQ ID NO: 3468:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3468:

TGTCCTAAT ATTTATGTTG TAAAAATGTA CAATCTAATT AAAGCAATAG TCTTGGGCA 59

25 (2) INFORMATION FOR SEQ ID NO: 3469:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3469:

35 TCCATGATCG TTCAACATTT AAATACACAA CTTAATAAGT ATCGTGTACA AGTTATG 57

(2) INFORMATION FOR SEQ ID NO: 3470:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3470:

50 CCCTGTTTCT GCTATCCTCT AAAGTGACGA TATAGAATAG CGATTAAATAT CGCGATAGT 59

(2) INFORMATION FOR SEQ ID NO: 3471:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3471:

TACGCCATCA nCGCCAGCTA ATCCGATTGC GACACCTAAT GCGAAATCAT

50

(2) INFORMATION FOR SEQ ID NO: 3472:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3472:

AACGTCATCA AATGGAAGTA CGTGACGTTT ACTACTCTCA CTATGGCCGT ATGT

54

(2) INFORMATION FOR SEQ ID NO: 3473:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3473:

TAATAGGCAT TCCCATTAGG TCGCTCGACA ACTGCAACGC AAGCATTGTA AACAGA

56

(2) INFORMATION FOR SEQ ID NO: 3474:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3474:

TTTTAAGAAT GTCGCGTTAT CTGCGCCCAT TGGATTGACA TACTTCATAC GTATA

55

(2) INFORMATION FOR SEQ ID NO: 3475:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

GCCTTTAGGT AAAATGGGCA GAAATGCTAA TCATTTTGGC GCGGAAATGA AAAA

54

(2) INFORMATION FOR SEQ ID NO: 3476:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3476:

15

AAAnCATTCTG CAATCGACCA TAATTTTTTA TGTAATTCAG CTTGTTGCTG

50

(2) INFORMATION FOR SEQ ID NO: 3477:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3477:

GGAnGACCAT TAATCGATAT CGGTACACAC GCTTTAGATT TAACGTTATG

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(2) INFORMATION FOR SEQ ID NO: 3478:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3478:

40

TGCCTCCTTA CGCCATGATG CTTATTCAAA GTAAATTGCT TTGCCGGACT TTGCAGACTG

60

(2) INFORMATION FOR SEQ ID NO: 3479:

45

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3479:

GGTCTTTTCAG CTGCTAACGA GTTCCTGTTA CTGTTCATGT CTATCACTTT GCGTTCCTC

60

55

(2) INFORMATION FOR SEQ ID NO: 3480:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3480:

CAAGTATCAT ATGGACGGCT CGCCCAACAC AAAACAAGnC CAAGCAAAAC

50

(2) INFORMATION FOR SEQ ID NO: 3481:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3481:

ATTAAACAAC ATAGCTCGGC TAATCCTTTA AAGCTTTTGA GTTTTCTGT TGTAGAACAA
GA

60

62

(2) INFORMATION FOR SEQ ID NO: 3482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3482:

TGTGGCTAGC TGTTTCTTTT TTAGGTGCTG TGTAGGAGAT GAACTGATCG T

51

(2) INFORMATION FOR SEQ ID NO: 3483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3483:

GCAGTTTATA AGTAGAGAGA CAGCTGATCA TGAGATAAAA ATGGGTAAAT ATTT

54

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3484:
TTATCTATCA CAGTACGAAT CCCCCAGAGT ACCGATTGTG ACAGCAACTT CTGCG 55

(2) INFORMATION FOR SEQ ID NO: 3485:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3485:
ATCTCTGGTT CGATTCCCGT CGAGACCGGC ATCATTACAT GTTTATTATG GG 52

25 (2) INFORMATION FOR SEQ ID NO: 3486:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3486:
TGTGTCACGA TAATAGGCGT AATATCACTC TTTGGCATGA TTGCCGGATG 50

(2) INFORMATION FOR SEQ ID NO: 3487:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3487:
TATTTTTGAT CACTCAAC GCACAAACGA ATGGCCTTTA CCTTCACAGA ATAATGGTCT 60
AATGTAA 67

(2) INFORMATION FOR SEQ ID NO: 3488:

55

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3488:

10

TAGGTGGTCA ATTACCTGGT ACTAGGTATA TCCGTGGATT GCGAGGACAA

50

(2) INFORMATION FOR SEQ ID NO: 3489:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3489:

CAATTGTACT TCATAACGTT TTGCATTTTCG CCACCTTCAC CACTATATTT TCCCATGGTC

60

25

(2) INFORMATION FOR SEQ ID NO: 3490:

(i) SEQUENCE CHARACTERISTICS:

30

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3490:

35

CTAAACTGAT TGTTTTACGT AACGTTTCAT CGGCTTCTTT CGCTTCTATC

50

(2) INFORMATION FOR SEQ ID NO: 3491:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3491:

TCGATTTACC TTTCATCATT GAAGAAGATC GCCATGACTA TACAATCAAT AT

50

52

(2) INFORMATION FOR SEQ ID NO: 3492:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3492:

AACCTTTTCA CAAATATCAT ATAACTCTTC TAATGGGATA ATCTCTTCAT GT

52

(2) INFORMATION FOR SEQ ID NO: 3493:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3493:

GGTTTTAAAC CGTCACGAAC ATCTGGCAAT GCACGAGCAA CGTACATACG TATCTAAAGT

60

TACGCTT

67

(2) INFORMATION FOR SEQ ID NO: 3494:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3494:

TACGTTATGT TATGTAAATA ACAGTTAATT ATACCGGTGG TCTGGGTCGA

50

(2) INFORMATION FOR SEQ ID NO: 3495:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3495:

CGCTTGTTGT TGTACTTTGG CAGTTCGCGT TGTGGATTGT GCCAGCGCTT TTAAACCGTA

60

(2) INFORMATION FOR SEQ ID NO: 3496:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3496:

GGCACCGGCT TCTCTATTGC TTCTTTAGCA TATCTGCAGC TCTCTCAAGG GACATG 56

5

(2) INFORMATION FOR SEQ ID NO: 3497:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3497:

CACCTTTAGG ATACGCGTCT AACCACTGTG TCGCGTCTCT ATATATCGCT AAACACGTA 59

15

(2) INFORMATION FOR SEQ ID NO: 3498:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3498:

AAGTAATATC TGAATGCGTA TATTGTCTAA TTTCAAATTC TACAGACATC GACGT 55

30

(2) INFORMATION FOR SEQ ID NO: 3499:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3499:

AnTGTAACAG TCCATCTTCA CATGACAACA ACGATATTTT GACCATCACA 50

40

(2) INFORMATION FOR SEQ ID NO: 3500:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3500:

55

(2) INFORMATION FOR SEQ ID NO: 3501:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3501:

TGTGTGCCTT TAAGTTGTTG ATGACACGCA TTCACGACAA CAGACATGAC AC 52

(2) INFORMATION FOR SEQ ID NO: 3502:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3502:

CTGGCTTCAA TGGCAACTTC TGTACCTGGT ACCAATGGGC GATGACCGAT 50

(2) INFORMATION FOR SEQ ID NO: 3503:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3503:

TGTCCGACTT GGCGGnATCG TAATTTAGCG CnTGTAATTC TAAAGGGACC 50

(2) INFORMATION FOR SEQ ID NO: 3504:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3504:

AACCTTCATA TTGCTTCTAA TAAGAAACCG AGCAGCGCAC CAAACCTGGC AGTACCTTTA 60

TCGC 64

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3505:
 TATTGATGTT GAAAACTGTT ATGTCCTTTC GATGGGCCAA CACnAAnATA 50

(2) INFORMATION FOR SEQ ID NO: 3506:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3506:
 GAATATGGTA TCAATGGTAT GCACTAAGGC TTTATGAAAT TCATTAAAA T 51

25 (2) INFORMATION FOR SEQ ID NO: 3507:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3507:
 CGGTTTTAAT CGGTAAATTA AATATGGATG AGTTTGCAAT GGTGTTTACA GAACATCTAT 60
 TTAA 64

40 (2) INFORMATION FOR SEQ ID NO: 3508:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3508:
 CAAGGCCTTG TTTTAAAGC AGCTACAGTT GGCAATATGT CCACTCATGT 50

(2) INFORMATION FOR SEQ ID NO: 3509:

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(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3509:

10 CAGATGCAAA TTGACATGGT CATCAACATC nGThCATTAA AAGATGGACG 50

(2) INFORMATION FOR SEQ ID NO: 3510:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 94 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3510:

ACAAGAGGGT CACCCAGCTC GGTGATTCC CACCGCCACA TCATGATATT TATTCATAGA 60

25 GTTTACGCAC TGTACATGAT TGAATGCGAT AAAG 94

(2) INFORMATION FOR SEQ ID NO: 3511:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3511:

ACTCAACAAT GGATATTCTT AACTGAAAA ATGGGTAATG GTGCAAACAT AGTA 54

(2) INFORMATION FOR SEQ ID NO: 3512:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3512:

50 CCGGATGCAC ATTTGATGAC TGAAGTCCGC GATAAAGGGA CAAnAGTCAn 50

(2) INFORMATION FOR SEQ ID NO: 3513:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3513:

GCATTAAATT GAAACAATCG GATTTACAAT TTTCTCTTAA TGCTGTCGTC TACACAGC 58

10

(2) INFORMATION FOR SEQ ID NO: 3514:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3514:

20

GTGTTTCGTGT TCATGCAAGG TGAATGCGAG TGATCTGTTG GTATGGGCTT TATGCATGGC 60

AATCTG 66

25

(2) INFORMATION FOR SEQ ID NO: 3515:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3515:

35

ATGCCACTGA TAATGChnCT GAACTTATTG ATGACTTCTC ATTAGACTAT 50

(2) INFORMATION FOR SEQ ID NO: 3516:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3516:

CGGCGACAAA GAGTAAACAC AGCGGAGGGA CAAAGCCCGC GACTAGCAAC 50

50

(2) INFORMATION FOR SEQ ID NO: 3517:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3517:

5 ATGCCTATGT AGCACCGAGT ACCGATACCG AACACTTAGC TACGCCAGTT C 51

(2) INFORMATION FOR SEQ ID NO: 3518:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3518:

GAGCATnAAG GTGATTTnGA TCGCTATCCG TTAGCTAAAT TTAAACGTTC 50

20 (2) INFORMATION FOR SEQ ID NO: 3519:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3519:

30 GATTGGTATT TAGCTTTAAA TTTATGGTTG GAATAGTAGG TGGCATATAT CGCTGTTAGT 60

ATCG 64

(2) INFORMATION FOR SEQ ID NO: 3520:

35

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3520:

45 TCTTCAATCT CAGGGGCATC TACTAACATA TCATCCAGTC AATATTGCGT CACATTGTTA 60

ATCGGTTCCG ATC 73

(2) INFORMATION FOR SEQ ID NO: 3521:

50

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3521:
 5 TCAAATTGGC AATTGGTACG AATGTCGACT GTACTAACAT CATTAGCTCA TGATTGCCAG 60
 GTGATTTCAT GGATG 75

(2) INFORMATION FOR SEQ ID NO: 3522:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3522:

TTCCAATGGG CTTCTGACTT TGGCGGTTTT AGTGCTTGGG TTGCCGGCGG TTTTGGA 57

20

(2) INFORMATION FOR SEQ ID NO: 3523:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 72 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3523:

TGGTGGAGGT TTTGTTTTTT CCGTGTCGGT TTTTGTTTTTC GTCTTGGTTT CTTTGTGTTT 60
 TGTGTTCTCT TT 72

35

(2) INFORMATION FOR SEQ ID NO: 3524:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3524:

ATATCACAAT ATACCGGTTT ATATGCTGTC TAATCATAGT TGAATAGTGA C 51

(2) INFORMATION FOR SEQ ID NO: 3525:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3525:

5 TAGACCGTCG TGGATAGTTT TGGGTACGGT AACCAATTTA TTTTGAAGAG ACCATCCTC 59

(2) INFORMATION FOR SEQ ID NO: 3526:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3526:

TAATAACGTT GCCCTCCCAT GTATATCCTA CCAACATGAC ATCTGTACA 50

(2) INFORMATION FOR SEQ ID NO: 3527:

20 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3527:

30 TTCCCAACGA GCAGTCGCAT GCGGTACTGC CACGGCATT TGTATGCAGGC CT 52

(2) INFORMATION FOR SEQ ID NO: 3528:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3528:

AAAGAAAnGA TnGnnnGnnn GnAnAAAnnn nnCCATnnnn nTAAAAAAA 50

45 (2) INFORMATION FOR SEQ ID NO: 3529:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

CATTAGCCTC ATCCCCTTCG TTTAGACTCG CTATAGATGC ACTAAATGGC GATATATTTT 60

TC 62

5

(2) INFORMATION FOR SEQ ID NO: 3530:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3530:

CACTACCACA AAAATTATAG GTGTTGACCT TCAGGnGCAA GTAGTATGAT 50

(2) INFORMATION FOR SEQ ID NO: 3531:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3531:

GAATGCAAAA TCCATTGTGA AGGAnATCGA ATGGTTTAGT AnCTCGTGCA 50

30

(2) INFORMATION FOR SEQ ID NO: 3532:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3532:

GGTAGAnCnC TGTTTAGTAC TAGGGGCCCC TCTCGGGTTA CCAATTCAGA 50

(2) INFORMATION FOR SEQ ID NO: 3533:

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3533:

55

(2) INFORMATION FOR SEQ ID NO: 3534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3534:

CGTCAACGAT GTAAAGTAAA GCCTTGTTCA GTTTAATTTA CGAGTGGCGT AA 52

(2) INFORMATION FOR SEQ ID NO: 3535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3535:

TTAATCCAGA AGTACCGGTG GATTAGTTA TTGACCACTC AGTTCAAGTG GATAGCTATG 60
 CAAATCCAGA AGCTCTTGAA CGTAATATGA AATTAGAATT TGAACGTAAC TATGAACGTT 120
 ATCAGTTTTT AAATTGGGCA ACGAAAGCAT TTGATAATTA CAATGCAGTT CCTCCTGCAA 180
 CTGGAATAGT TCACCAAGTT AACTTAGAAT ATTTAGCAAG TGTGTACAT GTTCGTGATG 240
 TAGATGGTGA AAAAAGTGA TTTCCAGATA CATTAGTTGG TACTGATTCA CATAACAACAA 300
 TGATAAATGG TATTGGCGTA CTAGGATGGG GTGTTGGTGG TATTGAAGCT GAAGCTGGAA 360
 TGCTTGGACA ACCTTCTTAT TTCCAATTC CAGAGTTAT 400

(2) INFORMATION FOR SEQ ID NO: 3536:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3536:

CGTATAGAGT GTCCTACAAC CCCAACAAGC AAGCTTGTTG GTTTGGGCTC TTCCCGTTTC 60
 GCTCGCCGCT ACTAAGGGAA TCGAATTTTC TTTCTCTTCC TCCGGGTACT AAGATGTTTC 120
 AGTTCTCCGG GTGTGCCTTC TGATATGCTA TGTATTCACA TATCGATAAC ATGACATAAC 180

GCATATCGTC GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGCGC 300
 CCTTAATAAC TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGCTCA CATACGGCTT 360
 5 CGTTTTCAAT ATTTTAAATG CTCATTTACA TAAGTAAACT CTGCTTTAAA ATAATTTAAC 420
 TCATTGTCTG CTAAACGTTT TCTTTTATAA AAAGATTTAA ACGCGTTATT AATCTTGTGA 480
 GTGTTCTTTC GAACACTAGC GATTATTTCT TATGAATTCA AGCTTATTTA AAACCTCTTA 540
 10 TTCACTCGGT TTTGCTTGGT AAAATCTATA TTTTACTTAC TTATCTAGTT TTCAATGTAC 600
 AATTTCTTTT TAGTCAAGCG CTCGCATACT GCTTTATTTT CAAAAAATCA AATGCTCATT 660
 15 TACAAAAGTA AACTCCGCTT TAATTTTCTT TAATGCATTG TCTAACAACC GCTTTCTTTA 720
 AAAAGAATAG ATTGTCAAGC GCTCGCATAA GCAATATCAC TTTAACCAAA AAATATTTGA 780
 ATGTTAAATA AACATTCAAA ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG 840
 20 AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT 900
 ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG 960
 TTACTIONCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT GACGGGCGGT GTGTACAAGA 1020
 25 CCCGGGAACG TATTCACCGT AGCATGCTGA TCTACGATTA CTAGCGCTCC AGCTTCATGT 1080
 AGTCGAGTGC AGACTACCAT CCGGACTGnG GACCAACT 1118

(2) INFORMATION FOR SEQ ID NO: 3537:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3537:

GGGGATCCCC AGCCAGAAGA TTTATTCAGT GCGATGATTC GTGAAATTGA AACGCAAGAT 60
 TTCGATATCG AACACCTGGC GACGGCAATT CGTAAGTTG AAACATCAAC ATTAGGTGAA 120
 GAAAGTGAAA ATGACTTTAT CGGTCTGTTC AGCGATATGG ATTTGAGTTC AACGCGACTA 180
 45 GGTAACAATG TCAAAGAACG TACTGCTTTA ATCTCTAAAG TCATGGTTAA TCTTGACGAC 240
 TTACCATTCTG TTCACAGTGA CATGGAAATT GATATGTTAG GTGATGCATA TGAATTCCTA 300
 50 ATTGGGCGCT TTGnGCGACA CGGGTAAAAA AAGCAGGCGA GTTCTATACA CCACAACAAG 360
 TATCTAAGAT ACTGGCGAnG ATTGTCACAG ACGGTAAAGA TAAATTACGT CACGTGTATG 420
 ACCC 424

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3538:

ATCTCATATG TTAAAAGGTA AACAAGGTCG TTTCCGTCAA AACTTACTTG GTAAACGTGT	60
TGACTATTCA GGACGTTTCAG TTATTGCAGT AGGTCCAAGC TTGAAAATGT ACCAATGTGG	120
TTTACCAAAA GAAATGGCAC TTGAACTATT TAAACCATTG GTAATGAAAG AATTAGTTCA	180
ACGTGAAATT GCAACTAACA TTAATAATGC GAAGAGTAAA ATCGAACGTA TGGATGATGA	240
AGTTTGGGAC GTATTGGAAG AAGTAATTAG AGAACATCCT GTATTACTTA ACCGTGCACC	300
AACACTTCAT AGACTTGGTA TTCAAGCATT TGAACCAACT TTAGTTGAAA GGTCTGCGCA	360
TTCGTCTACA TCCACTTGTA ACAACAGCTT ATAACGCTGA	400

(2) INFORMATION FOR SEQ ID NO: 3539:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3539:

AATAAGTAAG TTATTTTGTC TGGTGA CTAT AGCAAGGAGG TCACACCTGT TCCCATGCCG	60
AACACAGAAG TTAAGCTCCT TAGCGTCGAT GGTAGTCGAA CTTACGTTCC GCTAGAGTAG	120
AACGTTGCCA GGCAATGAC AAATCGGAGA ATTAGCTCAG CTGGGAGAGC ATCTGCCTTA	180
CAAGCAGAGG GTCGGCGGTT CGAACCCGTC ATTCTCCACC ATTTATTCTT AGATATAGCC	240
GGCCTAGCTC AATTGGTAGA GCAACTGACT TGTAATCAGT AGGTTGGGGG TTCAAGTCCT	300
CTGGCCGGCA CCATCTTTTG AGCCATTAGC TCAGCTGGTA GAGCATCTGA CTTTAAATCA	360
GAGGGTCAGA GGTTCGAATC CTCTATGGCT CATTACGATT TAATTTTAT ATTTAGCAAA	420
ATAATGCAGA AGTAGTTCAG CGGTAGAATA CAACCTTGCC AAGGTTGGGG TCGCGGGTTC	480
GAATCCCGTC TTCTGCTCCA TTATTTTGCC GGGGTGGCGG AACTGGCAGA CGCACAGGAC	540
TTAAAATCCT GCGGTGAGAG ATCACCGTAC CGGTTGATT CCGGTCCTCG GCACCATTTT	600
AGCGCCCGTA GCTCAATTGG ATAGAGCGTT TGACTACGGA TCAAGAGGTT ATGGGTTCGA	660

GAGCACTTGG TTTGGGACCA AGGGGTGCA GGTTCGAATC CTGTCTTCCC GATTACTTCT 780
 TAAATTCAT TTTATGGGG CTTAGCTCAG CTGGGAGAGC GCCTGCTTTG CACGCAGGAG 840
 5 GTCAGCGGTT CGATCCCGCT AGTCTCCACC ATTTATTTTT TACACGATGA ACATTGAAAA 900
 CTGAATGACA ATATGTCAAC GTTAATTCCA AAAAACGTAA CTATAAGTTA CAAACATTAT 960
 TTAGTATTTA TGAGCTAATC AAACATCATA ATTTTATGG AGAGTTTGAT CCTGGCTCAG 1020
 10 GATGAACGCT GCGGGCGTGC CTAATACATG CAAGTCGAGC GAACGGACGA GAAGCTTGCT 1080
 TCTCTGaTG TAGCGCGGA CGGGTGAGTA ACACGTGGgA TAACCTACCT ATAAGACTGG 1140
 15 GaTAACTTCG GGaAACCGGA GCTAATACCG G 1171

(2) INFORMATION FOR SEQ ID NO: 3540:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 601 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3540:

CTCGGCAGTG TGAAATCAAC GACTCGAAGA CACAATGTCT TCTCCCCATC ACAGCTCAGC 60
 30 CTTAACGAGT ACCGGATTG CCTAATACTC AGCCTTACTG CTTAGACGTG CAATCCAATC 120
 GCACGCTTCG CCTATCCTAC TCGTCCCCC CATCGATTAA AACGATTATA GGTGGTACAG 180
 GAATATCAAC CTGTTATCCA TCGCCTACGC CTGTCGGCCT CAGCTTAGGA CCCGACTAAC 240
 35 CCAGAGCGGA CGAGCCTTCC TCTGGAAACC TTAGTCAATC GGTGGACGGG ATTCTCACC 300
 GTCTTTCGCT ACTCACACCG GCATTCTCAC tTCTAAGCGC TCCACATGTC CTTACGATCA 360
 TGCTTCAACG CCCTTAGAAC GCTCTCCTAC CATTGTCCAA AGGCATwCrC ACAGCTTCGG 420
 40 TaATATGTTT AGCCCCGGTA CATTTTCGGC GCagTGTCAC TCGACTAGTG AGCTATTACG 480
 CACTCTTTAA ATGATGGCTG CTTCTnAGCC AACATCCTAG GTTGGTCTGG GGCACGcNAC 540
 ATCCTTTTCC ACTTAACATA TATTTTGGGG ACCTTGGCTG GTGGGTCTGG GGCTGnTTCC 600
 45 C 601

(2) INFORMATION FOR SEQ ID NO: 3541:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 1311 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3541:

5 GCnAGGACCT TnCCAAATTT GAAATCCTTT GACCACnTTT GGGGTAGAGC CCTTTCCnC 60
 GGGGACAAAG TGACCAGGTG GTGCATGGTT GTCGTCAGCT CGTGTCTGTA GATGTTGGGT 120
 TAAGTCCCCG CAACGAGCGC AACCTTAAG CTTAGTTGCC ATCATTAAAGT TGGGCACTCT 180
 10 AAGTTGACTG CCGGTGACAA ACCGGAGGAA GGTGGGGATG ACGTCAAATC ATCATGCCCC 240
 TTATGATTTG GGCTACACAC GTGCTACAAT GGACAATACA AAGGGCAGCG AAACCGTGAG 300
 nTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC TCGACTACAT 360
 15 GAAGCTGGAA TCGCTAGTAA TCGTAGATCA GCATGCTACG GTGAATACGT TCCCGGGTCT 420
 TGTACACACC GCCCCTCACA CCACGAGAGT TTGTAACACC CGAAGCCGGT GGAGTAACCT 480
 TTTAGGAGCT AGCCGTCGAA GGTGGGACAA ATGATTGGGG TGAAGTCGTA ACAAGGTAGC 540
 20 CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCTAAGGA TATATTCGGA ACATCTTCTT 600
 CAGAAGATGC GGAATAACGT GACATATTGT ATTCAGTTTT GAATGTTTGT TCATTCAAAT 660
 25 TAATGGGCCT ATAGCTCAGC TGGTTAGAGC GCACGCCTGA TAAGCGTGAG GTCGGTGGTT 720
 CGAGTCCACT TAGGCCCCACC ATTAATTTAA TACCTATTTG GGGGCTTAGC TCAGCTGGGA 780
 GAGCGCCTGC TTGCACGCA GGAGGTCAGC GGTTTCGATCC CGCTAGTCTC CACCATTATT 840
 30 TGTACATTGA AACTAGATA AGTAAGTAAA ATATAGATTT TACCAAGCAA AACCGAGTGA 900
 ATAAAGAGTT TTAAATAAGC TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAAGAACA 960
 CTCACAAGAT TAATAACGCG TTAAATCTT TTTATAAAAG AACGTAACCT CATGTTAACG 1020
 35 TTTGACTTAT AAAAATGGTG GAAACATAGA TTAAGTTATT AAGGGCGCAC GGTGGATGCC 1080
 TTGGCACTAG AAGCCGATGA AGGACGTTAC TAACGACGAT ATGCTTTGGG GAGCTGTAAG 1140
 TAAGCTTTGA TCCAGAGATT TCCGAATGGG GAAACCCAGC ATGAGTTATG TCATGTTATC 1200
 40 GATATGTGAA TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC 1260
 CGGAGGAAGA GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCGAAATG G 1311

(2) INFORMATION FOR SEQ ID NO: 3542:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3542:

CGCTAGAGTA GAACGTTGCC AGGCAAATGA CAAATCGGAG AATTAGCTCA GCTGGGAGAG 120
CATCTGCCTT ACAAGCAGAG GGTCGGCGGT TCGAACCCGT CATTCTCCAC CATTTATTCT 180
5 TAGATATAGC CGGCCTAGCT CAATTGGTAG AGCAACTGAC TTGTAATCAG TAGGTTGGGG 240
GTTCAAGTCC TCTGGCCGGC ACCATCTTTT GAGCCATTAG CTCAGCTGGT AGAGCATCTG 300
ACTTTTAATC AGAGGGTCAG AGGTTCGAAT CCTCTATGGC TCATTACGAT TTAATTTTTA 360
10 TATTTAGCAA AATAATGCAG AAGTAGTTCA GCGGTAGAAT 400

(2) INFORMATION FOR SEQ ID NO: 3543:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 804 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3543:

GTGAGAGTGA CGTTATGTTA TGTAATAAAC AGTTAATTAT ACCGGTGGTC GGGGTCGAAC 60
25 CGCACTCCAC AAGTGAAGA GaTTTTGAGT CCCGCGCGTC TGCCAATTCC GCCACACCGG 120
CTTAATGGTA AACAAAAAAC TTCCCTTTGG AAGCAATTAT GGAGCGGAAG ATAGGATTTA 180
CACCTATACC TCGTTCGGG aAGGAActGg TTcTAAAAGT TGAAC TACTC CCGCAAATAT 240
30 TAAATTATGG AGCGGAAGAT AGGATT TACA CCTATACCTC ATTCCAGGAA GGAATGTATT 300
CTAAGAGTTG AAATACTCCC GCATTATTAT TAAATTATGG AGCGGAAGAT AGGATTTGCA 360
CCTATACCTC GTTCCGGGAA GGackTGTTt CTAAAAGTTG AACTACTCCC GCATAAACCT 420
35 GGAGGCGGCA ACCGGATT TG AACCGGTGAT AAAGGTTTTG CAGACCTCTG CCTTACCACT 480
TGGCTATGcg CcAATAACTG GGCTAGCTGG ATTCTGAACCA ACGAGTGACG GATmAAAGTC 540
40 CGTTGCCTTA CCGCTTGGCT ATAGCCCAT TATAATAAGG GCGGCTGAAG GGGATCGAAC 600
CCTCGAATGT CGGAACCACA ATCCGATGTG TTAACCACTT cACCACAGCC GCCATGGCAG 660
GGGCAGTAGG AATCGAACCC ACACCAAAGT TTTGGaGACC TCTATTCTAC CGTTGAACTA 720
45 TGCCCCATT aAAAAATaTA ATkGGAGGGG GGCAGATTCTG AAnTGCCGAA CCCGAAGGAG 780
CGGGATTTAC ATTCCGCCGG GTTT 804

(2) INFORMATION FOR SEQ ID NO: 3544:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3544:

5 ATGATGTCGT TGCACAATCA ATTGATAAAT TACATTATAG CTTTAATCGT TTGAAGTATA 60
 GTTTGAAACC AGTAGTCACA GCTGTTCAAG GTCGTGCCIT AGGCGGTGGC TGTGAGCTTG 120
 TACTTTACTC ACCTATTGTT GTCGCTGCAA GTGAAACATA TATCGGTCTT GTTGAAGCAG 180
 10 GTGTTGGCTT ATTACCGAGT GGCGGTGGCC TTGCAGAAAT GGCTGATCGC ATATTACGCA 240
 CATCGCATAA GTTTGATKAC AAACAAGCTT CCATGACAAA AGTACTGACG AATATCGCAT 300
 TTGCGAAAGT CTCTACAAAT GCCTTTGAGG CACGTCGTTA TGGTTATTTA CGTGGATACA 360
 15 GATACGATTA TTTTCAATAC AGCACACGT GTCCGAAGTT 400

(2) INFORMATION FOR SEQ ID NO: 3545:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 474 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3545:

25 CCGGCATTCT CACTTCTAAG CGCTCCACAT GTCCTTACGA TCATGCTTCA ACGCCCTTAG 60
 AACGCTCTCC TACCATTGTC CAAAGGnATC nCACAGCTTC GGTAATATGT TTAGCCCCGG 120
 30 TACATTTTCG GCGCAGTGTC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGATGGC 180
 TGCTTCTAAG CCAACATCCT AGTTGTCTGG GCAACGCaCA TCCTTTTCCA CTTAACATAT 240
 35 ATTTTGGGAC CTTAGCTGGT GGTCTGGGCT GTTTCCCTTT CGAACACGGA CCTTATCACC 300
 CATGTTCTGA CTCCCAAGTT AAATTAATTG GcATTCTGGAG TTTGTCTGAA TTCGGTAACC 360
 CGAGAGGGGC cCCTCGTCCA AAcAGTGGCT CTACCTCCAA TAATCATCAn TTGAGGCTAG 420
 40 CCCTAAAGCT AATTCGGAGA GAACCAGTAT CTCCAGTTCG ATTGGAATTC TnCG 474

(2) INFORMATION FOR SEQ ID NO: 3546:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3546:

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GCAATTCGTA AAGTTGAAAC ATCAACATTA GGTGAAGAAA GTGAAAATGA CTTTATCGGT 120
 CTGTTTCAGCG ATATGGATTT GAGTTCAACG CGACTAGGTA ACAATGTCAA AGAACGTACT 180
 5 GCTTTAATCT CTAAAGTCAT GGTTAATCTT GACGACTTAC CATTTCGTTCA CAGTGACATG 240
 GAAATTGATA TGTTAGGTGA TGCATATGAA TTCCTAATTG GCGCCTTTGn GCGACACGGG 300
 TAAAAAAGC AGGCGAGTTC TATACACCAC AACCAAGTATC TAAGATACTG GCGAGATTGT 360
 10 CACAGACGGT AAAGATAAnT ACGTCACGTG TATGACCCAA 400

(2) INFORMATION FOR SEQ ID NO: 3547:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3547:

AACGTTTTCA CTTGCCAAG CCATTTTCTT TTGTGTTTAC TTTTATTTT GACGTTTTAG 60
 25 ACATAAAAAA AAGAGACCTT GCGGTCTCAA TCGGCTCAT CGCATCCATT TTTGCTGG 120
 CAACGTCTA CTCTAGCGGA ACGTAAGTTG GCTACCATCG ACGCTAAGAA CCTTCTTGA 180
 CTTGTGACAA TCGCTTGCTT CTTCTCTCTT CTTGGCTCT CGCTTACTCA TTTAGCTCTA 240
 30 CTAAACTCGT TCGCTCTTT TCTCGTTTCG TCAGATTCAA ACGTTTTCAC TTCGCCAAGC 300
 CATTTTCTT TGTGTTTGCT TTTTATTTTG ACGTTTTAGA CATAAAAAA AGAGACCTTG 360
 35 CGGTCTCAAT GCGGCTCATC GCATCCAnTT TTTGCTGGC 400

(2) INFORMATION FOR SEQ ID NO: 3548:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3548:

ATGATGTCGT TGCACAATCA ATTGATAAAT TACATTATAG CTTTAATCGT TTGAAGTATA 60
 50 GTTTGAAACC AGTAGCACA GCTGTTCAAG GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG 120
 TACTTTACTC ACCTATTGTT GTCGCTGCAA GTGAAACATA TATCGGTCTT GTTGAAGCAG 180
 GTGTTGGCTT ATTACCGAGT GGCGGTGGCC TTGCAGAAAT GGCTGATCGC ATATTACGCA 240

55

TTGCAAAGTC TCTACAAATG CCTTTGAGGC ACGTCGTTAT GGTATTATTAC GTGATACAGA 360
TACGATTATT TTCAATACAG CACAACGTGT CCGAAGTTGG 400

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(2) INFORMATION FOR SEQ ID NO: 3549:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3549:

20

AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC GGTGTGTACA 60
AGACCCGGA ACCTATTAC CGTAGCATGC TGATCTACGA TTAGTAGCGA TTCCAGCTTC 120
ATGTAGTCGA GTTGCACT ACAATCCGAA CTGAGAACAA CTTTATGGGA TTTGCTTGAC 180
CTCGCGTTT CGCTGCCCTT TGTATTGTCC ATTGTAGCAC GTGTGTAGCC CAAATCATAA 240
GGGGCATGAT GATTTGACGT CATCCCCACC TTCCTCCGGT TTGTCACCGG CAGTCAACTT 300
AGAGTGCCCA ACTTAATGAT GGCAACTAAG CTTAAGGGT GCGCTCGTTG CGGGACTTAA 360
CCCAACATCT CACGACACGA GCTGACGACA ACCATGCACC 400

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(2) INFORMATION FOR SEQ ID NO: 3550:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3550:

45

CGAACGGACG AGAAGCTTGC TTCTCTGATG TTAGCGGCGG ACGGGTGAGT AACACGTGGA 60
TAACCTACCT ATAAGACTGG GATAACTTCG GGAAACCGGA GCTAATACCG GATAATATTT 120
TGAACCGCAT GGTTCAAAAG TGAAAGACGG TCTTGCTGTC ACTTATAGAT GGATCCGCGC 180
TGCAATTAGCT AGTTGGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG CCGACCTGAG 240
AGGGTGATCG GCCACACTGG AACTGAGACA CGGTCCAGAC TCCTACGGGA GGCAGCAGTA 300
GGGAATCTTC CGCAATGGGC GAAACCTGAC GGAGCAACGC CGCGTGAGTG ATGAAGGTCT 360
TCGGATCGTA AACTCTGTT ATTAGGGAAG AACATATGTG 400

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(2) INFORMATION FOR SEQ ID NO: 3551:

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(A) LENGTH: 506 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3551:

10	ACAAGGTAGC CGTATCGGAA GGTGCGGCTG GATCACCTCC TTTCTAAGGA TATATTCGGA	60
	ACATCTTCTT CAGAAGATGC GGAATAACGT GACATATTGT ATTCAGTTT GAATGTTTAT	120
	TTAACATTCA AATATTTTTT GGTAAAGTG ATATTGCTTA TCGAGCGCT TGACAATCTA	180
15	TTCTTTTAA AGAAAGCGGT TGTTAGACAA TGCATTAAGA AAAATTAAAG CGGAGTTTAC	240
	TTTTGTAAAT GAGCATTTGA TTTTTGAAA ATAAAGCAGT ATGCGAGCGC TTGACTAAAA	300
	AGAAATTGTA CATTGAAAAC TAGATAAGTA AGTAAAATAT AGATTTTACC AAGCAAAACC	360
20	GAGTGAATAA AGAGTTTAA ATAAGCTTGA ATTCATAAGA aTAATCGCTA GTGTCGAAA	420
	GAACACTCAC AAGATTAATA ACGCGTTTAA ATCTTTTAT AAAAGAnAAC GTTTAGCAGA	480
25	CAATGAGTTA AATTATTTTA AAGCAG	506

(2) INFORMATION FOR SEQ ID NO: 3552:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3552:

	AAGCTGAGGC CGACAGTGGn GCGATGGATA ACAGGTTGAT ATTCCTGTAC CACCTATAAT	60
	CGTTTTAATC GATGGGGGA CGCATAGGAT AGGCGACGTG TCGATTGGAT TGCACGTCTA	120
40	AGCAGTAAGG CTGAGTATTA GGCAAATCCG GTACTCGTTA AGGCTGAGCT GTGATGGGA	180
	GAAGACATTG TGTCTTCgAG GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA	240
	AAATAGGTGC CCGTACCGCA AACCGACACA GGTAGTCAAG ATGAGAATTC TAAGGTGAGC	300
45	GAGCGAACTC TCGTTAAGGA ACTCGGCAA ATGACCCCGT AACTTCGGGA GAAGGGGTGC	360
	TCTTTAGGGT TAACGCCAG AAGAGCCGCA GTGAATAGGC CCAAGCGACT GTTTATCAAA	420
50	AACACAGGTC TCTGCTAAAC CGTAAGtGAn TGTATAGGGG CTGACGCCTG CCCGGTGCTG	480
	GAAGGTTAAG AGGAGTGGTT AGCTTCTGCG AAcTAcGaAT CGAAGCCCCA GTAAACGGCG	540
	GCCGTAAC TAACGGTCCT AAGGTAGCGA AATTCCTTGT CGGGTAAGTT CCGACCCGCA	600

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GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT 720
 5 GATATTGAAA TTCGGCACAG CTTGTACAGG ATAGGTAGGA GCCTTTGAAA CGTGAGCGCT 780
 AcTTaCgTGG aGGCGCTGGT GGGATACTAC CCTAGCTGTG TTGGCTTTCT AACCCGCACC 840
 ACTTATCGTG GTGGGAGACA GTGTCAGGCG GGCAGTTTGA CTGGGGCGGT CGCCTCCTAA 900
 10 AAGGTAACGG AGGCGCTCAA AGGTTCCCTC AGAATGGTTG GAAATCATT C ATAGAGTGTA 960
 AAGGCATAAG GGAGCTTGAC TGCAGACCT ACAAGTCGAG CAGGGTCGAA AGACGGACTT 1020
 AGTGATCCGG TGGTTCCGCA TGAAGGGCC ATCGCTCAAC GGATAAAAGC TACCCCGGGG 1080
 15 ATAACAGGCT TATCTCCCC AAGAGTTCAC ATCGACGGG AGGTTTGGCA CCTCGATGTC 1140
 GGCTCATCGC ATCCTGGGGC TGTAAGTCGGT CCCAAGGGT GGGCTGTTCTG CCCATTAAAG 1200
 CGGTACrmGg CTGGGTTCAG AACGTCGTGA GaCAGTTTCGG TCCCTATCCG TCGTGGGCGT 1260
 20 AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG 1320
 TACCAGTTGT CGTGCCAACG cATnAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA 1380
 AAcATnCTnA AGCATGAAGC CCCCCTCAAG ATGAGATTTC CCAACTTCGG TTATAAGATC 1440
 25 CCTCAAAGAT GATGAGGTTA ATAGGTTCTGA GGTGGAAGCA TGGTGACATG TgGGAGCTGA 1500
 CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACAAA tnCaCTTTTA 1560
 CTTACTATCT AGTTTTGAAT GTATAAATTA CATTATATG TCTGGTACT ATAGCAAGGA 1620
 30 GGTCACACCT GTTCCCATGC CGAACACAGA AGTTAAGCTC CTTAGCGTCG ATGGTAGTCG 1680
 AACTTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAGTTT TTTAATCAAA TTTTGTTAA 1740
 35 AAAATAAAAT GGACAAGATA AAAAAAGTTA TTGACTTAAA TGTTAATAAA ATGTATAATT 1800
 AATTCTTGTC GGTAAGAAAA ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT 1860
 TCCAAAAAAC GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT 1920
 40 CATAATTTTT ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA 1980
 CATGCAAGTC GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG 2040
 AGTAACACGT GGATAACCTA CCTATAAGAC TGGGATAACT TCGGGAACC GGAGCTAATA 2100
 45 CCGGATAATA TTTGAACCG CATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCACCTATA 2160
 GATGGATCCg CGCTGCATTA GCTAGTTGGt AAGGtAACGG CTTTACCCA 2209

(2) INFORMATION FOR SEQ ID NO: 3553:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 518 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3553:

5 CTAGATAAGT AAGTAAAATA TAGATTTTAC CAAGCAAAAC CGAGTGAATA AAGAGTTTTA 60
 AATAAGCTTG AATTCATAAG AAATAATCGC TA_gTGTTCTGA AAGAACACTC ACAAGATTAA 120
 TAACGCGTTT CCTGTAGGAT GGAAACATAG ATTAAGTTAT TAAGGGCGCA CGGTGGATGC 180
 10 CTTGGCACTA GAAGCCGATG AAGGACGTTA CTAACGACGA TATGCTTTGG GGAGCTGTAA 240
 GTAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT GTCATGTTAT 300
 15 CGATATGTGA ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC 360
 CCGGAGGAAG AGAAAGAAAA TTCGATTCCC TTAGTAGCGG CGAGCGAAAC GGGAAGAGCC 420
 CAAACCAACA AGCTTGCTTG TTGGGGTTGT AGG_aCACTCT ATACGGAGTT AC_aAAG_mCG 480
 20 ACATT_rGACG AaTCATCTGG gAAAG_wTGaT CCAAGGAA 518

(2) INFORMATION FOR SEQ ID NO: 3554:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 587 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3554:

AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG CAGATGCTCT CCCAGCTGAG 60
 CTAATTCTCC GATTTAAAC TGCTTGCAA CGTTCTACTC TAGCGGAACG TAAGTT_sGAC 120
 35 TACCATCGAC GCTAAGGAGC TTAAC_tTTCTG TGTTCGGCAT GGGAACAGGT GTGACCTCCT 180
 TGCTATAGTC ACCAGACATA TGAATGTAAT TTATACATTC AAAACTAGAT AGTAAGTAAA 240
 40 AGTGATTTTG CTTGCAAAA CATTTATTTT GATTAAGTCT TCGATCGATT AGTATTCGTC 300
 AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGAT 360
 CTTATAACCG AAGTTGGGAA ATCTCATCTT GAGGGGGGCT TCATGCTTAG ATGCTTT_cCAG 420
 45 CACTT_atCCC GTCCACACAT AGCTACCCAG CTATGCCGTT GGCACGACAA CTGGTACACC 480
 AGAGGTATGT CCATCCCGGT CCTCTCGTAC TAAGGACAGC TCCTCTCAA TTTCTACGC 540
 CCACGACGG_a TAGGG_aCCGA ACTG_tCTCAC GACGTTCTGA ACCCAGA 587

(2) INFORMATION FOR SEQ ID NO: 3555:

(i) SEQUENCE CHARACTERISTICS:

55 (A) LENGTH: 399 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3555:

	GAATCTGAAT CGCTATCTGA ATCCGAGTCA CTGTCGGAAT CTGAGTCACT GTCGGAATCT	60
10	GAATCGCTAT CTGAATCTGA ATCGCTGTCT GAATCTGAAT CGCTGTCTGA ATCTGAGTCG	120
	CTATCTGAGT CGGAATCGCT ATCTGAGTCG GAATCACTGT CGGAATCTGA ATCGCTGTCT	180
	GAGTCGGAAT CACTGTCTGGA GTCAGAATCG CTGTCTGAGT CGGAATCACT GTCGGAATCT	240
15	GAATCGCTAT CTGAATCTGA ATCGCTATCT GAATCCGAGT CACTGTCTGa GTCAGAATCG	300
	CTATCTGGAA TCTGGAGTCA CTGTCGGAAT CTGAGTCACT GGTCTGGAGT CAGAATCGCT	360
20	ATCTGGAATC CGAnGTCATG GTCTGAGTCG GGaATCGCT	399

(2) INFORMATION FOR SEQ ID NO: 3556:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3556:

	ATTCATCTTT CCAGATGATT CGTCTAATGT CGTCCTTTGT AACTCCGTAT AGAGTGTCTT	60
	ACAACCCCAA CAAGCAAGCT TGTTGGTTTG GGCTCTTCCC GTTTCGCTCG CCGCTACTAA	120
35	GGGAATCGAA TTTTCTTTCT CTTCCTCCGG GTACTAAGAT GTTTCAGTTC TCCGGGTGTG	180
	CCTTCTGATA TGCTATGTAT TCACATATCG ATAACATGAC ATAACTCATG CTGGGTTTCC	240
40	CCATTCGGAA ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG	300
	TAACGTCCTT CATCGGCTTC TAGTGCCAAG GCATCCACCG TCGGCCCTTA ATAACCTAAT	360
	CTATGTTTCC ATCCTACAGG AAACGCGTTA TTAATCTTGT	400

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(2) INFORMATION FOR SEQ ID NO: 3557:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 657 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3557:

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ACAACTGGTA CACCAGAGGT ATGTCCATCC CGTCCTCTC GTACTAAGGA CAGCTCCTCT 120
 CAAATTTCTT ACGCCACGA CGGATAGGGA CCGAACTGTC TCACGACGTT CTGAACCCAG 180
 5 CTCGCGTACC GCTTTAATGG GCGAACAGCA AnCCCTTGGG ACCGACTACA GCCCCAGGAT 240
 GCGATGAGCc GACATCGAGG TGCCAAACCT CCCCCTCGAT GTGAACTCTT GGGGGAGATA 300
 10 AGCCTGTTAT CCCCAGGGTA GCTTTTATCC GTTGAGCGAT GGCCCTTCCA TGCGGAACCA 360
 CCGGATCACT AAGTCCGTCT TTCGAcCCTG CTCGACTTGT AGGTCTCGCA GTCAAGCTCC 420
 CTTATGCCTT TACACTCTAT GAATGATTTC CAACCATTCT GAGGGAACtT TGAGCGCCTC 480
 15 CGTTACCTTT TAGGAGGCGA CCGCCCCAGT CAAACTGCCc GCcTGACACT GTCTACcmCC 540
 ACGATAAGTG GTGCGGGTTm GmAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGCCTn 600
 CCCACTAATA GCGCTCACGT TTCAAAGGCT CCTACCTATC CTGTACAAGC TGTGCCG 657

(2) INFORMATION FOR SEQ ID NO: 3558:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3558:

GAGTCCATGG GTGAAAGAAG CATCTGCAGC AACTGTAGCA GGTATTGCTG GAACTAATAA 60
 TGGTATTACT GTTGACAGCAG GTACTTTCAA CCCTGCTGAT ACAATTCAAG TTGTTGCAAC 120
 35 GCAAGGACAG CGGAGAGACA GTGAGTGATG AGCAACGTAT nnTnGATTTC ACAGTTGTCG 180
 CACCACAACC GAACCAAGCG ACTACTAAGA TTTGGCAAAA TGGTCATATT GATATCACGC 240
 CTAATAATCC ATCAGGACAT TTAATTAATC CAACTCAAGC AATGGATATT GCTTACACTG 300
 40 AAAAAAGTGGG TAATGGTGCA GAACATAGTA AGACAATTAA TGTGTTCGT GGTCAAATA 360
 ATCAATGGAC AATTGCGAAT AAGCCTGACT ATGTAACGTT 400

(2) INFORMATION FOR SEQ ID NO: 3559:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3559:

CGACACAAAA CAAGCCAAGC AAAACAAACG CATATAACGT AACACACAT GGAAACGGCC 120
 AAGTATCATA TGGCGCTCGC CAACACAAAA CAAGCCAAGC AAAACAAATG CATACAACGT 180
 5 AACACACAT GCAAACGGTC AAGTGTCTATA CGGAGCTCGC CCGACATACA AGAAGCCAAG 240
 TAAAACAAAT GCATACAATG TAACAACACA TGCAGATGGT ACTGCGACAT ATGGGCCTAG 300
 10 AGTAACAAAA TAAGTTTGTA ACTCTATCCA AAGACATACA GTCAATACAA AACATTACGT 360
 ATCTTTACAA CAGTAATCAT GCATTCTATG ATGCTTCTAA 400

(2) INFORMATION FOR SEQ ID NO: 3560:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 485 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3560:

TTTAGGTTAT ACAGCATTGC AGGCAGGATA CTTATCAATT ACTTATTTAA TCATGGTGTT 60
 25 ATTGATGATT CGAGTTGGTG AAAAATTATT ACAAAAAATG GGTCTAAGC GACCAATGTT 120
 ATTAGGTACA TTCATTGTGG TCATTGGTAT TGCATTATT TCATTAGTAT TCTTACCAGG 180
 30 CATATTTTAT GTTATCAGTT GTGTCGTAGG ATATTTATGT TTCGGACTION GCTTAGGTAT 240
 TTATGCAACA CCTTCTACAG ATACAGCTAT TTCGAATGCA CCGTTAGATA AAGTTGGCGT 300
 TGCTTCAGGT ATTTATAAAA TGGCTTCATC ACTTGGTGGG CGCATTCCGT GTCGCAATTA 360
 35 GTGGTGCTGT ATATGCTGGT GCAGTTGCTG CAACGAGCAT TCCATACAGG TGCGATGATT 420
 GCACTTTGGG TTAACGTATT GAATGGGGAA TCCATGGCCA TTTATCGCAA TTTTAATnCG 480
 CGATT 485

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(2) INFORMATION FOR SEQ ID NO: 3561:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3561:

AAATTATGTG AAGTAAAAGG AGTACGTCCA TGCAAAATTT AGATAAGAAT TTTCGACaTT 60
 TATCtCGTAA AGAAAAGTTA CaACAATTGG TTGATAAGCA ATGGTTATCA GAAGAACAAT 120

55

ATGTCATCGC GCAAGGTGCA TTACCCGTTG GATTATTACC GAATATCATT GTGGACGATA 240
 AGGCATATGT TGTACCTATG ATGGTGGAAG AGCCTTCAGT TGTCGCTGCA GCTAGTTATG 300
 5 GTGCAAAGCT AGTGAATCAG ACTGGCGGAT TTAAACGGT ATCTTCTGAA CGTATTATGA 360
 TAGGTCAAAT CGTCTTTGAT GCGGTTGACG ATACTGAAAA ATTATCAGCA GACATTAAAG 420
 CTTTAGAAAA GCAAATTCAT AAAATTGCGG ATGAGGCATA TCC 463
 10

(2) INFORMATION FOR SEQ ID NO: 3562:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 643 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3562:

AATTTAAACC CAATTGTCTG GCAAAACGTT TTCCTTTATA AAAAGATTTA AACGCGTTAA 60
 TTAATCTTGG TGCnGGTCTT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT 120
 25 TAAACTCTT TATTCACCTG GTTTTGCTTG GTAAATCTA TATTTTACTT ACTTATCTAG 180
 TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA CTGCTTTATT TTCAAAAAAT 240
 CAAATGCTCA TTTACAAAAG TAAACTCCGC TTAAATTTTT CTTAATGCAT TGTCTAACAA 300
 CCGCTTTCTT TAAAAAGAAT AGATTGTCAA GCGCTCGCAT AAGCAATATC ACTTTAACCA 360
 AAAAAATTTT GAATGTTAAA TAAACATTCA AACTGAATA CAATATGTCA CGTTATTCCg 420
 35 CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAG GAGGTGATCC AGCCGCACCT 480
 TCCGATACGG CTACCTTGtT ACGACTTCAC CCCAATCATT TGTCCACCT TCGACGGCTA 540
 GCTCCTAAAA GGTTACTCCA CCGGCTTCGG GTGTTACAAA CTCTCGTGGT GTGACGGGCG 600
 40 GTGTGTACAA GACCCGGGAA CGTATTCACC GTAGCATGCC TCG 643

(2) INFORMATION FOR SEQ ID NO: 3563:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3563:

GATAAATCCA AATAGTGCAC TATAAAAAAT AATATCTACT AAAGTATCTT TATGTAATCC 60
 55

TTCCATACCA TCGTACACTC AGTGGTCCTA AGTTAAATGC CACAGGATCT ATATAGTTAA 180
 ATACAATACC CATTCAACCT ACTCCTCACT CTTATGACTG TTCTTGATAA TTTCTTCATT 240
 5 TAATCTTTCA CTAAATTCTT CGGCCGTGTT AATGCCCATG ATATTTAATC GATAGTTCAT 300
 TGCAGCGACC TCAATAATTA CCGCAACATT TCTACCAGGT CTTACAGGTA TTGGTTTTTT 360
 TTAGTGGnTT TCAGTATCTA AAATACTTAG CGTCTCTTCA 400

(2) INFORMATION FOR SEQ ID NO: 3564:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3564:

TCGTCAGCnC nTGTCGTGAG ACgTTGGGTT AAGTCCCGCA ACGAGCGCAA CCCTTAAGCT 60
 TAGTTGCCAT CATTAAgTTG GGCACtCTAA GTTGACTGCC GGTGACAAAC CGGAGGAAGG 120
 25 TGGGGATGAC GTCAAATCAT CATGCCcCTT ATGATTTGGG CTACACACGT GCTACAATGG 180
 ACAATACAAA GGGCAGCGAA ACCGCGAnGT CAAGCAAATC CCATAAAGTT GTTCTCAGTT 240
 CGGATTGTAG TCTGCAACTC GACTACATGA AGCTGGAATC GCTAGTAATC GTAGATCAGC 300
 30 ATGCTACGGT GAATACGTTC CCGGGTCTTG TACACACCGC CCGTCACACC ACGAGAGTTT 360
 GTAACACCCG AAGCCGGTGG AGTAACtTTT AGGAGCTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3565:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3565:

CAAACCATTt GTAGCTATTt GTAActCTTA TATTGATATT GTTCCTGGAC ATGTTCACTT 60
 GAGAGAGCTT GCAGATATAG CTAAAGAAGC AATTAGAGAA GCCGGTGCCA TTCCATTtGA 120
 50 ATTCAATACA ATTGGTGTtG ATGATGGAAT AGCTATGGGA CATATCGGAA TGCGATATTC 180
 TCTACCATCA CGTGAAATTA TTGCAGATGC AGCTGAAACT GTAATTAAACG CTCATTGGTT 240
 TGACGGCGTA TTTTACATTc CTAATTGTGA CAAGATTACA CCCGGTATGA TTTTAGCAGC 300

TGCACATGGA AAAGCATTAA CACTTTCATC AATGTTTGAA

400

(2) INFORMATION FOR SEQ ID NO: 3566:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 420 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3566:

AAATTACGTA CATATTTAAA GCTGACGGCA CTATGACTGC AGGAACATCT GCCCCACTTT 60
 CTGATGGTGC AGGATTTGTA GTTTTAATGT CTGGAGATAA AGTGAAAGAA CTCGGcGTGA 120
 CACCTATTGC ACGATTCTGT GGTTTTAAGG CAGTAGGCGT TGACCCGAAA ATTATGGGTA 180
 TTGGGCCTGC ATATGCGATT CCTGAAGTAT TGTCCTCAG CAATCTATCT GTTGAAGACA 240
 TTGATTGAT CGAATTGAAC GAAGCATTTG CTTCTCAAAC GATTGCATCT ATTAAAGAAG 300
 TAGGTCTAGA TATATCACGT ACGAATGTGA ATGGTGGCGC TATTGCTTka GGTCATCCAT 360
 TAGGTGCTAC AGGCGCaATG TTAACCGCGC GTTFACTTAA TGAAATGGGT AGACGTCCCG 420

(2) INFORMATION FOR SEQ ID NO: 3567:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3567:

TACGGGAAGT AGCTCAGCTT GGGTAGAGCA CTTGGTTTGG GACCAAGGGG TCGCAGGTTc 60
 GAATCCTGTC TTCCCGATAT ACTGTAATTA TTATGGGGGC TTAGCTCAGC TGGGAGAGCG 120
 CCTGCTTTGC ACGCAGGAGG TCAGCGGTTC GATCCCGCTA GTCTCCACCA TATTATTTAC 180
 AAATATATA AGGCGGTGTA GCTCAGCTGG CTAGAGCGTA CGGTTcATAC CCGTGAGGTC 240
 GGGGGTTCGA TCCCCTCCAC CGCCACTATT TATTAGTTGT AAAATTATAT TTAGGACCTT 300
 TAGCTCAGTT GGTTAGAGCT AACGGCTCAT AACCGTTcGG TCGCAGGTTc GAGTcCTGCA 360
 GGTCCCATAT AATTTTGGAG GAATACCCAG TCCGGCTGAA 400

(2) INFORMATION FOR SEQ ID NO: 3568:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3568:

	TTAGCCAATC CCCATTCTGG ACGTACCTCA CTCCAATCAC TCGCAAACCG CTGCGCTTCT	60
10	TCCACTGGAT GATTACACAG ACCAATCGTT GGCAGTTTGT CCAAACGTTT GCGATTCCGT	120
	GTTTCAGAAA TCATCGGCAT CGCGTCATTC AATGATTCAT ATGCATCTAA AGCAATAGAA	180
	GATAATGTGT CTGGCACATA TACCCATGCC AACGTATCAG TAGACGTATG ATGTTCTGCT	240
15	ACCGCAAAAA CAGTTGTCTC TGGAnTATAC ACACCTGATT GTTTTAATCC TTGTCTGACA	300
	TTTGACGAT TACATATCAT CGCTAATAAC TTAGCATtnA AAACCGCTTG ATGCGCCACC	360
20	ACAAGCCCCA CATTTCAAGT GATGGCATGG nTGTTGGTTn	400

(2) INFORMATION FOR SEQ ID NO: 3569:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3569:

	CCCCGACCTC ACGGGTATGA ACCGTACGCT CTAGCCAGCT GAGCTACACC GCCTTATATA	60
	GTTTGTAAT AATATGGTGG AGACTAGCGG GATCGAACCG CTGACCTCCT GCGTGCAAAG	120
35	CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC ATAATAATTA CAGTATATCG GGAAGACAGG	180
	ATTGGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT ACCAAGCTGA GCTACTTCCC	240
	GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT CTTGATCCGT AGTCAAACGC	300
40	TCTATCCAAT TGAGCTACGG GCGCATATGT TTTTATTGAA AATGGTGCCG AGGACCGGAA	360
	TCGAACCGGT ACGTGATCAC TCACCGCAGA TTTTAAGTCC	400

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(2) INFORMATION FOR SEQ ID NO: 3570:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 542 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3570:

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GTTTTTATCC GTTGAGCGAT GGCCnTCCCA TGGGGACCTA CCGGATCACT AAGTCCGTCT 120
 TTTTCGACCCT GCTTCGACTT GTAGGTCTCG CAGTCAAGCT CCCTTATGCC TTTACACTCT 180
 5 ATGAATGATT TCCAACCATT CTGAGGGAAC CTTTGAGCGC CTCCGTTACC TTTTAGGAGG 240
 CGACCGCCCC AGTCAAAGCT CCCGCCTGAC ACTGTCTCCC ACCACGATAA GTGGTGCGGG 300
 10 TTAGAAAGCC AACACAGCTA GGGTAGTATC CCACCAGCGC CTCCACGTaA GyTAGCGCTC 360
 ACGTTTCAAA GGCTCCTACC TATCCTGTAC AAGCTGTGCC GAATTTCAAT ATCAGGCTAC 420
 AGTAAAGCTC CACGGGGTCT TTCCGTCTCG TCGCGGGTAA CCTGCATCTT CACAGGTAAT 480
 15 ATGATTTTAC CGAGTCTCTC GTTGAGACAG TGCCCAAATC GTTACGCCTT TCGTGCGGGT 540
 CG 542

(2) INFORMATION FOR SEQ ID NO: 3571:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 619 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3571:

30 ATGCCCCGACC ACATGGAGCT TCCAATCCCA TTGCTCTAAC CAATGAGCTA CTGAACCATA 60
 aTaAAAATGT AATGATGGCG GTCTCGACGG GAATCGAACC CGCGATCtCh GCGTGACAGG 120
 CAGGCGTGTT AACCCCTACA CTACGAGACC TATAAAATAT TGCGGGAGGC GGATTTGAAC 180
 35 CACCGGACTT CGGGTTATGA GCCCCGACGAG CTACCGAACT GCTCCATCCC GCGATAATAA 240
 AAAATAATGG CGGAGGAAGA GGGATTCGAA CCCCCGCGGC CCGTTAAGGc CCTGTGCGTT 300
 TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCTCTC ATTATTATAG GTAAATCGCT 360
 40 ATTAATTATA AAATTAAATG GCGGTCTCGA CGGGAATCGA ACCCGCGATC TCCTGCGTGA 420
 CAGGCAGGCG TGTTAACCGC TACACTACGA GACCATTAGT AAAACGGAGG AAGAGGGATT 480
 CGAACCCCCG CGAGCCGTTA AGCCCCGTGC GGTTTTCAAG ACCGATCCCT TCAGCCGGAC 540
 45 TTGGGTATTCTCCTCAAAATT ATATGGACCT TGCAGGACTC GAACCTkCGA CCGAACGGTT 600
 ATGAGCCGTT AGCTCTAAC 619

(2) INFORMATION FOR SEQ ID NO: 3572:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3572:

5 GGTGAAGACA TCACGTATCA AGAAGCATGG GCAGATGAAG AATATCGTGA AGACTTAAAA 60
 GCAGAATTAA TTGATCAAGC GGTACTTCA TTGAGCCACA AGATTTATTC AGTGCGATGA 120
 TTCGTGAAAT TGAAACGCAA GATTTCGATA TAGAACATCT AGCGACGGCG ATTCGCAAAG 180
 10 TTGAAACATC TACATTAGGT GAAGAAAGTG AAAATGACTT TATCGGGCTG TTCAGCGATA 240
 TGGATTTGAG TTCAACGCGA CTAGGTAACA ATGTCAAAGA ACGTACTGCT TTAATCTCTA 300
 AAGTCATGGT TAATCTTGAC GACTTACCAT TCGTTCACAG TGACATGGAA ATTGATATGT 360
 15 TAGGTGATGC ATATGAATTC CTAATCGGGC GCTTTGCGGC 400

(2) INFORMATION FOR SEQ ID NO: 3573:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3573:

CAAATCGTAA CTCGCCGTT CATTCTACAA AAGGCACGCC ATCACCATT AACGGGCTCT 60
 30 GACTACTTGT AAGCACACGG TTTCAGGTTC TATTTCACTC CCCTTCGGG GTGCTTTTCA 120
 CCTTCCCTC ACGGTACTGG TTCACTATCG GTCACTAGAG AGTATTTAGC CTTAGGAGAT 180
 GGTCCCTCCA GATTCCGACG GAATTTACG TGCTCCGTCG TACTCAGGAT CCACTCAAGA 240
 35 GAGACAACAT TTTCGACTAC AGGATTATTA CTTCTTTGA TTCATCTTTC CAGATGATTC 300
 GTCTAATGTC GTCCTTTGTA ACTCCGTATA GAGTGTCTA CAACCCCAAC AAGCAAGCTT 360
 GTTGGTTTGG GGCTCTTCCC ATTTGCTCG CGGCTACTAA 400

(2) INFORMATION FOR SEQ ID NO: 3574:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 1051 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3574:

50 TCCCTCAAAG ATGGATGAGG TTAATAGGTT CGAGGTGGAA GCATGGTGAC ATGTGGCAGC 60

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TTTACTTACT ATCTAGTTTT GAATGTATAA ATTACATTCA TATGTCTGGT GACTATAGCA 180
 AGGAGGTCAC ACCTGTTCCC ATGCCGAACA CAGAAGTTAA GCTCCTTAGC GTCGATGGTA 240
 5 GTCGAACTTA CGTTCGGCTA GAGTAGAACG TTGCCAGGCA TAATATTAAT CCACAGTAGC 300
 TCAGTGGTAG AGCTATCGGC TGTAAACCGA TCGGTCGTAG GTTCGAGTCC TACCTGTGGA 360
 GCCATGGCTC cTtGGTCAAG CGGTTAAGAC ACCGCCCTTT CACGGCGGTA ACACGGGTTC 420
 10 GAGTCCCGTA GnAGTCATTA TTTTGGAGAA TTAGCTCAGC TGGGAGAGCA TCTGCCTTAC 480
 AAGCAGAGGG TCGGCGGTTC GAACCCGTCA TTCTCCACCA TTTTGATTAT TAAATTATAT 540
 15 GAATAAGCTG GAGGGGTAGC GAAgTGGCTA AACGCGCGCG ACTGTAAATC CGCTcCTTCG 600
 GGTTCGGCAG TTCGAATCTG CCCCCCTCCA CCATCTATAT ATTGGGCTAT AGCCAAGCGG 660
 TAAGGCAACG GACTTTGACT CCGTCACTCG TTGGTTCGAA TCCAGCTAGC CCAGCCATTA 720
 20 GAGCCATTAG CTCAGTTGGT AGAGCATCTG ACTTTTAATC AGAGGGTCAG AGGTTCGAAT 780
 CCTCTATGGC TCACTACTTG CACTTTCCAT TTTTGGGAAG TGCTTTTTTT TAGGTTCTcC 840
 ACCAAATGTG GTGGGtATAT AATTTAAAGA ACTATTTTIA AAATACAAC TTTAGAGCTT 900
 25 TTATTATTAG GCGGCCAGTC CATTATTGGG CTTGGTTGTC TTCTTTTTTT CTCCTTTGtA 960
 CAAGCTGAAA ATCATCATTA TACGTGctTA AAGTGTGAAA TTTCTGTAAC CAAAAGAATn 1020
 30 CACTTGATTA ATInnATCTA TATAATGCCT C 1051

(2) INFORMATION FOR SEQ ID NO: 3575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3575:

GTGGAGCGCT TAGAAGTGAG AATGCAAGTG TGAgTAGCGA AAGACGGGTG AGAATCCCGT 60
 CCACCGATTG ACTAAGGTTT CCAGAGGAAG GCTCGTCCGC TCTGGGTTAG TCGGGTCCTA 120
 45 AGCTGAGGCC GACACGTATG GCGATGGATA ACAGGTTGAT ATTCCTGTAC CACCTATAAT 180
 CGTTTTAATC GATGGGGGGA CGCATAGGAT AGGCGAcGTG sCGATTGGAT TGCACGTCTA 240
 50 AGCAGTAAGG CTGAGTATTA GGCAATCCG GTACTCGTTA AGGCTGAGCT GTgATGGGGA 300
 GAAGACATTG TGTCTTCGAG TCGTTgATTT CACACTGCCG AGAAAAGCCT CTAGATAGAA 360
 AATAgGTGCC CGTaCCGCAA AaCCGACACA GGTAGTCCAA GATGnGAATT CTAAnGTGAA 420

(2) INFORMATION FOR SEQ ID NO: 3576:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3576:

TTTGTTCTT TTTTAATTTA TATATTTAAA ATACACATAT TCAAGAGCTC GAGATATAAG 60
 TCAATGTACT AGGCACACAA TTTAATATTG ACAGTAATTA ACCGAACGAA AATGCGCCCC 120
 GGGGCCCCAA CATAGAGAAT TCGAAAAGA AATTCTACAG ACAATGCAAG TTGGCGGGGC 180
 CCCAACATAG AAGCTGGCCA ATAGTTAGCT TTCAATAATG TGCAAGTTGG GGTAAGGGCC 240
 CCAACACAGA AGCTGGCCAA TAGTCAGCTT TCAATAATGT GCAAGTTGGG GTAAGGGCCC 300
 CAACACAGAG AATTTGAAA AGAAATTCTA CAGACAATGC AAGTTGGCGG GGCCCCAACA 360
 CAGAAGCTGG GCCAATAGTC AGCTTTTCCA ATAATGTGGC 400

(2) INFORMATION FOR SEQ ID NO: 3577:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3577:

TGCATCTTCA CAGGTACTAT GATTTCACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 60
 TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT 120
 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAC TAACCACTCC 180
 TCTTAACCTT CCAGCACCGG GCAGGCGTCA GCCCTATACA TCACCTTACG GTTTAGCAGA 240
 GACCTGTGTT TTTGATAAAC AGTCGCTTGG GCCTATTAC TCGGCTCTT CTGGGCGTTA 300
 ACCCTAAAGA GCACCCCTTC TCCCGAAGTT ACGGGGTCAT TTTGCCGAGT TCCTTAACGA 360
 GAGTTCGCTC GCTCACCTTA GAATTCTCAT CTTGACTAAC 400

(2) INFORMATION FOR SEQ ID NO: 3578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3578:

5 TAACTTAACA CGACTTCTTA AGTCATTTAG TTTTAATGTT TGATGTGTTT CTGCTAAACC 60
 AATCTCCCAA GGAACACCGG CATGCTGAAT ACTCGTTTTG GGTGAAGCCC TGTACCACCA 120
 TCGTAACCAC TGATGACAAT TTTATCTGCA AATGCTTTTG CCACCCAGCA TGCAATGGTA 180
 10 CCAACACCTG TTTTCGAAAC TAATTTTACC GCGATATCTG CATCTTTATT CGCATTTTTC 240
 AAATCATGTA TCAGTTGCGC TAAATCTTCT ATTGAATAAA TATCATGATG TGGCGGTGGT 300
 GAAATCAGAC CGATACCTGG CGTTGGACCC TCTTGCTTTC GCAATCCACG GATATACCTT 360
 15 AGTACCAGGT AATTGGACCA CCTTCACCAG GCTTTCACCC 400

(2) INFORMATION FOR SEQ ID NO: 3579:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3579:

AGCTACACCG CCTTATATAG TTTGTAAATA ATATGGTGGA GACTAGCGGG ATCGAACCGC 60
 30 TGACCTCCTG CGTGCAAAGC AGGCGCTCTC CCAGCTGAGC TAAGCCCCCA TAATAATTAC 120
 AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC AAGTGCTCTA 180
 CCAAGCTGAG CTACTTCCCG TATAATTAAC GCGCCCGATA GGAGTCGAAC CCATAACCTC 240
 35 TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTT TTTATTGAAA 300
 ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA TTTTAAGTCC 360
 TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3580:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3580:

50 ACGTAAATAA CCATAACGAC GTGCCTCAAA GGCATTTGTA GAGACTTTCG CAAATGCGAT 60

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5 TATGCGATCA GCCATTTCTG CAAGGCCACC GCCACTCGGT AATAAGCCAA CACCTGCTTC 180
 AACAAAGACCG ATATATGTTT CACTTGCAGC GACAACAATA GGTGAGTAAA GTACAAGCTC 240
 ACAGCCACCG CCTAAGGCAC GACCTTGAAC AGCTGTGACT ACTGGTTTCA AACTATACTT 300
 CAAACGATTA AAGCTATAAT GTAATTTATC AATTGATTGT GCACGACATC ATCTACAAGA 360
 10 CCGTCTTCCA TGC GCCTTTT TCCATTAAGA AAGGGTTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3581:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3581:

ATGTCATTGT TGGTACGGCT TTTCCAGAAG GATTACAAGG CAAAACATT GCACGAACGA 60
 TTGCATTGCG TGC GGATTAT CTGACACGGT ACCGGGTCAA ACAGTGAATC GCTACTGCTC 120
 25 ATCAGGATTA CAAACCATGC GATTGCAGCC AATCAAATTA TGGCTGGTCA AGGAGATATA 180
 CTTGTAGCTG GTGCGTTGAA TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCACAA 240
 ACAATCCAAC CTTACAATAT GATGATATAG GTGCGTCATA TCCTATGGGT TTAAGTCTG 300
 30 AAAATGTAGC ATCCCAATTT GACGTATCAC GCGAAGATCA AGATGCTTAT GCTGTCAGAA 360
 GTCATCAACG TGCCTATGAC GCACAACGTG ATGGGTCCGG 400

35 (2) INFORMATION FOR SEQ ID NO: 3582:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3582:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT 60
 TTTTCTTTGT GTTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGA GACCTTGCGG 120
 50 TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT 180
 AAGTTGGCTA CCATCGACGC TAAGAACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT 240
 CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC 300

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ATTTTGACGT TTTAGACATA AAAAAAAGAG ACCTTGCGGT

400

(2) INFORMATION FOR SEQ ID NO: 3583:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3583:

AAGCAGGCGC TCTCCAGCT GAGCTAAGCC CCCAAATAGG TATTAAATTA ATGGTGGGCC	60
TAAGTGGACT CGAACCACCG ACCTCACGCT TATCAGGCGT GCGCTCTAAC CAGCTGAGCT	120
ATAGGCCCAT TAATTTGAAT GAACAAACAT TCAAACTGA ATACAATATG TCACGTTATT	180
CCGCATCTTC TGAAGAAGAT GTTCCGAATA TATCCTTAGA AAGGAGGTGA TCCAGCCGCA	240
CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC ATTTGTCCCA CCTTCGACGG	300
CTAGCTCCTA AAAAGGTTAC TCCACCGGCT TCGGGTGTTA CAAACTCTCG TGGTGTGACG	360
GGCGGTGTGT ACAAGACCCG GGAACGTATT TCACCGTAGC	400

(2) INFORMATION FOR SEQ ID NO: 3584:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3584:

ACTTATTTGG CGATATTTTA AGTGATGAAG CTTCAGTGAT TCCTGGTTCA CTTGGTTTAT	60
CACCTTCTGC TAGTTTTAGT AACGATGGTC CAAGATTGTA TGAGCCTATT CATGGATCAG	120
CACCAGATAT TGCAGGTAAG AACGTTGCCA ATCCATTTGG AATGATTCTA TCTTTAGCGA	180
TGTGTTTACG TGAAAGCTTA AATCAACCAG ATGCTGCAGA TGAATTAGAA CAACATATTT	240
ATAGCATGAT TGAACATGGG CAAACGACAG CAGATTTAGG CGGCAAATTG AATACTACTG	300
ATATTTTCGA AATTCTATCT CAAAAATTGA ATCACTAAGG GGGGAGATGT AAATGGGGTC	360
AAACATTATT TGACAAGTG TGGGACAGAC ATGTGTTATA	400

(2) INFORMATION FOR SEQ ID NO: 3585:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3585:

ACTGATGACA ATTTTATCTG CAAATGCTTT TGCCACCCCA GATGCAATGG TACCAACACC 60
 10 TGTTCGAA ACTAATTTTA CCGCGATATC TGCATCTTTA TTCGCATTTT TCAAATCATG 120
 TATCAGTTGC GCTAAATCTT CTATTGAATA AATATCATGA TGTGGCGGTG GTGAAATCAG 180
 ACCGATACCT GCGGTGACC CTCTGTCTT CGCAATCCAC GGATATACCT TAGTACCAGG 240
 15 TAATTGACCA CCTTCACCAG GCTTGCACC TTGCGCAACT TTAATTTGAA TTTCTTTGGG 300
 CATGTTGTAA ATAATCACTA GTTACACCAA AACGCCAGA AGCAACTTGT TTAATCGCAC 360
 TTACTTTGGT GGCTTCCATC AACTTGTA CTATAACGGT 400

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(2) INFORMATION FOR SEQ ID NO: 3586:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3586:

TACAAGTATT ACCATTATCT CnAGAGGATT CTAGATAAGG GGCATGGATC ATTTGTCTTC 60
 TTATGAATTT GAGCCAGATA AAGAATCTAT CTTAAGTGTA ATCTTGACCT CAATATGTTG 120
 35 AGAGTTTGAT TTACGGAACA ATATTAGACG CAAAAGCAAG TGAGCATGCA ACACGTATGA 180
 CTGCGATGAA AAATGCCACT GATAATGCAA CTGAACTTAT TGATGACTTA TCATTAGAAT 240
 ATAACAGAGC GAGACAAGCA GAAATTACGC AACAAATTAC TGAAATTGTT GGTGGTCCG 300
 40 CAGCGCTTGA ATAATATTTA AnGGAGGAAA ATAGCATGGG AATTGGCCGT GTACTCAAGT 360
 TATGGGTCCT GTAATTGATG TTCGATTGA ACATAACGAG 400

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(2) INFORMATION FOR SEQ ID NO: 3587:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3587:

AGGATTGCGAA CCTGCGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120
 CCCGTATAAT TAACGCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180
 5 CGCTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTTATT GAAAATGGTG CCGAGGACCG 240
 GAATCGAACC GGTACGTGAT CACTCACC GC AGGATTTTAA GTCCTGTGCG TCTGCCAGTT 300
 CCGCCACCCC GGCACTATAA AAATGGAGCA GAAGACGGGA TTCGAACCCG CGACCCCAAC 360
 10 CTTGGCAAGG TTGTATTCTA CCGCTGAACT ACTTCTGCAT 400

(2) INFORMATION FOR SEQ ID NO: 3588:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3588:

TACTATTGAC ATGTGTGAAC CCTATGTCCG ATTATTTTCG GACCTATTTT CTAATGCAGC 60
 25 TATTATTTTT GACAGATTCC ATATCGTTCA ACATTTAAAT AGAGAACTTA ATAAGTATCG 120
 TGTACAAGTT ATGAATGAAT ACCGTAATAA AAAAGGACCT GATTATACAA TTTTAAAGAA 180
 TAACTGGAAG GTCCTATTGA TGGATACTAG TAAAACCATA TTTAGTAAAT ACAGATGGAA 240
 30 TAAATCTTTT AAGGGCTTAT AAACGCTCAT CTGACATTGT AGAATTCATG CTTTCAAAAG 300
 ACGATATACT ACGCACTCC TACGAACTTG TCCAGGGATT ACGAAAAGAC CTAAGGGTAT 360
 35 GTAATTGGGC CTAAATTTAT TAATCGTTTA AATTCCGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3589:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3589:

AGAGCGAACG GACGAGAAGC TTGCTTCTCT GATGTTAGCn GCGGACGGGT GAGTAACACG 60
 TGGATAACCT ACCTATAAGA CTGGGATAAC TTCGGGAAAC CGGAGCTAAT ACCGGATAAT 120
 50 ATTTTGAACC GCATGGTTCA AAAGTGAAAG ACGGTCTTGC TGTCATTAT AGATGGATCC 180
 GCGCTGCATT AGCTAGTTGG TAAGGTAACG GCTTACCAAG GCAACGATGC ATAGCCGACC 240

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AGTAGGGAAT CTTCCGCAAT GGGCGAAAGC TGACGGAGCA ACGnCGCGTG AGTGATGAAG 360
 GTCTTCGGAT CGTAAAACTC TGTTATTAGG GAAGAACATA 400

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(2) INFORMATION FOR SEQ ID NO: 3590:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 509 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3590:

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GTTAgGAGAG CGTTCTAAGG GCGTTGAAGC ATGATCGTAA GGACATGTGG AGCGCTTAGA 60
 AGTGAGAATG CCGGTGTGAG TAGCGAAAGA CGGGTGAGAA TCCctCCACC GATTGACTAA 120
 GGTtTCCAGA GGAAGGCTCG TCCGCTCTGG GTTAGTCGGG TCCTAAGCTG AGGCCGACAg 180
 gTaaGGCGAT GGATAACAGG TTGATATTCC TGTACCACCT ATAATCGTTT TaATCGATGG 240
 GGGGACGCAT AGGATAGGCG AACGTGcGAT TGGATTGCAC GTCTAAGCAG TAAGGCTGAG 300
 TATTAGGCAA ATCCGGTACT CGTTaAGGCT GAGCTGTGAT GGGGAGAAGA CATTGwGTCT 360
 TCGAGTCGTT GATTTCACAC TGCCGAGAAA AgCCTCTAGA TAGAAAATAG GTGCCCCGTAC 420
 CGCAAACCGA CACAGGTAAT CCAAGATGAG AATTCTAAGG TGAGCGAGCG AACTCTCGTT 480
 AAGGAACTCG GCAAAATGAC CCCGTAAC 509

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(2) INFORMATION FOR SEQ ID NO: 3591:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3591:

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ATTTCTTATG AATTCAAGCT TATTTAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA 60
 TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA 120
 TCGAACCGCT GACCTCCTGC GTGCAAAGCA GGCCTCTCC CAGCTGAGCT AAGCCCCCAA 180
 ATAGGTATTA AATTAATGGT GGGCCTAAGT GGACTCGAAC CACCGACCTC ACGCTTATCA 240
 GGCGTGCGCT CTAACCAGCT GAGCTATAGG CCCATTAATT TGAATGAACA AACATTCAAA 300
 ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 360

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(2) INFORMATION FOR SEQ ID NO: 3592:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 440 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3592:

TGGGnAACGC AACATCCTTT TCCAACCTAA CATATATTTT GGGACCTTaG CTGGTGGTCT 60
 GGGCTGTTTC CCTTTCGAAC ACGGACCTTA TCACCCATGT TCTGACTCCC aAGTTAAATT 120
 AATTGGCATT CGGAGTTTGT CTGAATTCGG TAACCCGAGA GGGGCCCTC GTCCAAACAG 180
 TGCTCTACCT CCAATAATCA TCACTTGAGG CTAGCCCTAA AGCTATTTTCG GAGAGAACCA 240
 GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCTCA GTTCATCCGC TCACTTTTCA 300
 ACGTAAGTCG GTTCGGTCct CCATTcAGTG TTACCTGAAC TTCAACCTGa CCAAGGGTAG 360
 ATCACCTGGT TTCcGsGTsT ACGACCAAAT AsTAAACGCC CTATTCAGAC TCGCTTTTCG 420
 TanGGCTCCA CATTACTGGn 440

(2) INFORMATION FOR SEQ ID NO: 3593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3593:

TAAACGAACC AATTTTATTT GGTGCACCAC TAGTATTGAA TCCTGTGTTT TTTATTCCAT 60
 TTGTATTAGC ACCAATTGTT AACGTATGGA TTTTCAAAC TTTGTTGAA GTGTTAGGAA 120
 TGAATAGTTT TAGTGTGAAT TTACCTTGGA CAACACCAGG TCCATTGGGC ATTATCATGG 180
 GTACAGGTTT TGGTTTATGG TCATTCGTAC TAGCTATTAC TTTGATTGTT GTAGATATTA 240
 TTATnTACTA CCCATTCTTA AAAGTTTATG ATAGTGAAAT TCTTGATGAA GAAGAAGGAC 300
 GTAAAGAAAG TAATTcAGAT TTAAAGAAA AAGTTGCAGC AAACCTTTGA TACGAAAAAA 360
 GCTGATTCAA TTTTAGCGGC AAGTGGTGTA TCAGACGATG 400

(2) INFORMATION FOR SEQ ID NO: 3594:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 409 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3594:

	AAGGGAATCG AATTTTCTTT CTCTTCCTCC GGGTACTAAG ATGTTTCAGT TCTCCGGGTG	60
10	TGCCTTCTGa TATGCTATGT ATTCACATAT CGATAACATG ACATAACTCA TGCTGGGTTT	120
	CCCCATTTCGG AAATCTCTGG ATCAAAGCTT aCTaCAGCTC CCCAAAGCAT ATCGTCGTTA	180
	GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA	240
15	TCTATGTTTC CACCATTTTT ATAAGTCAAA CGCTCACATA CGGCTTCGTT TTCATTATTT	300
	TAAATGCTCA TTTACATAAG TAAACTCTGC TTTAAATAA TTAACTCAT TGTCTGCTAA	360
	ACGTTTTCTT TTATAAAAAG ATTTAAAcGC GTTAtTAATC CTCTCGCTC	409

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(2) INFORMATION FOR SEQ ID NO: 3595:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3595:

	AATATAAGCC CTGGATCATA CATGACCTGT ATTTGGGCAA TCCCTTCTGC TACATCTTCT	60
	GCCCACTCAT TCAATATTTG TTTTGCAATA TCATCACCTT CTTAGCTGC TTCAAACAAT	120
35	ACTGGCACAT GTGTGCTTCT CGTAAATCCT CCGGCAATCA TCGGCTTTTT CAATGCACTC	180
	GTTCAGCAC GTTGCTCAAA CGTTGTATTT TCAAGTTGGAC GATACAATAA ATACCCAAC	240
	TCATTTGCCT TATGAAGCTC ACCATTATCA ATATGACCTT GGATTATTCT TGTACGCACC	300
40	CCCAATGGCC TGGTACCAAG CGTCCATACA AAAGATCCGT TCTGGCTTGG ATATTGGATG	360
	GTAATTTCCA ATTCGGCCTA GTTAATGGCA GCGGTTTTAA	400

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(2) INFORMATION FOR SEQ ID NO: 3596:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 596 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3596:

CTGCCGAACC CGAAGAGCGG ATTTACAGTC CGCCGCGTTT AGCCACTTCG CTACCCTCCA 120
 GCTTATTCAT ATAATTTAAT AATCAAAATG GTGGAGAATG ACGGGTTCGA CCGCCGACCC 180
 5 TCTGCTTGTA AGGCAGATGC TCTCCCAGCT GaGCTAATTC TCCAAAATAA TGA CTCCTAC 240
 GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGtGTCT TAACCGCTTG ACCAAGGAGC 300
 CATGGCTCCA CaGGTAGGAC TCGAACCTAC GACCGATCGG TTAACAGCCG ATAGCTCTAC 360
 10 CACTGAGCTA CTGTGGaTTA ATATTATGCC TGGcAACGTT CTACTCTAGC GGAACGTAAG 420
 TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 480
 15 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTA 540
 AGTAAAAGTG ATTTTGCTTC GCAAAACATT TATTTTGATT AAGTCTTCGA TCGATT 596

(2) INFORMATION FOR SEQ ID NO: 3597:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3597:

TCATCTTGAG GGGGGCTTCA TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC 60
 30 TACCCAGCTA TGCCGTTGGC ACGACAAC TGACACCAGA GGTATGTCCA TCCCGGTCCT 120
 CTCGTACTAA GGACAGCTCC TCTCAAATTT CCTACGCCCA CGACGGATAG GGACCGAACT 180
 GTCTCACGAC GTTCTGAACC CAGCTCGCGT ACCGCTTTAA TGGGCGAACA GCCCAACCCT 240
 35 TGGGACCGAC TACAGCCCCA GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT 300
 CGATGTGAAC TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG 360
 40 CGATGGCCCT TCCATGCGGA ACCACCGGAT CAATAAAGTC 400

(2) INFORMATION FOR SEQ ID NO: 3598:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 397 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3598:

AACCAACGGC AGCAACTACA TGACCTAATT CTTGTGCTGA CTCTACATTT AGTAGCTCTA 60

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CACTTCAATT GTACCAATCA ATCGTTGACG ATCTTGATCG TAACGCCATG TAGCAATACC 180
 ACGATACTGT CCGTCACGAC TCGCGTATGC ATGCGCACTT GCTTCTGCAC CACGCGTATC 240
 5 ATTTCTCTGTT GCTAAAACAA CAGCATGTAT GCCATTCATA ACACCTTTAT TATGTGTTGC 300
 TGCACGATGA ATATCTACTT GGGCCAATAC AGAAGCACGT TCCATCGTTT GcaACCTCTT 360
 CTCCAGTTCT CTCGCCCCCTT GGCTAAATCT TTAACAT 397

(2) INFORMATION FOR SEQ ID NO: 3599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3599:

AACCCTTGGG ACCGACTACA GCCCCAGGAT GCGATGAGCC GACATCGAGG TGCCAAACCT 60
 CCCCCTCGAT GTGAACTCTT GGGGGAGATA AGCCTGTTAT CCCCAGGGTA GCTTTTATCC 120
 25 GTTGAGCGAT GGCCCTTCCA TCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG 180
 CTCGACTTGT AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTC 240
 CAACCATTCT GAGGGAACCT TTGAGCGCCT CCGTTACCTT TTAGGAGGCG ACCGCCCCAG 300
 30 TCAAAGTGCC CGCCTGACAC TGTCTCCAC CACGATAAGT GTGCGGGTGA GAAAGCCAAC 360
 ACAGCTAGGG TAGTATCCCA CCAGCGCCTC CAACGTAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3600:

ATCTGAATCT GAGTCGTTGT CTGAGTCCGA ATCGCTATCT GAATCTGAGT CGCTATCTGA 60
 GTCTGAGTCG CTATCTGAAT CTGAGTCGCT GTCTGAATCT GAATCACTGT CTGAGTCTGA 120
 50 GTCGCTGTCT GAGTCTGAAT CGCTGTCAGA ATCTGAGTCG CTATCTGAGT CTGAATCTGA 180
 ATCACTGTCT GAGTCCGAAT CGCTATCTGA ATCTGAATCG CTATCTGAGT CTGAGTCGCT 240
 ATCCGAATCT GAGTCGCTAT CTGAGTCTGA GTCGCTATCC GAGTCTGAAT CGCTGTCTGA 300

GGTCTGGAAT CTGAnTCGCT AACTGAAATC TGAGTCGCTA

400

(2) INFORMATION FOR SEQ ID NO: 3601:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3601:

ATTTAATACC TATTGGGGG CTTAGCTCAG CTGGGAGAGC GCCTGCTTTG CACGCAGGAG 60
 GTCAGCGGTT CGATCCCGCT AGTCTCCACC ATTATTTGTA CATTGAAAAC TAGATAAGTA 120
 AGTAAATAT AGATTTTACC AAGCAAAACC GAGTGAATAA AGAGTTTTAA ATAAGCTTGA 180
 ATTCATAAGA AATAATCGCT AGTGTTTCGAA AGAACATCCA CAAGATTAAT AACGCGTTTA 240
 AATCTTTTAA TAAAGAACG TAACTTCATG TTAACGTTTG ACTTATAAAA ATGGTGGAAA 300
 CATAGGTAA GTTATTAAGG GCGCACGGTG GGATGCCTTG GCACTAGAAG CCGATGAAGG 360
 GnCGTTACTA ACGACGATAT GCTTTGGGGA GCTGTAAGTA 400

(2) INFORMATION FOR SEQ ID NO: 3602:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3602:

GCTGTCTGAG TCGGAATCAC TGThGGAGTC AGAATCGCTG TCTGAGTCGG AATCACTGTC 60
 GGAATCTGAA TCGCTATCTG AATCTGAATC GCTATCTGAA TCCGAGTCAC TGTCTGAGTC 120
 AGAATCGnTA TCTGAATCTG AGTCACTGTC GGAATCTGAG TCACTGTCTG AGTCAGAATC 180
 GCTATCTGAA TCCGAGTCAT TGTCTGAGTC GGAATCGCTC GCTGAGTCGG AATCGCTTGC 240
 TGAATCTGAA TCACTCGCTG AGTCTGAATC ACTTGCTGAA TCTGAATCAC TCGCTGAATC 300
 TGAACCACTA TCTGATGTAG GAATCACTAC CCGAATCTGA AnCGCTATCT GAATAAGAAT 360
 CGCTGCCAGA TCTGAACCTG GGGTCAGAAT CTGAAT 396

(2) INFORMATION FOR SEQ ID NO: 3603:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 529 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3603:

TTTCTTATCT GTAATTTTAT CGTAAGATTT TTTGCAATG AGATTGGAT CGTnTTTGTC 60
 10 CACTACAATA TCTAATAGTT TTACTTTAAG TCCAGCATT CAAAAAGTG CTGCCAGTTG 120
 AGCGCCCAT GTGCCTGCGC CAAGAACGGT TACTTTATTA ATTGTCATAG TGATTCCTCC 180
 AATTAGTTG AGGATAAGAT AACCATTAAG ATAATTGGAA TAACGTTGCT ATTTTATAAA 240
 15 ATTAATTAAG TATCTTTGAC AGTCATCTTA GCCTCTTATT TAAGGaAAAA GCTTTATGCT 300
 TAAATAAGT CTTTTTTAGT GAAATTAATG CATCTCATAT AATTATTTGC TATTTATACG 360
 AAAGCmGaAT CTCCAGTCaA AGCGCGTCCA ATTACTAAGG CATTAAATTC ATGTGTACCT 420
 20 TCGTACGTGT AAATCGCTTC TGCATCAGAG AAGAAACGTG CAATATCATA ATCGTCAGCT 480
 AGTATGCCAT TACCACCTGT AATACCGCGG CCCATAGCTA CTnTCTCAC 529

(2) INFORMATION FOR SEQ ID NO: 3604:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3604:

35 CACAAGATAA GCATTGTAGA TGTGGATGCT TTAAGTGGC AAGCGATTGG TCGTCCTAAA 60
 ACAGGTACAT ATGCGCTATC TGACCTAGTC GGTTTAGATA TTGCAGTGTC TGTAATTAAA 120
 GGCATGCAAC AAGTACCTGA AGAAACACCT TATTTTCATG ATGTCAAAAT TGTAAATACG 180
 40 TTGTTTGACA ATGGCGCACT CGGACGTAAA ACGAAACAAG GATTTTACAA AAAGGATAAA 240
 GAAACTAAAG CTCGACTTGT TTACGATGTT GAAAAACAAG ATTATGTACC TGTATCGCAA 300
 CCACAATTAC CAATTTTAAA TGAATTTAAT AAAGACTTAG TGCaTAACCT TGATACCATA 360
 45 TTCCAATGCG CAAGACGAGC GGGGACTATT TTTATGGGG 399

(2) INFORMATION FOR SEQ ID NO: 3605:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3605:

5 ATCACTTGAG GCTAGCCCTA AAGCTATTTT GGAGAGAACC AGCTATCTCC AGGTTCGATT 60
 GGAATTTCTC CGCTACCCTC AGTTCATCCG CTCACCTTTT AACGTAATCG GTTCGGTCCT 120
 CCATTCACTG TTACCTGAAC TTCAACCTGA CCAAGGGTAG ATCACCTGGT TTCGGGTCTA 180
 10 CGACCAAATA CTAAACGCCC TATTCAGACT CGCTTTCGCT ACGGCTCCAC ATTTACTGCT 240
 TAACCTTGCA TCAAATCGTA ACTCGCCGGT TCATTCTACA AAAGGCACGC CATCACCCAT 300
 TAACGGGCTC TGGACTACTT GTAAGCACAC GGTTTCAGGT TCTATTTTAC TCCCCTTCCG 360
 15 GGGTGGCTTT TCACCTTTCC CTCACGGTAA TGGGTTCACT 400

(2) INFORMATION FOR SEQ ID NO: 3606:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3606:

AAATCCTGCG GTGAGTGATC ACTAACCCGG TTCGATTCCG GTCCTCGGCA CCATTTTCAA 60
 30 TAAAAACATA TCGCCCCGTA GCTCAATTGG ATAGAGCGTT TGAACAGGA TCAAGAGGTT 120
 ATGGGTTTCA CTCCTATCGG GCGCGTTAAT TATACGGGAA GTAGCTCAGC TTGGTAGAGC 180
 ACTTGTTTGG GGACCAAGGG GTCGCAGGTT CGAATCCTGT CTTCCCGATA TACTGTAATT 240
 35 ATTATGGGGG CTTAGCTCAG CTGGGGAGAG CGCCTGCTTT GCACGCAGGA GGTCAGCGGT 300
 TCGATCCCGC TAGTCTCCAC CATATTATTT ACAAACTATA TAAGGCGGTG TAGCTCAGCT 360
 GGCTAGAGCG TACGGTTCAT ACCCGTGAGG TCGGGGGTTC 400

40 (2) INFORMATION FOR SEQ ID NO: 3607:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3607:

GGGTGTGCTT CTGATATGCT ATGTATTCAC ATATCGATAA CATGACATAA CTCATGCTGG 60
 GTTTCCTTTC CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 120

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TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGTTAA CATGAAGTTA CGTTCCTTTA 240
TAAAAAGATT TAAACGCGTT ATTAATCTTG TGAGTGTCTT TTCGAACACT AGCGATTATT 300
5 TCTTATGAAT TCAAGCTTAT TTAAGACTCT TTATTCACCTC GGTTTTGCTT GGTAAAATCT 360
ATATTTTACT TACTTATCTA GTTThCAATG TACAAATAAT 400

(2) INFORMATION FOR SEQ ID NO: 3608:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3608:

20 TAGTTTTCAA TGTACAAATA ATGGTGGAGA CTAGCGGGAT CGAACCGCTG ACCTCCTGCG 60
TGCAAAAnAGC CGCTCTCCCA GCTGAGCTAA GCCCCCAAAT AGGTATTAAA TTAATGGTGG 120
GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCCTCT AACCAGCTGA 180
25 GCTATAGGCC CATTAAATTG AATGAACAAA CATTCAAAAC TGAATACAAT ATGTCACGTT 240
ATTCCGCATC TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC 300
GCACCTTCCG ATACGGCTAC CTTGTTACGA CTTCACCCCA ATCATTGTGC CCACCTTCGA 360
30 CGGCTAGCTC CTAAAAGGTT ACTCCACCGG CTTCCGGGTG 400

(2) INFORMATION FOR SEQ ID NO: 3609:

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3609:

AGGGCACTCT TACTGGGCGT GTTAAATTAC TAAnTTCAAT CAGCAGAAGA ACTAGGACAT 60
45 GGCGCTTTTA AAATTATTGA AACACATGCA TTAAGAGATG TACAAGCAGT ATTGGGTTTT 120
CATAATGACC CATCGCGTTC GGTAGGTACA TTTGCAATCA AAACAGGGGC AATTACATCA 180
GCAGTAGATC GTTTTGAGTT TCATATTAAA GGCGTGGGTG GTCATGCTGC AAACCAGAAC 240
50 AATGCAACGA TCCAGTTATT GTGTTGGCGC AATTGATTAA TAGTATTCAA TCCATAGTTA 300
GTAGAAATCT ATCTGCGTTT GATGAAGCGG TAGTAACAAT TGGACAAATA TCATGTGGTA 360

(2) INFORMATION FOR SEQ ID NO: 3610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3610:

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AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT      60
GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC      120
CCCATTCCGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA      180
GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA      240
TCTATGTTTC CACCATTTTT ATAAGTCAAA CGCTCACATA CGGCTTCGTT TTCATTATTT      300
TAAATGCTCA TTTACATAAG TAAACTCTGC TTTAAATGA ATTTAACTCA TTGTCTGCTA      360
AACGTTTTGC TTTTATAAAA AGATTTAAAC GCGTTGATTT      400

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(2) INFORMATION FOR SEQ ID NO: 3611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3611:

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GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTCG AACCGCCGAC      60
CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT      120
GGCAACGTTT TACTCTAGCG GAATTAAGTT GAACTACCAT CGACGCTAAG GAGCTTAACT      180
TCTGTGTTTC GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG      240
TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAAACATTTA      300
TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC ACATGTCACC ATGCTTCCAC      360
CTCGAACCTA TTAACCTCAT CATCTTTGAG GGATCTTAAT      400

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(2) INFORMATION FOR SEQ ID NO: 3612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3612:

5 ACCCAGCTCG CGTACCGCTT TAATGGGCGA ACAGCAATCC CTTGGGACCG ACTACAGCCC 60
 CAGGATGCGA TGAGCCGACA TCGAGGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG 120
 GAGATAAGCC TGTATCCCC GGGGTAGCTT TTATCCGTTG AGCGATGGCC CTTCCATGCG 180
 10 GAACCACCGG ATCACTAAGT CCGTCTTTTC ACCCTGCTCG ACTTGTAGGT CTCGCAGTCA 240
 AGCTCCCTTA TGCCTTTACA CTCTATGAAT GATTTCCAAC CATTCTGAGG GAACCTTTGA 300
 15 GnGCCTCCGT TACCTTTTAG GAGGCGACCG CCCCAGTCAA ACTGCCCCGCC TGACACTGTC 360
 TCCCACCACG ATAAGTGTCn GGGGGTTAGA AAGCCAACAC 400

(2) INFORMATION FOR SEQ ID NO: 3613:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3613:

ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCaA 60
 30 GGCATCCACC GTGCGCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA 120
 CGCTCACATA CGGCTTCGTT TTCATTATTT TAAATGCTCA TTTACATAAG TAAACTCTGC 180
 TTTAAAATAA TTAACTCAT TGTCTGCTAA ACGTTTTCTT TTATAAAAAG ATTTAAACGC 240
 35 GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG AATTCAAGCT 300
 TATTTAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA TCTATATTTT ACTTACTTAT 360
 CTAGTTTTCA ATGTACAAAT AATGGTGGG CTAAGTGGAC TCGAACCACC GACCTCACGC 420
 40 TTATCAGGCG TCGCTCTAA CCAGCTGAGC TATAGGcCCA TTTTTTTGaA TGTTAAATAA 480
 ACATTCA 487

45 (2) INFORMATION FOR SEQ ID NO: 3614:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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ACCGTACGCT CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG 60
 AGACTAGCGG GATCGAACCG CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG 120
 5 CTAAGCCCCC ATAATAATTA CAGTATATCG GGAAGACAGG ATTCGAACCT GCGACCCCTT 180
 GGTCCCAAAC CAAGTGnTCT ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT 240
 AGGAGTCGAA CCCATAACCT CTTGATCCGT AGTCAAACGC TCTATnCAAT TGAGCTACGG 300
 10 GCGCATATGT TTTTATTGAA AATGGTGCCG AGGACCGGAA TCGAACCGGT ACGGTGATCA 360
 CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GChAGTTCCG 400

15 (2) INFORMATION FOR SEQ ID NO: 3615:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3615:

25 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTGTTG CGCTCTTTTC TCGTTTCGTC 60
 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 120
 30 GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCTACTCTA 180
 GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT 240
 TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 300
 35 TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT 360
 TTACTTTTTTA TTTTGACGTT TAGGCATAAA AAAAAGAGAC 400

40 (2) INFORMATION FOR SEQ ID NO: 3616:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 420 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3616:

50 TnGTGTCTTT CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT AAAACTCTTT 60
 ATTCACTCGG TTTTGCTTGG kAAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA 120
 55 CAATTTCTTT TTAGTCAAGC GCTCGCATAA GCAATATCAC TTTAACCAAA AAATATTTGA 180

AAGATGTTCC GAATATATCC TTAGAAAGGA GGNATCCAG CCGCACCTTC CGATACGGCT 300
 ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG 360
 5 TTACTIONACC GGCTTCGGGT GTTACAAACT CTCGTnGGTG TGACGGGCGG TGTGTACAAG 420

(2) INFORMATION FOR SEQ ID NO: 3617:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3617:

CACTAGCGAT TATTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC ACTCGGTTTT 60
 20 GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTC AATGTACAAT TTCTTTTTAG 120
 TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT TAAATAAACA 180
 25 TTCAAAACTG AATACAATAT GTCACATTAT TCCGCATCTT CTGAAGAAGA TGTTCCGAAT 240
 ATATCCTTAG AAAGGAGGTG ATCCAGCCGC ACCTTCCGAT ACGGCTACCT TGTTACGACT 300
 TCAACCCAAT CATTGTGCCC ACCTTCGACG GCTAGCTCCT AAAAGGTTAC TCCACCGGCT 360
 30 TCGGGTGTTA CAACTCTCG TGGTGTGACG GCGGGTGTGT 400

(2) INFORMATION FOR SEQ ID NO: 3618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3618:

GATATACGCT ATGGCTGGAG CAGTGTGGCC AAATGGCGGA AGACAAACGT TTAATGCGAT 60
 45 ATACTTAGCG CAAAATATTG GTGTGGCTGT CCGTGCTGCA ATGGGCGGCT TTGTGCGAGA 120
 ATTTAGCTTT AACTATATCT TTTTAGCCAA TCTTATTATG TATGTTGTGT TTGCGCTTGT 180
 CCGGTTAACH AATTTAATAT TGAAATTAAT GCGAAAGTTA AATATCCAAC TCATTAGAT 240
 50 ATTACTGGTA AAAAGAATAA AGCAAGATTT ATTTTCATTAG TACTAATTTG TGCAATGTTT 300
 GCAATTTGTT GGGTTGCATA TATTCAATGG GGAGTCTACA ATCGCTTCAT TTTACACAAT 360
 55 CTATTAATAT TTCAATGGGC ACAATATAGT GTTTTATGGG 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3619:

TCGCACGCCT TCGCCTATCC TACTGCGTCC CCCCATCGAT TAAAACGATT ATAGGTGGTA 60
 CAGGnAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTCTG GCCTCAGCTT AGGACCCGAC 120
 TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC 180
 ACCCGTCTTT CGCTACTCAC ACCGGCATTTC TCACTTCTAA GCGCTCCACA TGTCTTACG 240
 ATCATGCTTC AACGCCCTTA GAACGCTCTC CTACCATTGT CCAAAGGAAA TCCACAGCTT 300
 CGGTAATATG TTTAGCCCCG GTACATTTTC GGCGCAGTGT CACTCGACTA GTGAGCTATT 360
 ACGCACTCTT TAAATGATGG CTGCTTCTAA GCCAACATCC 400

(2) INFORMATION FOR SEQ ID NO: 3620:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3620:

TTAAGTCTTC GATCGATTAG TATTCGTCAG CTCCACATGT CACCATGCTT CCACCTCGAA 60
 CCTATTAACC TCATCATCTT TGAGGGATCT TATAACCGAA GTTGGGAAAT CTCATCTTGA 120
 GGGGGGCTTC ATGCTTAGAT GCTTTTCAGCA CTTATCCCGT CCACACATAG CTACCCAGCT 180
 ATGCCGTTGG CACGACAACCT GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA 240
 AGGACAGCTC CTCTCAAATT TCCTACGCCC ACGACGGATA GGGACCGAAC TGTCTCACGA 300
 CGTTCTGAAC CCAGCTCGCG TACCGCTTTA ATGGGCGAAC AGCCCAACCC TTGGGACCGA 360
 CTACAGnCCC AAGGATGCGA TGAGCCGACA TCGAGGTGCC 400

(2) INFORMATION FOR SEQ ID NO: 3621:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 475 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3621:

5 CCACACCCGc AAATGGTGag CCATAGcAGG ATTCGgaACC TCTGcACCCT CTGATTAAAA 60
 GTCAGcATGC TCTACCAACT GaGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 120
 ACCCCCAACC TACTGATTAC AAGTCAGTTG CTCTACCAAT TGAGCTAGGC CGGCAATATG 180
 10 TAAGAATAAA TGGTGGAGAA TGACGGGTTC GAACCGCCGA CCCTCTGCTT GTAAGGCAGA 240
 TGCTCTCCA GCTGAGCTAA TTCTCCGATT TAAAACTGCC TGGCAACGTT CTACTCTAGC 300
 GGAACGTAAG TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA 360
 15 ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTAATTTA TACATTCAAA 420
 ACTAGATAGT AAGTAAAAGT GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGT 475

(2) INFORMATION FOR SEQ ID NO: 3622:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3622:

30 TGGACGAAAC TTTATATCGA TCAATTTCTA TCGAGTTGGA CAATGCCGAA GCGTGACAAA 60
 AGTTTTTACC ATGCATGGTT GCATTTAGCG CAACATGACC ATAGTTTTAC TAAAGCACAG 120
 CGChCAAGTG ATTAAAGGCT TACCCAATGA TCCTGAAATG ACGATAGAGT CAGTATTAAAC 180
 35 TCATTTTTCA ATAGATCAGG AAGACTACCA AGCTTATGTT GAAGGACATC TTTTGGCGTT 240
 ACCGGGTTGG GCAGGTATGT TGTATTACCG TTCACAACAG CATCACTTTG AACAACTTT 300
 40 GTTAACGGAT TATTTGGCAA TTCGGTTAGT TGTCGAACAA TTGCTAGTTG GTGGATGAGT 360
 TTTAAGTCAG TCGCTAAAGA TTGTGGAAAG TAAGATCCGG 400

(2) INFORMATION FOR SEQ ID NO: 3623:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3623:

55 TAGATGCTTT CAsACTTATC CCGTCCACAC ATAGCTACCC AGCTATGCCG TTGGACGACA 60

ATTCCTACG CCCACGACGG ATAGGGACCG AACTGTCTCA CGACGTTCTG AACCCAGCTC 180
 GCGTACCGCT TTAATGGGCG AACAGCCAAC CCTTGGGACC GACTACAGCC CCAGGATGCG 240
 5 ATGACCGACA TCGAGGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG GAGATAAGCC 300
 TGTATCCCC GGGGTAGCTT TTATCCGTTG AGCGATGGCC TTCCATGCGG GAACACCGGA 360
 TCACTAAGTC CGTCTTTCGA CCCTGCTCGA CTTTGTAGGn 400
 10

(2) INFORMATION FOR SEQ ID NO: 3624:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3624:

GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTCTG AACCGCCGAC 60
 CCTCTGCTTG TAAGGCAGAT GCTCTCCAG CTGAGCTAAT TCTCCGATT AAAACTGCCT 120
 25 GGCAACGTTT TACTCTAGCG GAAnTAAGTn GnACTACCAT CGACGCTAAG GAGCTTAACT 180
 TCTGTGTTCTG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240
 30 TAATTTATAC ATTCAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAACATTTAT 300
 TTTGATTAAG TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC 360
 TCGAACCTAT TAACCTCATC ATCTTTGAGG GGATCTTATA 400

35 (2) INFORMATION FOR SEQ ID NO: 3625:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3625:

TTAAAGAACG CTAATAACTG ATCGTAACCA CTATATATAT TGTTGTGACC TCTAACAGCA 60
 TAATGTCTAA ATGTTTGTGG GATATATTGA AGCAATCCTT TTGCTGGATT GCCCTGTAAA 120
 50 ACGTTGATGT CTCTAAGCGA ACTAGATTGA GTTATACCTG CATTTCTCTC TGATTCGTGT 180
 TGAATCAAGC TAATGATATT TCCTACGTCA GCCGAAGTAA CATTACACC CATTCGTTTT 240
 55 GCTGCACGAC GTATATCGCC TGCCCAAGCA GATGCAGCCT TATTAACACC TGAACCACTT 300

CCTGGATGCG ACCCTTGCAT CAnTTGGGAA ATGTAnGTGT

400

(2) INFORMATION FOR SEQ ID NO: 3626:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3626:

15	GATTGTGGTT CCGACATTCG AGGGTTCGAT CCCCTTCAGC CGCCCTTATT ATTAATGGGC	60
	TATAGCCAAG CGGTAAGGCA ACGGACTTTG ACTCCGTCAC TCGTTGGTTC GAATCCAGCT	120
	AGCCCAGTTA TTGGCGGCAT AGCAAGTGGT AAGGCAGAGG TCTGCAAAAC CTTTATCACC	180
20	GGTTCAAATC CGGTTGCCGC CTCCAGGTTT ATGCGGGAGT AGTTCAACTT TTAGAACACG	240
	TTCTTCCCG GAAGAGGTAT AGGTGCAAAT CCTATCTTCC GCTCCATAAT TTAATAATAA	300
	TGCGGGAGTA TTTCAACTCT TAGAATACAT TCCTTCCTGG AATgAGGTAT AGGTGTAAAT	360
25	CCTATCTTCC GCTCCATAAT TTAATATTG cGGGAGTAGT TCAACTTTTA GAAACAGCTC	420
	CTTCCCGGAA CCGAGGTATA GGTGTAAATC CTATCTTCCG C	461

(2) INFORMATION FOR SEQ ID NO: 3627:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3627:

40	TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTTCCTG GCAACGTTCT ACTCTAGCGG	60
	AACGTAAGTT GGCTnAnATC GACGCTAAGA ACCTTTCTTG ACTTGTGACA ATCGCTTGCT	120
45	TCTTTCCTCT TCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGCGCTCTT	180
	TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTTCT TTGTGTTTGC	240
	TTTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA TGCGGCTCAT	300
50	CGCATCCATT TTTTGCTTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTC GACTACCATC	360
	GACGCTAAGG GAGCTTAACT TCTGTGTnCG GGCATGGGGG	400

(2) INFORMATION FOR SEQ ID NO: 3628:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3628:

10 ATGCTTTCAG CACTTATCCC GTCCACACAT AGCTACCCAC CTATGCCGTT GGCACGACAA 60
 CTGGGTACAC CAGAGGTATG TCCATCCCGG TCCTCTCGTA CTAAGGACAG CTCCTCTCAA 120
 ATTTCTTACG ACCCAGGACG GATAGGGACC GAACTGTCTC ACGACGTTCT GAACCCAGCT 180
 15 CGCGTACCGC TTTAATGGGC GAACAGCCCA ACCCTTGGGA CCGACTACAG CCCCAGGATG 240
 CGATGAGCCG ACATCGAGGT GCCAAACCTC CCCGTCGATG TGAACCTCTG GGGGAGATAA 300
 GCCTGTTATC CCCGGGGTAG CTTTTATCCG nTGAGCGATG GGCCTTCCAT GCGGnACCAC 360
 20 CGGnTTACTA AGTCCGTCTT TCGAnCCTGC TCGACTTGTA 400

(2) INFORMATION FOR SEQ ID NO: 3629:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3629:

TTTATAAATA TCCCAGTCTG AACGCGATTG CCATAACGGA TCAATGGCAG GATTGAAAGG 60
 35 ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGT TTTTCATACC AAGTCGCTGC 120
 CGGCAAAACA ATGTCAGAAT ATAACGGTGT TGCCGTCATT CTGAAGTCTA AAGAGACCAC 180
 40 TAAATCTAAC TTACCTGTTG TTTCTTCACG CCACGTAATT TCTTCTGGCT TTTCATCTTC 240
 ATTTGGTGTA GCTAATAACC CTGATTTTGT GCCAAGTAAA TGCTTCATAA AGTATTCTTG 300
 ACCTTTTGCA GAACTTGAAA TTAAGTTTGA ACGCCATATA AATAATGATT TTGGATGATT 360
 45 CThTTTCAAA TCAGGATCTT CTATTGCAAA TGGGGTTTGT 400

(2) INFORMATION FOR SEQ ID NO: 3630:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 589 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

5 TTTAAGTTGT nGATTTAAAA TATTAATAAA GTGTAAATTT GACTATTGAn ATTckrACAA 60
 ATACATATTA AAATAATATT TGTTGAATTA ATTGAGTTAG GAAATTTATT TTTTAGAAAT 120
 AAAATAATTA AAAATAATTC TTGACTTACA AAAACTTACG AGTTATAATT AAATCTTGTA 180
 AGTGACAAAC GAACATTGAA AACTGAATGA CAATATGTCA ACGTTAATTC CAAAAACGTA 240
 10 ACTATAAGTT ACAAACATTA TTTAGTATTT ATGAGCTAAT CAAACATCAT AATTTTTATG 300
 GAGAGTTTGA TCCTGGCTCA GGATGAACGC TGGCGGCGTG CCTAATACAT GCAAGTCGAG 360
 CGAACGGACG AGAAGCTTGC TTCTCTGATG TTAGCGGCGG ACGGGTGAGT AACACGTGGA 420
 15 TAACCTACCT ATAAGACTGG GATAACTTCG GGAAACCGGA GCTAATACCG GATrATATTT 480
 TGAACCGCAT GGTTCAAAAG TGAAAGACGG TCTTGCTGTC ACTTATAGAT GGATCCGCGC 540
 TGCATTAGCT AGTTGGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATA 589

(2) INFORMATION FOR SEQ ID NO: 3631:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3631:

CCAACTGAGC TAATGGCTCT TCCATGGTGC CGGCCAGAGG ACTTGAACCC CCAACCTACT 60
 GATTACAAGT CAGTTGCTCT ACCAATTGAG CTAGGCCGGC AATATGTAAG AATAAATGGT 120
 35 GGAGAATGAC GGGTTCGAAC CGCCGACCCT CTGCTTGTA GGCAGATGCT CTCCCAGCTG 180
 AGCTAATTCT CCGATTTAAA ACTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTTCG 240
 ACTACCATCG ACGCTAAGGA GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC 300
 40 CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT TCAAACTAG ATAGTAAGTA 360
 AAAGTGATTT GCTTCGCAA ACATTTATTT TGATTAAGTC 400

(2) INFORMATION FOR SEQ ID NO: 3632:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3632:

TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 120
 AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACACTA GCGATTATTT CTTATGAATT 180
 5 CAAGCTTATT TAAAACTCTT TATTCACCTCG GTTTTGCTTG GTAAAATCTA TATnTTACTT 240
 ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCGCTGACC 300
 10 TCCTGGCGTG CAAAGCAGGC GCTCTCCCAG CTGAGCTAAn GCCCCCAnAT AGGTATTAAA 360
 TTAATGGGGG GGCCTAAGTG GACTCGAACC ACCGACCTCA 400

(2) INFORMATION FOR SEQ ID NO: 3633:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3633:

25 ATATGTCAAC GTTAATTCCA AAAAACGTAA CTATAAGTTA CAAACATTAT TTAGTATTTA 60
 TGAGCTAATC AAACATCATA ATTTTATGG AGAGTTTGAT CCTGGCTCAG GATGAACGCT 120
 GGCGGCGTGC CTAATACATG CAAGTCGAGC GAACGGACGA GAAGCTTGCT TCTCTGATGT 180
 30 TAGCGGCGGA CGGGTGAGTA ACACGTGGAT AACCTACCTA TAAGACTGGG ATAACCTCGG 240
 GAAACCGGAG CTAATACCGG ATAATATTTT GAACCGCATG GTTCAAAAGT GAAAGACGCT 300
 CTTGCTGTCA CTTATAGATG GATCCGCGCT GCATTAGCTA GTTGGTAAGG TAACGGCTTA 360
 35 CCAAGGCnAC GATGCATAGC CGACCTGAGA nGGTGATCGG 400

(2) INFORMATION FOR SEQ ID NO: 3634:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3634:

TGAGCTAGGC CGGCAATATG TAAGAATAAA TGGTGGAGAA TGACGGGTTC GAACCGCCGA 60
 50 CCCTCTGCTT GTAAGGCAGA TGCTCTCCA GCTGAGCTAA TTCTCCGATT TAAAACTGCC 120
 TGGCAACGTT CTACTCTAGC GGAACGTAAG TTCGACTACC ATCGACGCTA AGGAGCTTAA 180
 55 CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 240

TATTTTGATT AAGTCTTCGA TCGATTAGTA TTCGTCAGCT CCACATGTCA CCATGCTTCC 360
 ACCTCGAACC TATTAACCTC ATCATCTTTG AGGGATCTTA 400

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(2) INFORMATION FOR SEQ ID NO: 3635:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3635:

TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT TTAGCTCTAC 60
 TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC 120
 ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAA GAGACCTTGC 180
 GGTCTCAAAT GCGGCTCATC GCATCCATT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA 240
 CGTAAGTTGG GCTACCATCG ACGCTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT 300
 CTTTCTCTT CTTGGCTCT CGCTTACTCA TTAGCTCTA CTAAACTCGT TCGCTCTTT 360
 TCTCGTTTCG TCAGATTCAA ACGTTTTTAC TTCGCCAAGC 400

30

(2) INFORMATION FOR SEQ ID NO: 3636:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3636:

40

TACTTATCTA GTTTTCAATG TACAATTTCT TnTAGTCAA GCGCTCGCAT ACTGATTTTC 60
 AAAAAATCAA ATGCTCATTT ACAAAGTAA ACTCCGCTTT ATTTTCTTA ATGCATTGTC 120
 TAACAACCGC TTTCTTTAAA AAGAATAGAT TGTCAAGCGC TCGCATAAGC AATATCACTT 180
 TAACCAAAAA ATATTTGAAT GTTAAATAAA CATTCAAAAC TGAATACAAT ATGTCACGTT 240
 ATTCCGCATC TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC 300
 GCACCTTnCG ATACGGCTAC CTTGTTACGA CTTCACCCCA nTCATTTGTn CCACCTTCGA 360
 CGGCTAGCTC CTAAAAGGTT ACTCCACCGG CTTGGGTGT 400

50

(2) INFORMATION FOR SEQ ID NO: 3637:

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- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3637:

10 AGCGCTCGCA TAAGCAATAT CACTTTAACC AAAAAATATT TGAATGTTA AATAAACATT 60
 CAAAACTGnA ATACAATATG TCACATTATT CCGCATCTTC TGAAGAAGAT GTTCCGAATA 120
 TATCCTTAGA AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT 180
 15 CACCCCAATC ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTTACT CCACCGGCTT 240
 CGGGTGTTAC AAACTCTCGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC 300
 ACCGTAGCAT GCTGATCTAC GATTACTAGC GATTCCAGCT TCATGTAGTC GAGTTGCAGA 360
 20 CTACAATCCG AACTGAGAAC CACTTATGGG ATTGCCTnAC 400

(2) INFORMATION FOR SEQ ID NO: 3638:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3638:

TTCTCCGATT TAAAACTGCC TGGCAACGTT CTA CTCTAGC GGAAGTAAGT CGAnCTACCA 60
 35 TCGACGCTAA GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGCTA 120
 TAGTCACCAG ACATATGAAT GTAATTTATA CATTCAAAAC TAGATAGTAA GTAAAAGTGA 180
 40 TTTTGCTTCG CAAAACATTT ATTTTGATTA AGTCTTCGAT CGATTAGTAT TCGTCAGCTC 240
 CACATGTCAC CATGCTTCCA CCTCGAACCT ATTAACCTCA TCATCTTTGA GGGATCTTAT 300
 AACCGAAGTT GGGGAAATCT CATCTTGAGG GGGGCTTCAT GCTTAGATGC TTTCAGCACT 360
 45 TATCCCGTCC ACACATAGCT ACCCAGCTAT GCCGTTGGCA 400

(2) INFORMATION FOR SEQ ID NO: 3639:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 551 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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ATGTCTCTAA CGCCTTTAAT AGTATTGAAC ACAATTGGGA AAAAAGCAGC GATAAAAATA 60
 ATCGCAATCG CTGGCAAACCT ACCAATACCA AACCATAGAA CAACAAATGG TGCCCATGCT 120
 5 ATCGGAGATA TCGGCCTAAT CAATTGAAAT AGCGGTTCTGA TAGCGTTGTA TAGCCAACGA 180
 TTCCTTCCAA GCAAGAAGCC CAATGGAATA GCAACCAACA ATGCGACAAC AAAGCCCGCT 240
 ACAAATCTCC ATAACTAAT TGCTAAATGT TGGAAAATTT CTCCAGTAAC AATGAAAGAC 300
 10 CATATACTTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA 360
 ATAAAGACCA TTCCCAAAT GCCTAAGAAA aTAATAAATG TGATAATAGG TAATATAAAT 420
 15 TTGTTATTTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCACAA 480
 AGTCATCCAT ATGCAGGTGG ATTAAACAAA TGATGTTGTT TTACCAAGTC GTAATTTCTT 540
 GATAGCCGGA T 551

20 (2) INFORMATION FOR SEQ ID NO: 3640:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3640:

CACTAAACTA AATTAATGAA GTGCCTTATG TATAAAAATT ATAACCTGAT CCAACTTACA 60
 CTACCAATAG AAACCTCTGT TAGAATTCCT CAAATTGATA TTTCGCGATA TGTTAATGAA 120
 ATTGTTGAAA CGATACCTGA TAGCGAATTC GATAAATTCA GACATCATCG TGGCGCAACA 180
 35 TCCTATCATC CAAAAATGAT GTTAAAAATC ACCTTATATG CATATACTCA ATCTGTATTT 240
 TCTGGTCGTA GAATAGAGAA ATTACTTCAT GACAGTATTC GAATGATGTG GTTAGCTCAA 300
 AATCAAACAC CTTCTTATAA AACTATTAAT CGTATTAGAG TGAATCCTAA TACTGATGCG 360
 40 TTAATTGAAT CTTTATTTAT CCAGTTTCAT AGTCAATGTT 400

(2) INFORMATION FOR SEQ ID NO: 3641:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 398 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3641:

55

GATTGTCCTT TGGcAATGGT AGGAGAGCGT TCTAAGGGCG TTGAAGCATG ATCGTAAGGA 120
 CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CGAAAGACGG GTGAGAATCC 180
 5 CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCGTC CGCTCTGGGT TAGTCGGGTC 240
 CTAAGCTGAG GCCGACAGnG TAGGCGATGG ATAACAGGTT GATATTCCTG TACCACCTAT 300
 AATCGTTTTTA ATCGATGGGG GGrCGCATAG GATAGGCGAA CGTTGCGATT GGATTGCACG 360
 10 TCTAAGCAGT AAGGCTGGAG TATTAGGCAA ATCCGGTA 398

(2) INFORMATION FOR SEQ ID NO: 3642:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 439 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3642:

TAATGTCTAC ACTTTGCTTG CGATCATTCA TTTTAAAGCC AGACTTTTTA TAATCTTGTA 60
 25 CAAATGCTTG CGCTACATCC TTGTGTTGAT CAAGCAATTC CCCTCTCAGT ACTAGCACAC 120
 AGCAATACGC ATCAGGtATA ACGTCATCAC CATGTTTCAA AGTCTTACCT TTGCCTAACT 180
 TTTCACCCAG TGCACCGAAT GGTTCTGGCTA CAGAATACCC TGTaATTCTG TGTTCACTCA 240
 30 ATGCGGCTGG CATTTCTGCT GGCGACATTT CATGATAGCT AAAATGCCCC GGTTTAATCT 300
 TTAATTGTTT ACGTAATTCC TCAAGTAAAA GATAATGTGt TGAATAACgA TGTGGtATAC 360
 35 CAAAATGGkA ATCATCGCCA TTAtTATTAA ATTCaTTTAA GTGCATACCT TTTTGTCCCA 420
 TAATGACATT GCCTTCATG 439

(2) INFORMATION FOR SEQ ID NO: 3643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3643:

ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA 60
 50 TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA 120
 TCGAACCGTG ACCTCCTGCG TGCAAAGCAG GCGCTCTCCC AGCTGAGCTA AGCCCCCAAA 180

GCGTGCCTC TAACCAGCTG AGCTATAGGC CCATTAATTT GAATGAACAA ACATTCAAAA 300
 CTGAATACAA TATGTCACGT TATTCCGCAT CTTCTGAAGA AGATGTTCCG AATATATCCT 360
 5 TAGAAAGGAG GTGATCCAGC CGCACCTTnC GATACGGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3644:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3644:

GCGAACTGT ACGGAGCAAC GCCGCGTGAG TGATGAAGGT CTTCCGATCG TAAAACTCTG 60
 20 TTATTAGGGA AGAACATATG TGTAAGTAAC TGTGCACATC TTGACGGTAC CTAATCAGAA 120
 AGCCACGGCT AACaCGTGCC AGCAGCCGCG GTAATACGTA GGTGGCAAGC GTTATCCGGA 180
 ATTATTGGGC GTAAAGCGCG CGTAGGnGTT TTTTAAGTCT GATGTGAAAG CCCACGGnTC 240
 25 AACCGTGGAG GGTCAATTGGA AACTGGAAAA CTTGAGTGCA GAAGAGGAAA GTGGAATTCC 300
 ATGTGTAGCG GTGAAATGCG CAGAGATATG GAGGAACACC AGTGGCGAAG GCGACTTTCT 360
 GGTCTGTAAC TGACGCTGAT GTGCGAAACG TGGGGATCA 399

30 (2) INFORMATION FOR SEQ ID NO: 3645:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3645:

TATTATACTT TACATTTCTC GTTTCGTCAG ATTCAAACGT TTTCAC TTCG CCAAGCCATC 60
 TTTCTTTGTG TTGCTTTTA TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT 120
 45 CAATGCGGCT CATCGCATCC ACTTTTTGCC TGGCAACGTT CTACTCTAGC GGAACGTAAG 180
 TnCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA 240
 CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATnAT ACATTCAAAA CTAGATAGTA 300
 50 AGTAAAAGTG GATTTTGCTT CGCAAAACAT TTATTTTGGA TTAAGTCTTC GATCGGATTA 360
 GTATTGCTCA GCTCCACATG TCACCATGGC TTCCACCTCG 400

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 758 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3646:

10 AGATAAGTAA GTAAATATA GATTTTACCA AGCAAAACCG AGTGAATAAA GAGTTTAAAA 60
 TAAGCTTGAA TTCATAATA ATCGCTAGTG TTCGAAAGAC ACGAnCAAGA TTAATAACGC 120
 15 GTTTAAATCT TTTTATAAAA GAACGTAAC TCACTGTTAAC GTTTGACTTA TAAAAATGGT 180
 GGAAACATAG ATTAAGTTAT TAAGGGCGCA CGGTGGATGC CTTGGCACTA GAAGCCrATG 240
 AAGGACGTTA CTAACGACGA TATGCTTTGG GGAGCTGTAA GTAAGCTTTG ATCCAGAGAT 300
 20 TTCCGAATGG GGAAACCCAG CATGAGTTAT GTCATGTTAT CGATATGTGA ATACATAGCA 360
 TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA GAAAGAAAAA 420
 TCGATTCCCT TAGTAGCGGC GAGCAnAACG GGAAGAGCCC AAACCAACAA GCTTGCTtGg 480
 25 GGGTnTGTA GACTCTAT ACGGATTACA AAGGACGACA TTAGACGAAT CATCTGGaAA 540
 GATGAATCAA AGAAGGTAAT AATCCTGTAG TCGAAAATGT TGTCTCTCTT GAGTGGATCC 600
 TGaGTACGAC GGAGCACGTG AAATTCCGTC GGAATCTGGG GAGGaCCATC TCCTAAGGCT 660
 30 AAATACTCTC TAGTGACCGA TAGTGGAACC aGTaCCGTGA GGGAAAGGTg AAAAGCACCC 720
 gGAAGnAGT TGAAATaGAA ctGGAAACCG TGTGCTTA 758

(2) INFORMATION FOR SEQ ID NO: 3647:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3647:

45 ACAAACTCCG AATGCCAATT AATTAACTT GGGAGTCAGA ACATGGGTGA TAAGGTCCGT 60
 GTTCGAAAGG GAAACAGCCC AGACCACCAG CTAAGGTCCC AAAATATATG TTAAGTGGAA 120
 AAGGATGTGG CGTTGCCAG ACAACTAGGA TGTTGGCTTA GAAGCAGCCA TCATTTAAAG 180
 50 AGTGCgTAAT AGCTCACTAG TCGAGTGACA CTGCGCCGAA AATGTACCGG GGCTAAACAT 240
 ATTACCGAAG CTGTGGATTG TCCTTTGGnA TGGGTAAGGA GAGCGTTCTA AGGGCGTTGA 300

AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAAGGTT

400

(2) INFORMATION FOR SEQ ID NO: 3648:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 521 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3648:

15 GTCATTGGAA ACTGGAAAAC TTGAGTGCAG AAGAGGAAAG TGAATTCCA TGTGTAGCGG 60
 TGAAATGCGC AGAGATATGG AGGAACACCA GTGGnCGAAG GCGACTTTCT GGTCTGTAAC 120
 TGACGCTGAT GTGCGAAACG TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC 180
 20 GTAAACGATG AGTGCTAAGT GTTAGGGGGT TTCCGCCCTT TAGTGCTGCA GCTAACGCAT 240
 TAAGCACTCC GCCTGGGGAG TACGACCGCA AnGTTGAAAC TCAAAGGAAT TGACGGGGAC 300
 CCGCACAAGC GgTGGaGCAT GTGGTTTAAT TCGAAGCAAC GCGAAGAACC TTACCAAATC 360
 25 TTGACATCCT TTGACAACTC TAGAGATAGA GCcTTCCCCT TCGGGGGACA AAGTGACAAG 420
 TGGTGCATGG TGTCGTCAAC TCCTGTCTGTT GAGATGTTGG GGTAAnTCCC CGCAAnGAGC 480
 GCACCCCTTAA GCCTTAGTTT nCATCATTAA GTTGGGCACT C 521

(2) INFORMATION FOR SEQ ID NO: 3649:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3649:

CCAAAGTTCA TCTTTTACGA ATGAGAAATA GGTGTTGCAT ATTCAATGGT CTCATCTTGT 60
 TTATAAAAGC CACCATCTAA ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC 120
 45 ATACGTGTTT TAACACGTTT GTATCCCATC GCATCCCATC ATTGGAATGG ACCAAGTTTC 180
 CAGTTGAACC CCCAGACAAG CGCACGGTCT ATGTCTCGGA AATCATCGGT AGCTTTAGGT 240
 ACATTGATAG CAGAGTAATA GAAATTATTA CGTAATGTCT CCCATAAAAA TAGTCCCGCT 300
 50 TCGTCTTGcG CATTGAATAT GGTATCAAkG TTATGCACTA aGTCTTTATT AAATTCATTT 360
 AAAATTGGTA ATTGTGGTTG CGATACAGGT ACATAATCTT 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3650:

GCGATAATAA AAAATAATGG CGGAGGAAGA GGGATTGAA CCCCCGCGGn CCGTTAAGGC 60
 CCTGTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC ATTATTATAG 120
 GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA CGGGAATCGA ACCCGCGATC 180
 TCCTGCGTGA CAGGCAGGCG TGTTAACCGC TACTACTACGA GACCATTAGT AAAACGGAGG 240
 AAGAGGGATT CGAACCCCCG CGAGCCGTTA AGCCCTGTC GGTTTTCAAG ACCGATCCCT 300
 TCAGCCGGAC TTGGGTATTC CTCCAAAATT ATATGGACCT TGCAGGACTC GAACCTGCGA 360
 CCGAACGGTT ATGGAGCCGT TAGCTCTAAn CAACTTGAGC 400

(2) INFORMATION FOR SEQ ID NO: 3651:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3651:

TGGCGCTGTG CTTTAGTAAA ACTATGGTCA TGTTGCGCTA AATGCAACCA TGCATGGTAA 60
 AAACTTTGCT CACGCTTCGG CATTGTCCAA CTCGATAGAA ATTGATCGAT ATAAAGTTTC 120
 GTCCATTAA TCATTGACG ATTCACCTGT TCGCTAAGTG GCTCACCTTG TTCATCTATT 180
 ATTGCATCAC TCATCGGACG TACATCATAG TGATGATATG ATTCAGCCAT ATCACGTTTT 240
 GATTTTTCTA ATAGTAGATC AGCAACAACA TCAACATTTG AATGATTCAT ATATGATGGC 300
 AGGTACGTCT TTTAATGTTT TAATGTTATC AATATAAAGA TGATGTAGTG TTGCGGGATA 360
 TGTAGTGAnG TTCAAGTAAC ATATCAGTAA CAAGTTGATT 400

(2) INFORMATION FOR SEQ ID NO: 3652:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3652:

CATTGTCCAA AGGACAATCC ACAGCTTCGG TAATATGTTT AGCCCCGGTA CATTTTCGGC 60
 5 GCAGTGTAC TCGACTAGTG AGCTATTACG CACTCTTTAA ATGATGGCTG CTTCTAAGCC 120
 AACATCCTAG TTGTCTGGGC AACGCCACAT CCTTTTCCAC TTAACATATA TTTTGGGACC 180
 TTAGCTGGTG GTCTGGGCTG TTTCCCTTTC GAACACGGAC CTTATCACCC ATGTTCTGAC 240
 10 TCCCAAGTTA AATTAATTGG CATTTCGGAGT TTGTCTGAAT TCGGTAACCC GAGAGGGGCC 300
 CCTCGTCCAA ACAGTGCTCT ACCTCCAATA ATCATCACTT GAGGGCTAGC CCTAAAGCTA 360
 ATTTCCGAGA GAACCAGCTA TCTCCAGGTT CGATGGAATT 400

(2) INFORMATION FOR SEQ ID NO: 3653:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3653:

GGTTCGGTCC TCCATTCAGT GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG 60
 TTTCGGGTCT ACGACCAAAT ACTAAACGCC CTATTCAGAC TCGCTTTCGC TACGGGTCCA 120
 30 CATTTACTGC TTAACCTTGC ATCAAATCGT AACTCGnCGG TTCATTCTAC AAAAGGCACG 180
 CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTTCAGGT TCTATTTAC 240
 TCCCCTTCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG 300
 35 AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTCA CGTGCTCCGT 360
 CGTACTCAAG nATCCACTCA AGAGAGACAA CATTTTCGAC 400

40 (2) INFORMATION FOR SEQ ID NO: 3654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3654:

50 AAAGGTCCTA AATATAATTT TACAACTAAT AAATAGTGGC GGTGGAGGGG ATCGAACCCC 60
 CGACCTCACG GGTATGAACC GTACGCTCTA GCCAGCTGAG CTACACCGCC TTATATAGTT 120

55

GCGCTCTCCC AGCTGAGCTA AGCCCCCATA ATAATTACAG TATATCGGGA AGACAGGATT 240
 CGAACCTGCG ACCCCTTGGT CCCAAACCAA GTGCTCTACC AAGCTGAGCT ACTTCCCGTA 300
 5 TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGnTCT 360
 ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT 400

(2) INFORMATION FOR SEQ ID NO: 3655:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3655:

20 TATTGAAGCC TGAGTCAACA CGTACGCAA TCGATCAAAT CATCGATGAA GCGAAACATA 60
 CAATTTTAAA TCTGTATGTG TGAATCCAAC ACATGTTAAA TATGCAGCAG AGCnnCTAGC 120
 TGATTCAAGAG GTGCTCGTTT GTACGGTAAT AGGATTCCCA TTAGGTGCGT CGACAACTGC 180
 25 AACGAAAGCA TTTGAAACAG AAGATGCAAT TCAAAATGGT GCAGATGAAA TTGACATGGT 240
 CATCAACATC GGCGCATTAA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 300
 AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGGAT TATTGAGACG GTATTGTTGG 360
 30 GACCATGACG AAATTGTAAG AGCGAGTGGA ATTAACCAAA 400

(2) INFORMATION FOR SEQ ID NO: 3656:

- (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 530 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3656:

GATGAGTCGC TgNtGATCT GAACGCTGTC TGAGnCCGAA CGCTACTGAA CTGAGTCGCT 60
 45 GTCTGAGTCT GAATCGCTAT CTGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTGTCTGA 120
 GTCTGAGTCG CTGTCTGAGT CTGAATCGCT ATCTGAATCT GAGTCGCTGT CTGAGTCTGA 180
 GTCGCTATCT GAGTCTGAGT CGCTGTCTGA ATCTGAGTCG CTGTCTGAAT CTGAATCGCT 240
 50 GTCTGAGTCT GAATCGCTAT CTGAGTCTGA ATCGCTATCT GAGTCTGAAT CACTGTCTGA 300
 GTCCGAGTCA CTGTCTGAAT CTGACTCACT ATCTGATTCT GAGTCGCTAT CTGATTCTGA 360

ATCTGAACCT GAGTCGCTGT CTGAGCCTGA AGTCACTGGT CTGAATCCGA ATCCGGATCC 480
 GGGTCTGGGG CTTGGGTTCC GGTTCCTGGGT CTGGGACTTG GGTTCCTGGGA 530

(2) INFORMATION FOR SEQ ID NO: 3657:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3657:

GTTTTAACTA CGCAAGACAT CGAAGAAGCT GACGGTGTCA TAATTGCAGC TGATAAACAA 60
 GTTGATCTGT CCCGATTGTG TGGTAAACGG TTGATTAAATG AAAATGTTCG CGAAGGGATT 120
 CATAATCCGA GAGGTCTAAT TCAACGTATC ATTAATCAAG ATGCGCCTAT TTATCAATCT 180
 GAAACAAATT ATCATTTCGAA AGATCGCGGT AAGTCTAAAA ATGGTATTCA AATGGTGTAT 240
 CAACATTTAA TGAACGGTGT ATCGTTTATG GTTCCTTTTA TCGTAGTTGG TGGACTCCTT 300
 ATCGCCATCG CGCTGGACTC TAGGCGGTGA ACGACATCAA AAGGATTAGT CATCCCAGAT 360
 GGATTCATTT TGGGAAATCC ATTGGAAAAC ATTGGGTAGT 400

(2) INFORMATION FOR SEQ ID NO: 3658:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 668 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3658:

GAAGAAGTTT ATGAAACGGT TATGAATAAG CCATACACTA GATATCCAGT GTACGAGGGA 60
 GATATTGATA ACATTATTGG GGTGTTTCAT TCTAAATATC TGTGGCTTG GAGTAATAAA 120
 AAAGAAAATC AAATTACAAA CTATTCAGCT AAGCCATTAT TTGTGAATGA ACACAATAAA 180
 GCTGAATGGG TATTACGTAA GATGACTATT TCTAGAAAAC ATTTAGCAAT TGTGTTGGAC 240
 GAATTGTTG GTACTGAAGC GATAGTGTCA CATGAAGACT TAATTGAAGA ATTATTAGGT 300
 ATGGAAATTG AAGATGAGAT GGAATAAAAG GAAAAAGAAA AACTTTCTCA ACAGCAAATT 360
 CmATTTC AACCGAAAAA TCGCmACGTA TCTATATAAG GmGCGAACAG CTATGTGGTA 420
 ATAAGAATCG ACTTACTCAA ATGTTAAGTA TTGAATATCC AATTATACAA GCAGGTATGG 480

TAGGCGCGGT TACTTTAATA CGCAGCAATT GGAAGATGAA ATAGATTATG GTACGCCAAT 600
 TAACGTCAAA TTCTTTTGGC GTAAATGTCT TTGGTACCAA GTCAACAATC ATATACCACT 660
 5 AGTCAAAT 668

(2) INFORMATION FOR SEQ ID NO: 3659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3659:

AAAAGAATGG TAAGTTGAAT AAAGTATTGA AATCAATTGC CAATATCTTT ATACCGTTGA 60
 20 TTCCTGnATT TATTGGAGCT GGATTAATTG GTGGTATTGC AGCAGTACTG AGTAACTTAA 120
 TGGTGGCAGG CTATATTTCA GGTGCTTGGG TTACGCAACT TATAACAGTA TTAAATGTCA 180
 TTAAAGACGG TATGTTAGCA TACTTAGCTA TTTTCACTGG TATTAATGCG GCTAAAGAAT 240
 25 TTGGTGCGAC ACCAGGACTT GGTGGCGTGA TTGGTGGTAC AACGTTATTA ACGGGTATTG 300
 CTGCTAAAAA TATTTTAAATG AATGTCTTCA CTGGAGAACC ATTGCAACCT GGACAAngTG 360
 GGATTATTGG CGTTATTTTG CCGTTTGGAA TTAAAGTAAT 400

(2) INFORMATION FOR SEQ ID NO: 3660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3660:

CTGAGCTAAT GGCTCTTCCA TGGTGCCGGC CAGAGGACTT GAACCCCAAA CCTACTGATT 60
 ACAAGTCAGT TGCTCTACCA ATTGAGCTAG GCCGGCAATA TGTAAGAATA AATGGTGGAG 120
 45 AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 180
 AATTCTCCGA TTAAAACTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTCGGACT 240
 ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG TGACCTCCTT 300
 50 GCTATAGTCA CCAGACATAT GAATGTAATT TATACATTCA AACTAGATA GTAAGTAAAA 360
 GTGATTTTGTn TTTCGCAAAA CATTTATTTT GGATTAAGTC 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3661:

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10  TGATGTTTGA TTAGCTCATA AATACTAAAT AATGTTTGTA ACTTATAGTT ACGTTTTTTG      60
    GAATTAACGT TGACATATTG TCATTCAGTT TTCAATGTTT ATTTTCTTA CCGACAAGAA      120
    TTAATTATAC ATTTTATTAA CATTTAAGTC AATAACTTTT TTTATCTTGT CCATTTTATT      180
15  TTTTAACCAA AATTTGATTA AAAAAGTCC TGGCAACGTT CTACTCTAGC GGAACGTAAG      240
    TTCGACTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA      300
    CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTA      360
20  AGTAAAAGTG ATTTTGCTC GCAAACATTT ATTTTGATTA      400
  
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(2) INFORMATION FOR SEQ ID NO: 3662:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 742 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3662:

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    CGCTCAACGT CTGCCTTCGT AATGGCTTTT GTAGAAATTC TAACTAAATA ATTTGGAATG      60
35  CTATCATTGA TTGTTTCAAC AGCTTGATGC TTTTGTTCAG GCTTTTGTAT CAATTTTCTA      120
    TCGTCTTTTG TAATTTGCGG AATGTCTTCA AACATTGATA AGACAATCTG ACCCACATTT      180
    TGTAATTTCTT TTTGAGTTTC TTGTAATGCA ACACCAGGTG CGTGATAAAC AAGATCTTTG      240
    TTTAAGTGCT GAGGTTTATA GTCATCAGCA ATATCTTTAC CTGGGACAAG CTTTGTAACA      300
    ATCCATGCTA AACCTGCTAC AAATGGTAAT TGAATCAAAG TATTTGTTAT GTTGAAGATA      360
45  CCATGTGATA CTGCAATCGT CATCGCTGGT TTTAAGTGCC ATAAATCTTG TAACAAACTA      420
    ATCAAATGAA TCACAACTGG CAAGAAAATT GTGAAGATAA TTACCCCGAT TAAGTTAAAG      480
    ATGACGTGTA CAAGCGCCGC ACGTTTGTCA GCGATTGAGC CGGCTAAACT AGCTAAGATA      540
50  GCTGTAATCG TGGTACCAAT GTTATCGCCT AGTAACACAG GGATkGCTGC GTTTAAGCTA      600
    ATTAAATCTT GTTGATAAAA TTCTTGTAAG ATACCAATCG TCGCACTTGA ACTTTGAACT      660
  
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AGCATTAAAT TGGCTTnAAA TC

742

(2) INFORMATION FOR SEQ ID NO: 3663:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3663:

15 ATGAATTCAA GCTTATTTAA AACTCTTTAT TCACTCGGTT TTGCTTGGTA AAATCTATAT 60
 TTTACTTACT TATCTAGTTT TCAATGTACA ATTCTTTTTT AGTCAAGCGC TCGCATACTG 120
 CTTTATTTTC AAAAAATCAA ATGCTCATTT ACAAAGTAA ACTCCGCTTT AATTTTTCTT 180
 20 AATGCATTGT CTAACAACCG CTTTCTTTAA AAAGAATAGA TTGTCAAGCG CTCGCATAAG 240
 CAATATCACT TTAACCAAAA AATATTTGAA TGTTAAATAA ACATTCAAAA CTGAATACAA 300
 TATGTCACGT nATTCCGCAT CTTCTGAAGA AGATGTTCCG AATATATCCT TAGAAAGGAG 360
 25 GTGATCCAGC CGCACCTTCC GATACGGGCT ACCTnGTnAC 400

(2) INFORMATION FOR SEQ ID NO: 3664:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 636 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3664:

AACTAATAGT TCACTTTTAC TTTTCTTTT TTCAATTATTA TCCATTATTT TTTCACCGCC 60
 40 AAAACGAATT TCATGATGTT AATTTAAATG TTCTATGACA AAATTAAGCA ACGATGTTtT 120
 ATATTTATTT CCAACTATGT CTAGATTAAA TTTCTAAAAA TAKACATCAT TTAAAAGGAG 180
 CTTGGGACAT AAATCAATGT CCTAGGGTCT ATAATATTAT AktGCTAGTA GTTGA CTGAA 240
 45 TGAAAATGCG CTTGCAACAA GCTTTTTTCA ACTCTAGTCA GGGGCCCAAA CACAGAGAAT 300
 TTCGAAAAGA AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCAACA CAGAGAATTT 360
 CGAAAAGAAA TTCTACAGGC AATGCGAGTT GGGGTGTGGG CCCCAACACA GAGAATTTTCG 420
 50 AAAAGAAAtt CTACAGGCAA TGCGAGTTGG GGTGTGGGCC CCAACATAGA GAAATGGaTT 480
 CCCAaTTTCT ACAGACAATG CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC 540

55

TACAATAATG nGCAAGTTGG CGGGGnCCCC AACACA

636

(2) INFORMATION FOR SEQ ID NO: 3665:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 404 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3665:

TATCATTTCC TGTTGCTAAA ACAACAGCAT GTATGCCATT CATAACACCT TTATTATGTG 60
 TTGCTGCACG ATGAATATCT ACTTGGGCCA ATACAGAAGC ACGTTCCATT CGTTTGGCAA 120
 CCTCTTCTCC AGTTCTCTCG CCCCTTGCTA AATCTTTAAC ATCAATTTCG CCTTGAACTT 180
 TAACAACGGA CGCTGTTGCA TGATTGGATA AAATACTCAT TAAAATGTCG CTTTGGGAAA 240
 tTCATTTTTT AAAAATGCAG TTATGGCCTC TAAAATCGTA TTAAGCATAT TAGCGCCCAT 300
 AGCATCTTTC GTATCAACAA ATACTTTTAA AGATAGTAAC TGtTGcTCAG GrAATGTakC 360
 mAtCGCTATA CGtTGGTAAC CACCACCACG CGCTTTAATA GGAA 404

(2) INFORMATION FOR SEQ ID NO: 3666:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3666:

GTGGTTCCAG TAGCAATTAT TGAACGATAT TAGGCTATCT AGTCGGCATA TTTGTAAAAC 60
 AAGATCCAAT TAAATATCAA CAGGAATAAC GAATAATATA AAAGAGGTTG GGACATAAAT 120
 CCCTAAAAAA ACAGCAGTAA GATAATTTTC AATTAGAAAA TATCTTACTG CTGTTCTCTA 180
 TTTATACAAT ACTTCGTATT GAATGGCTTC GCTTTCCTAG GGTGCCGTCT CAGCCTCGGT 240
 CTTGACTGG CACTGCTCCC TCAGGAGTCT CGCCATTAAT ACTACGTATT AACGTGTAAT 300
 TTTACTTTGA AATACTTTAA AAAAATAAGA CACTTTGCCC AACTGCACA TAAATGTAAA 360
 ATTCAATAAA ATAAATTTCT GTGTTGGATC CCTnCGTATA 400

(2) INFORMATION FOR SEQ ID NO: 3667:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3667:

	CCAACAAATC TGTCTGTCGC ATCGCCTTTG TCGTTCCAAA TAAATATGTA CAAACGAATC	60
10	CACCAGCATA CGCnCCAAGT AATCCTGCAA TATAACCTAA ATACATATTA TCTGAGATTA	120
	ATGGTAATAG TGACACACCA CTTGGGCCTA TTGCTTTGGC ACCAATATGT CCAATTCCAC	180
	CTATTACAGC GCCACCAATA CCACCACCAA TACAAGCAGT TAAGAAAGGT CGACCTAATG	240
15	GCAAAGTCAC ACCATAGATT AATGGTTCTC CGATACCTAG GGAAACCAAC TGGCAATGCA	300
	CCTTTTAAAG TATTACGTAA TGTTGTGTTG CGGTTTACAT CTTACCCAAA GTGCTAATGC	360
20	GGGCACCTAC TTGGTCCCAG CACCAGCCAT CGCTGCAATT	400

(2) INFORMATION FOR SEQ ID NO: 3668:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3668:

	ACTAAGATGT TTCAGTTCTC CGGGTGTGCC TTCTGATATG CTATGTATTC ACATATCGAT	60
	AACATGACAT AACTCATGAC TGGGTTTCCC CATTGCGAAA TCTCTGGATC AAAGCTTACT	120
35	TACAGCTCCC CAAAGCATAT CGTCGTTAGT AACGTCCTTC ATCGGCTTCT AGTGCCAAGG	180
	CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA AACGCGTTAT	240
40	TAATCTGTG AGTGTTCTTT CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT	300
	AAAACCTCTT ATTCACTCGG TTTTGCTTGG TAAATCTAT ATTTTACTTA CTTATCTAGT	360
	TTTCAATGTA CAATTCTTT TTAGTCAAGC GCTCGCATAA	400

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(2) INFORMATION FOR SEQ ID NO: 3669:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3669:

5 GAGCGCTACT TACTGGnAGG CGCTGGTGGG ATACTACCCT AGCTGTGTTG GCTTTCTAAC 120
 CCGCACCCT TATCGTGGTG GGAGACAGTG TCAGGCGGGC AGTTTGACTG GGGCGGTCGC 180
 CTCCTAAAAG GTAACGGAGG CGCTCAAAGG TTCCCTCAGA ATGGTTGGAA ATCATTCTATA 240
 GAGTGTAAG GCATAAGGGA GCTTGACTGC GAGACCTACA AGTCGAGCAn GGTGAAAGA 300
 10 CGGACTTAGT GATCCGGTGG TTCCGCATGG AAGGGCCATC GCTCAACGGA TAAAAGCTAC 360
 CCCGGGGGAT AACAGGCTTA TCTCCCCCAA GAGTTCACAT 400

(2) INFORMATION FOR SEQ ID NO: 3670:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3670:

25 ATACTTTACA TTTCTGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATCTTTC 60
 TTTGTGTTTG CTTTTATTTT GACGTTTTAG ACATAAAAAA AGAGACCTTG CCGTCTCAAT 120
 GCGGCTCATC GCATCCACTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTTC 180
 30 ACTACCATCG ACGCTAAGGA GCTTAACCTC TGTGTTCCGGC ATGGGAACAG GTGTGACCTC 240
 CTGCTATAG TCACCAGACA TATGAATGTA AATTATACAT TCAAACTAG ATAGTAAGTA 300
 AAAGTGATTT TGCTTCGCAA AACATTTATT TTGATTAAGT CTTCCGATCG ATTAGTATTC 360
 35 CGTCAGCTCC ACATGTCACC ATGCTTCCAC CTCGAACCT 400

(2) INFORMATION FOR SEQ ID NO: 3671:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3671:

50 CACCCGAAGA TATTGCTCAG ACAAAGTCAT CATATACAGG AAAGTATTTA AAAGAAGTAC 60
 TTGAACGAGA TAAACAAAAT ACTGAAGATA AATAAGATTA AAAGAAGTGA AGGATGTTAT 120
 AAATTATCC TTCGTTCTT TTTATTAATT TAGTAATGAA TAGTAGAAAG AAAAGATGCG 180
 TAAAAGAAT TATGTTAAGA TAGGGTCAAT CTAGAGTAGT TAAACATAAA TCGAACTGGG 240

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TTAGCCACAG CTATTGTGTA CTTAAAAATA GGAATGCATG AGTGCACCnA nAGGnAGAAT 360
 ACTAATTTCC AAAGAAAAAG TATTCCTTAT GTTGGGGCCC 400

5 (2) INFORMATION FOR SEQ ID NO: 3672:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 461 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3672:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAG ATTCCATTCTG AGAAAGAACG 60
 TAAATTTAAT cCTGATTTAG CmCCaGGGAC aGAAAAAGTA mCmAGaGAAG GACaAAAAGG 120
 20 TGAGAAGACA ATaACGACAC CAACACTAAA AAATCCATTA ACTGGAGTAA TTATTAGTAA 180
 AGGTGAACCA AAAGAAGAAA TCACAAAAGA TCCGATTAAT GAATTAACAG AATACGGACC 240
 AGAAACGATA ACACCAGGTC ATCGAGACGA ATTTGATCCG AAGTTACCAA CAGGAGAGAA 300
 25 AGAAGAAGTT CCAGGTAAAC CAGGAATTAA GAATCCAGAA ACAGGAGACG TaGTTAGACC 360
 ACCGGTCGAT AGCGTAACAA AATATGGACC TGTAAAAGGA GACTCGATTG TAGAAAAAGA 420
 AGAGATTCCA TTCAAAACGT AAATTTAATC CGGATTTAGC A 461

30 (2) INFORMATION FOR SEQ ID NO: 3673:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3673:

CTTATGAATT CAAGCTTATT TAAAACCTCTT TATTCACCTCG GTTTTGCTTG GTAAAACTTA 60
 TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA 120
 45 ACCGCTGACC TCCTGCGTGC AAAGCAGGCG CTCTCCAGC TGAGCTAAGC CCCCAAAnAG 180
 GTATTAAATT AATGGGGGGC CTAAGTGGAC TCGAACCACC GACCTCACGC TTATCAGGCG 240
 50 TGCGCTCTAA CCAGCTGAGC TATAGGCCCA TTAATTTGAA TGAACAAACA TTCAAAACTG 300
 AATACAATAT GTCACGTTAT TCCGCATCTT CnGAAGAAGA TGTCCGAAT ATATCCTTAG 360
 AAAGGAGGTG ATCCAGCCGC ACCTTCCGAn ACGGCTACCT 400

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3674:

10 ACATGAAGAC TTAATTGAAG AATTATTAGG TATGGAAATT GAAGATGAGA TGGATAAAAA 60
 GGAAAAAGAA AAACCTTCTC AACAGCAAAT TCAATTTCAA CAACGGAAAA ATCGCAACGT 120
 15 ATCTATATAA GGAGCGAACA GCTATGTGGG AATAAGAATC GACTTACTCA AATGTTAAGT 180
 ATTGAATATC CAATTATACA AGCAGGTATG GCAGGAAGTA CGACACCGAA ATTAGTTGCA 240
 TCAGTAAGTA AACAGTGGTG GGTTAGGCAC AATAGGCGCG GTTACTTTAA TACGCGCCAA 300
 20 TTGGAnGATG GAnATnGATT ATGTACGCCA TTAACGTCAA ATTCTTTTGG CGTAAATGTC 360
 TTTGTACCAA GTCAACAATC ATATACCAGT AGTCCAAATT 400

(2) INFORMATION FOR SEQ ID NO: 3675:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3675:

35 AGCTAGGCCG GCAATATGTA AGAATAAATG GTGGAGAATG ACGGGTTCGA ACCGCCGACC 60
 CTCTGCTTGT AAGGCAGATG CTCTCCCAGC TGAGCTAATT CTCCGATTTA AAACGCCTG 120
 GCAACGTTCT ACTCTAGCGG AACGTAAGTT CGACTACCAT CGACGCTAAG GAGCTTAACT 180
 40 TCTGTGTTTCG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 240
 TAATTTATAC ATTCAAAACT AGATAGTAAG TAAAAGTGAT TTTGCTTCGC AAAACATTTA 300
 TTTTGATTAA GTCCTCGTCG TTAGTATTCG TCAGCTCCAC ATGTCACCAT GCTTCCACCT 360
 45 CGGACCTATT AACCTCATCA ACCTTGAGGG nTCTTATAAA 400

(2) INFORMATION FOR SEQ ID NO: 3676:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3676:

5 TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG ACATGTGGAG 60
 CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC CCGTCCACCG 120
 ATTGACTAAG TTTCCAGAGG AAGGCTCGTC CGCTCTGGGT TAGTCGGGTC CTAAGCTGAG 180
 10 GCCGACAGCG TAGGCGATGG ATAACAGTTG ATATTCTGT ACCACCTATA ATCGTTTTAA 240
 TCGATGGGGG GACGCATAGG ATAnGCGAAAn GTGCGATTGG ATTGCACGTC TAAGCAGTAA 300
 GGCTGAGTAT TAGGCAAATC CGGTACTCGT TAAGGCTGAG CTGTGATnGG GAGAAGACAT 360
 15 TGAGTCTTCG AGTCGTTGAT TTCACACTGC CGAGAAAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3677:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3677:

AAAGCGCCAC ATGGTGCCAA GTCTGGAGTT AATCCAGCAA TTGCTTGTTT TAAGCTATTA 60
 TATTTTCTT CTACTTTTGT TTTTCTGCG GCAATTTGTT GGTCACTCGC ATCACCATTG 120
 30 TTAATAACAT TTTGTGCATT TGTGATTCT GTTGACCCG CACGTTTAGC ATTTTCATAT 180
 GCTTGGATTG ATGATTGTGT CATACCATCA GTAGTTACTG ATTTATTGAT TTCTTCATCA 240
 35 AGTTTCGTCT TAGCAGTTTT TAAAGCACTA TTATCAGCTA AAGGTACTAA TTGGATTAAT 300
 TGCTTGC GTT AATCGCTCAT TGACACGATT TACATTTGTT AACGCAGATT GCACTTCTTG 360
 TACTGTTCTT AATGGGCTTT TGGAATAATA GCATTAGCGC 400

40 (2) INFORMATION FOR SEQ ID NO: 3678:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 648 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3678:

ACAGTCAATT GnTCTACCAA TTGAGCTAGG CCGTTAAGA AATGGTTCCA GGACAGAGTC 60
 GAATGCCGAC ACATGGAGCT TCAATCCATT GCTCTAACCA ACTGAGCTAC TGAACCATAA 120

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AGGCGTGTTA ACCGCTACAC TACGAGACCT ATAAAATATT GCGGGAGGCG GATTTGAACC 240
 ACCGTACTTC GGGTTATGAG CCCGACGAGC TACCGAACTG CTCCATCCCG CGATAATAAA 300
 5 AAATAATGGC GGAGGAAGAG GGATTCTGAAC CCCC GCGGCC CGTTAAGGCC tGTCGGTTTT 360
 CAAGACCGAT CCCTTCAGCC GGACTTGGGT ATTCTCCAT TATTATAGGT AAATCGCTAT 420
 10 TAATTATAAA ATTAAATGGC GGTCTCGACG GGAATCGAAC CCGCGATCTC tGCGTGACAG 480
 GCAGGCGTGT TAAyCGCTAC ACTACGAGAC CATTAGTAAA ACGGAGGAAG AGGGATTCTGA 540
 ACCCCCCGCA GCCGTTAAGC CCCTGTCGGT TTTCAAGACC GATCCCTTCA GCCGGGACTT 600
 15 GGGGTATTCC TCCAAAATTA TATGGGACCT TGCAGGACTC GAACCTGC 648

(2) INFORMATION FOR SEQ ID NO: 3679:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3679:

CTGATCCCGT TGTGCTTCAC ACCCGATAGA TAGGGATTTA CAGATAAATT CAGGTCTCTT 60
 30 CCACGTCATA TTTGGACCCA TCGAAAATTC GGGTTCTCAA ATCATCGAAC ATAACAAAAG 120
 AAGCTAAGCA ACATGTAGGC CGTTGTCACT TAACTTCTTG TTTTCCGAT GACAGCTTCT 180
 ATTTAGAGAA TGTCATGATT ATTTTATATT CACTTCAATG TTATCAATAT TAGTGCCATC 240
 35 TATGACATCT GCCATGCGAT TTTCTTGTA TTTTGTGTC AATTCAAACG TGTACTTTCC 300
 ACCGTTTTTC ATTTAATAA CAATTTTACC TGAACCAACG TTACCGTACA GATTATTTTT 360
 TTCAATAAGT TGTTTTCTCA ATTTAAATC AAGTTCTTTC 400

40 (2) INFORMATION FOR SEQ ID NO: 3680:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3680:

TCAATGCGGC TCATCGCATT CATTTCTTGT CTAGCAACGT TCTACTCTAG CGGAAnTAAG 60
 TTAGCTACCA TCCTCGCTAA GAACCTTTCT TGACTTGTGA CAATCGCTTG CTTCTTTCCT 120

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TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT 240
 TTGACGTTTT AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCCTGG CAACGTTCTA 300
 CTCTAGCGGA AGTAAGTTGG CTACCATCGT CGCTAAAGAC CTTTCTTGAC TTGTGACAAT 360
 CGCTTGGCTT CTnTCCTCTC CTTCGGnTCT CGGCITACTC 400

(2) INFORMATION FOR SEQ ID NO: 3681:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3681:

TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTAGCTCT ACTAAACTCG TTGCGCTCTT 60
 TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTTCT TTGTGTTTAC 120
 TTTTATTTT GACGTTTTAG ACATAAAAAA AGAGACCTCA CGGTCTCAAC TTGCCTGGCA 180
 ACGTTCTACT CTAGCGGAAC GTAAGTTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT 240
 TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT 300
 AAACTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 360
 TTTTCTTTG TGGTTTACTT TTTATTTTGA CGGTTTAGGC 400

(2) INFORMATION FOR SEQ ID NO: 3682:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 414 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3682:

TTGAACATGT TGAATCTAAT GAAATCTTGT TTCGTCGTCT AGTTGAAGAG AACGGCGTTG 60
 AGCATGAAGG TGAATTAGAT CGCTATCCAT TAGCTAAATT TAAACGTTCA AACTCAGGTA 120
 CATGTTACAA CCAACGTCCA ATCGTTGCAG TTGGAGATGT TGTTGAGTAT AACGAGATTT 180
 TAGCAGATGG ACCATCTATG GAATTAGGAG AAATGGCATT AGGTAGAAAC GTATAGTTGG 240
 TTTCATGACT TGGGACGGTT ACAACTATGA GGATGCCGTT ATCATGAGTG AAAGACTTGT 300
 GAAAGATGAC GTGTATACTT CTATTCATAT TGAAGAGTAT GAATCAGAAG CACGTGATAC 360

(2) INFORMATION FOR SEQ ID NO: 3683:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3683:

TTGGAATTTT TCCGCTACCC TCAGTTCATC CGCTCACTTT TCAACGTAAG TCGGTTTCGGT 60
 CCTCCATTCA GTGTACCTG AACTTCAACC TGACCAAGGG TAGATCACCT GGTTCGGGT 120
 CTACGACCAA ATACTAAACG CCCTATTGAG ACTCGCTTTC GCTACGGCTC CACATTTACT 180
 GCTTAACCTT GCATCAAATC GTAACGCGCC GGTTCATTCT ACAAAGGCA CGCCATCACC 240
 CATTAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTC ACTCCCCTTC 300
 CGGGGTGCTT TTCACCTTTC CCTCACGGTA CTGGGTTTAC TATCGGTCAC TAAAGAGATA 360
 TTTAAGCCTT AAGAGATGGT CCTCCCAGAT TCCCACGGG 400

(2) INFORMATION FOR SEQ ID NO: 3684:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3684:

GATATATGAT GAAAACTAT CTGACTGCTG TTTCACTTTT TATAAGACTT CTGAATGTCT 60
 TCACTTATAC TTCTAGTCAC AGATTAAAT AATCAAAAGT GCACATTATT AAAATATCAA 120
 TTTCACTC AATGCGGCTC ATCGCATTCA TTTCTGTCT AGCAACGTTT TACTCTAGCG 180
 GAACGTAAGT TAGCTACCAT CTCGCTAAG AACCTTTCTT GACTTGTGAC AATCGCTTGC 240
 TTCTTTCTC TCCTTCGGCT CTCGCTTACT CATTAGCTC TACTAACTC GTTGCCTCT 300
 TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA GCCATTTTTC TTTGTGTTTA 360
 CTTTTTATT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA CTTGCCTGGG 420
 CAACGTTCTA CTCTAGCGGA ACGTAAGTTG GCTACCATCG TCGCTAAAGA CCTTCTTGA 480
 CTTGTGACAA TCGCTTGCTT CTTCCTCTC CTTCGGCTCT CGGTACT 528

(2) INFORMATION FOR SEQ ID NO: 3685:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3685:

10 AAATTATGGT CGATTGCGAA TGATTTAAGA GGGAnCATGG ATGCGAGTGA ATTCCGTAAT 60
 TACATTTTAG GCTTGATTTT CTATCGCTTC TTATCTGAAA AAGCCGAACA AGAATATGCA 120
 GATGCCTTGT CAGGTGAAGA CATCACGTAT CAAGAAGCAT GGCAGATGA AGAATATCGT 180
 15 GAAGACTTAA AAGCAGAATT AATTGATCAA GTCGGTTACT TCATTGAGCC ACAAGATTTA 240
 TTCAGTGC GA TGATTCGTGA AATTGAAACG CAAGATTTCG ATATAGAGCA TCTAGCGACG 300
 GCGATTCGCA AAGTTGAAAC ATCTACATTA GGTGAnGAAA GTGAAAATGn CTTTATCGGG 360
 20 CTGTTCA GCG ATATGGATTT GAGTTCAACG CGGCTAGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3686:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 403 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3686:

TTAAATTATT GGTCTATCGG TTCTTGGGGT GGCCATGGTA TCTGTTCCT CTTCGGTGGT 60
 35 GCAGTTGCGA CAACTATGGG TTGGAGATGG ATTTTCATCT TCTCAATTAT CGTTGCCGTA 120
 CTTTCAATGT TACTCATCAA AGGGACGCCT GAAACGAAAT CAGAAATTAC CAATACACAT 180
 AAATTTGACG TTGCAGGGCT AATTGTTCTA GTAGTTATGT TGCTAAGTTT AAACGTTGTC 240
 40 ATTACTAAAG GTGCAGCACT TGGTTACACA TCATTATGGT TCTTTGGTTT GATTGCAATC 300
 GTAATTGTAG CATTCTTTAT TTTCTTAAAT GTTGAGAAAA AAGTAGATAA TCCACTTATT 360
 GATTTTAAAT TATTgAAAAT AAACCATATA CAGGTGCAAC GGT 403

45

(2) INFORMATION FOR SEQ ID NO: 3687:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 449 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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TATGAGCCCG ACGAGCTACC GAACTGCTCC ATCCCGCGAT AATAAAAAAT AATGGCGGAG 60
 GAAGAGGGAT TCGAACCCCC GCGGCCCGTT AAGGnCTGT CGGTTTTCAA GACCGATCCC 120
 5 TTCAGCCGGA CTTGGGTATT CCTCCATTAT TATAGGTAAA TCGCTATTAA TTATAAAATT 180
 AAATGGCGGT CTCGACGGGA ATCGAACCCG CGATCTCCTG CGTGACAGGC AGGCGTGTTA 240
 ACCGCTACAC TACGAGACCA TTAGTAAAAC GGAGGAAGAG GGATTCGAAC CCCC GCGAGC 300
 10 CGTTAAGCCC CTGTCGGTTT TCAAGACCGA TCCCTTCAGC CGGACTTGGG TATTCCTCCA 360
 AAATTATATG GACCTTGCAG GACTCGAACC TGCGACCGAA CGGTATGAGC CGTAGCnCTA 420
 ACCACTGGGC TAAAGTCCTA ATATAATTT 449
 15

(2) INFORMATION FOR SEQ ID NO: 3688:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3688:

AAAACGTCGT AATATGCAAA TTGAAGGTGC CAAGGTTGTT ATTCAAGGTT TCnATAATGC 60
 CGGAAGTTTC TTAGCTAAAT TCTTATATGA TTTAGGTGCA AAAATTGTAG GTATCTCTGA 120
 30 TGCTTACGGT GCATTACACG ATCCAAATGG CTTAGATATA GATTATTTAT TAGACCGTCG 180
 AGATAGTTTT GGTACGGTAA CAAATTTATT TGAAGAAACA ATCTCAAATA AAGAATTGTT 240
 TGAATTAGAT TGTGACATTT TAGTACCAGC GGCTATTTCA AACCAAATTA CAGAAGACAA 300
 35 TGCACATGAT ATTAAAGCTA GTATCGTTGT TGAAGCTGCT AATGGACCTA CAACACCAGA 360
 AGCAACACGT ATTTTAACTG AACGTGGTAT ATTATTAGTT 400

40 (2) INFORMATION FOR SEQ ID NO: 3689:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3689:

50 CACGCTTATC AGGCGTGCGC TCTAACCAGC TGAGCTATAG GCCCATTAAAT TTGAATGAAC 60
 AAACATTCAA AACTGAATAC AATATGTCAC GTTATTCCGC ATCTTCTGAA GAAGATGTTT 120

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CGACTTCACC CCAATCATTT GTCCACCTT CGACGGCTAG CTCCTAAAAG GTTACTCCAC 240
 CGGCTTCGGG TGTACAAAC TCTCGTGGTG TGACGGGCGG TGTGTACAAG ACCCGGGAAC 300
 5 GTATTCACCG TAGCATGCTG ATCTACGATT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT 360
 TGCAGACTAC AATCCGAAC GAGAACT TATGGGGAA 400

(2) INFORMATION FOR SEQ ID NO: 3690:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 553 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3690:

GCnGCGTTTT AGGCCATTG GGTACCCCC nTTCCATAAA TGGTGCCCGG CCAGAGGACT 60
 TGAACCCCCC AACTTACTGA TTACAAGTCA GTTGCTCTAC CAATTGAGCT AGGCCGGCTA 120
 AGAAATGGTT CAGGACAGAG TCGAACTGCC GACACATGGA GCTTCAATCC ATTGCTCTAC 180
 25 CAACTGAGCT ACTGAACCAT AATAAAAATG TAATGATGGC GGTCTCGACG GGAATCGAAC 240
 CCGCGATCTC tGCGTGACAG GCAGGCGTGT TAACCGCTAC ACTACGAGAC CTATAAAATA 300
 TTGCGGGAGG CGGATTGAA CCACCGaCtT CGGGTTATGA GCCCGACGAG CTACCGAACT 360
 30 GCTCCATCCC GCGATAATAA AAAATAATGG CGGAGGAAGA GGGATTGAA CCCCCGCGG 420
 CCGTTAAGGC CCTGTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC 480
 ATTATTATAG GTAnATCGCT ATTAATTATA AnATTAAAT GGCGGTCTCG ACGGGAATCG 540
 35 AACCCGCGGA TCT 553

(2) INFORMATION FOR SEQ ID NO: 3691:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3691:

TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA 60
 50 GTTGGCTACC ATCGACGCTA AGAACCTTTC TTGACTTGTG ACAATCGCTT GCTTCTTTCC 120
 TCTTCTTCGG CTCTCGCTTA CTCATTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGT 180

TTTGACGTTT TAGACATAAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 300
 ATTTTTTGCC TGGCAACGTT CTA CTACTCTAGC GGAACGTAAG TTCGGACTAC CATCGACGCT 360
 5 AAGGGAGCTT AACTTTCTGT GTTCGGGCAT GGGGAACAGG 400

(2) INFORMATION FOR SEQ ID NO: 3692:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 410 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3692:

TCGAATACTG TCATGAAGTA ATTTCTCTAT TCTACGACCA GAAATACAG ATTGAGTATA 60
 20 TGCATATAAG ATGTTTTTAA CATCATTTTT GGATGATAGG ATGTTGCACC ACGATGATGT 120
 CTGAATTCAT CGAATTCCTA TCAGGTATCG TTTCAACAAT TTCATTAACA TATCGCGAAA 180
 TATCATTTTG AGAATTCTAA CGAATTTCTT ATTGGTAGTG TAAGTTGGGG TCATGTTATA 240
 25 ATTTTATAC ATAAGGCACC TCTTTAATT AGTTTAGTAG TATTTATTAA ATTATACGAG 300
 GGACCCAACA CAGAAAATTC ATTTTATTGa ATTTTACATT TATGTGmCAA GTTGGGaAAA 360
 ATGTCTTATT TTTTCAAAGT ATTTAAAAGT AAAaTTACAT GTTAATACGT 410

(2) INFORMATION FOR SEQ ID NO: 3693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3693:

ACTTCATATA ATTTATGAAA TAAACCTGTC AATTTTGGAT TGATTATGCT TTGTGATTCT 60
 TTTTATTTCT GCGTAATAAC GCTAAACCTA AAATGCTAAA TAATCCGCCG AACACATGC 120
 45 CGTTGTTTGT TGATTCTTCT CCACCTGTTT CAGTAGTTCA GATTTCTTAG ATTGTGCTTT 180
 TTTAGTTGGT ACCACTGcTT TAACCTTTTC ATTGATTCA ATAACAGGTG TTACTACTTT 240
 ACCTTGTTCC ACTGGTTTAG AAGGTTTTTT AGGTTCTTCT TTAGCAGGTG GTaTTGGTTT 300
 50 ACCAGGTTCA GTTGGTACCT CTGGCGTTGG CGGTGTTGGT GTTTCCGGCT CGCTTGGTAC 360
 TTCTGGTGTC GGTGGTGTG GGTGTTThCC GGCTTCGCTT GGTACTTCTG GGTGTTGGT 420

(2) INFORMATION FOR SEQ ID NO: 3694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3694:

GCATCGTTGC CTTGGTAAGC CGTTACCTTA CCACTAGCT AATGCAGCGG GAGTCCATCT 60
 ATAAGTGACA GCAAGACCGT CTTTCACITT TGAACCATGC GGTCAAATn ATTATCCGGT 120
 ATTAGCTACG GTTTCCTCGAA GTTATCCCAG TCTTATAGGT AGGTTATCCA CGTGTTACTC 180
 ACCCGTCCGC CGCTAACATC AGAGAAGCAA GCTTCTCGTC CCGTTCGCTC GACTTGCATG 240
 TATTAGGCAC GCCGCCAGGT TCCATCCTGA GCCAGGATCA AACTCTCCAT AAAAATTATG 300
 ATGTTTGATT AGCTCATAAA TACTAAATAA TGTTTGTAAC TTATAGTTAC GTTTTTTGGG 360
 AATTAACGTT GGACATATTG TCATTCCAGT TTTCAATGTT 400

(2) INFORMATION FOR SEQ ID NO: 3695:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3695:

ACCTAATATA TAGACAGGTT CATCACTTAA TGACTTTGCA AGTTCGGCAA TGTCTGTGC 60
 GTCGCGTTTG ACACGATAAT CACTGTCAGG GTTTGAAGCG GAATCAGGGA GTGGTTCAGT 120
 TAACTCGCTT TCTCCATAAT CACGACGATC AACGGCTACA ACAGTAAAT GGTCTTTTAA 180
 CTGTTCTGCA AGAGGCAGAA AAATGTCTCC GGTACCGTTT GCACCAGGAA TAAAGATGAG 240
 CACGGGTCCT TGTCCGACTT GGTGGTATCG TAATTTAGCG CCTTGTAATT CTAAAGTTTC 300
 CATATTCAAT GACCTCCATT TGTTAATTGT TAGGTGATAA ACCTAATAAT TTAGCACCAT 360
 TTGGTATAAC TTAATTTcnc CTTTTCCTTC ATCnGGTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3696:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3696:

5 TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCTC CGGGTGTGCC TTCTGATATG 60
 CTATGTATTTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT 120
 CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 180
 10 TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 240
 CATTTTTATA AGTCAAACGC TCACATACGG CTTCTGTTTT ATTATTTTAA ATGCTCATT 300
 ACATAAGTAA ACTCTGCTTT AAAATAATTT AACTCATTGT CTGCTAAACG TTTTCTTTTA 360
 15 TAAAAAGATT TAAACGCGTT GATTAACTG TGAGTGTCT 400

(2) INFORMATION FOR SEQ ID NO: 3697:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3697:

CACTTTAACC AAAAAATATT TGAATGTAA ATAAACATTC AAAACTGAAT ACAATATGTC 60
 30 ACGTTATTCC GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC 120
 CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCCAATCAT TTGTCCCACC 180
 TTCGACGGCT AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG 240
 35 TGTGACGGGC GGTGTGTACA AGACCCGGA ACGTATTCAC CGTAGCATGC TGATCTACGA 300
 TTACTAnCGA TTCCAnCTTC ATGTAGTCGA GTTGCACT ACAATCCGAA CTGAGAACAA 360
 CTTTATGGGA TTTGCTTGAC CTCGCGGTTT CGCTnCCCTT 400

(2) INFORMATION FOR SEQ ID NO: 3698:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3698:

50 AAGGGAATCG AATTTCTTT CTCTTCTCC GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60

CCCCATTTCGG AAATCTCTGG ATCAAAGCTT ACTTACAGCT CCCCAAAGCA TATCGTCGTT 180
 AGTAACGTCC TTCATCGGCT TCTAGTGCCA AGGCATCCAC CGTGCGCCCT TAATAACTTA 240
 5 ATCTATGTTT CCATCCTACA GGAAACGCGT TATTAATCTT GTGAGTGTTT TTTCGAACAC 300
 TAGCGATTAT TTCTTATGAA TTCAAGCTTA TTTAAAACTC TTTATTCACT CGGTTGTGCT 360
 TGGnAAAATC TATATTTTAC TTACTIONTATCT AGGTTTCAAT 400

10

(2) INFORMATION FOR SEQ ID NO: 3699:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3699:

TTTATGGCAT ACACGCATCA TAATACAGCC CAACACCACT AATGGTGCGAG TTGCAAATCC 60
 AAATTCTTCC GCTCCAAGCG CACATGCGTA CGCTACATCT TTACCAGTTA ATAACCTTACC 120
 25 GTCTGTTTCT AACTTAACAC GACTTCTTAA GTCATTTAGT TTTAATGTTT GATGTGTTTC 180
 TGCTAAACCA ATCTCCCAAG GAACACCGGC ATGCTGAATA CTCGTTTTGG GTGAAGCCCC 240
 TGTAnCACCA TCGTAACCAC TGATGACAAT TTTATCTGCA AATGCTTTTG CCACCCCAGA 300
 30 TGCAATGGTA CCAACACCTG TTTTCGAAAC TAATTTTACC GCGATATCTG CATCTTTATT 360
 CGCATTTTTT AAATCATGTA TCAGTTGCGC TAAATCTTCT 400

35

(2) INFORMATION FOR SEQ ID NO: 3700:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3700:

CGACGTACCA TCGACGCTAA GGAGCTTAAC TTTCTGTGT TCGGCATGGG AACAGGTGTG 60
 ACCTCCTTTG CTATAGTCAC CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG 120
 TAAGTAAAG TnATTTTGCT TCGCAAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG 180
 50 TATTCGTCAG CTCCACATGT CACCATGCTT CCACCTCGAA CCTATTAAACC TCATCATCTT 240
 TGAGGGATCT TATAACCGAA GTTGGGAAAT CTCATCTCnC GGGGGGCTTC ATGCTTAGAT 300

55

GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA

400

(2) INFORMATION FOR SEQ ID NO: 3701:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3701:

AACCAAGCCC AATAATGGAC TGGCCGCCTA ATAATAAAAG CTCTAAAAGT TGTATTTTAA 60
 AAATAGTTCT TTAAATTATA TACCCACCAC ATTTGGTGGA GAACCTAAAA AAAAGCACTT 120
 CCCAAAAATG GAAAGTGCAA GTAGTGAGCC ATAGAGGATT CGAACCTCTG ACCCTCTGAT 180
 TAAAAGTCAG ATGCTCTACC AACTGAGCTA ATGGCTCTAA TGGCTGGGCT AGCTGGATTC 240
 GAACCAACGA GTGACGGAGT CAAAGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA 300
 TAGATGGTGG AGGGGGGCAG ATTCGAACTG CCGAACCGA AGAGCGGnTT TACAGTCCGC 360
 CGCGTTTAGC CanTTCGnTA CCCCTCCAGn TTATTTCATAT 400

(2) INFORMATION FOR SEQ ID NO: 3702:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3702:

TTTAAGTCCT GTGCGTCTGC CAGTTCCGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA 60
 CGGGATTCTGA ACCCGCGACC CCAACCTTGG CAAGGTTGTT ATTCTACCGC TGAAGTACTT 120
 CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA AGgTTAGaTC CTAAGTCTAG 180
 TGCGTCTGCC AATTCGCGCA CACCCGCAA TGGTGAGCCA TAGAGGATTC GAACCTCTGG 240
 ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGGCTCT TCCATGGTGC 300
 CGGCCAGAGG ACTTGGAACC CCCAACCTAC TGGATTACAA GTCAGTTGGC TCTACCAATT 360
 GAnGCTAAGG CCGGCAATAT GTTAAGnATn AATGGTGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3703:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3703:

	CAACTAATAA ATAGTGGCGG TGGAGGGGAT CGAACCCCGG ACCTCACGGG TATGAACCGT	60
10	ACGCTCTAGC CAGCTGAGCT ACACCGCCTT ATATAGTTTG TAAATAATAT GGTGGAKACT	120
	AGCGGGATCG AACCGCTGAC CTCCTGCGTG CAAAGCAGgC GCTCTCCCAG CTGAGCTAAG	180
	CCCCCATAAT AATTACAGTA TATCGGGAAG ACAGGATTCG AACCTGCGAC CCCTTGGTCC	240
15	CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGCGC CCGATAGGAG	300
	TGAACCCAT AAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG CTAACGGGCG	360
	CATATGTTTT TAATTGAAAT GGTGCCCGAG GACCGGAATG	400

20

(2) INFORMATION FOR SEQ ID NO: 3704:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3704:

30

	CTAACGCCTA CGCGTTACAT GAAAAACGGA GAACAAGCAG AACAAATTATT ACGTCAGCTT	60
	ATAGAAAAAG ATGAAGCACT AGCTAAGTAT GTCATGGTTT GTGATGAAAC AGCTTGGTGG	120
35	TCATATATGG GTCAAGATAA TGATATTTTC AAAGATCAAT TAGGTCACTT AACTGTTTCT	180
	CTAAGAAAGT ATCCCGAAGT GCTAGCCAAA AATGATACGC AACAGCTAGT GTCAATGGCA	240
	GCACTCGCGG CAAATGATCG CACTTTATAT CAAATGATTT GTGGAAAAGA TAATATTTCT	300
40	AAAAATGATG TCATGACGTT ATTTGAAGAT ATCGCGCAAG TCTTTTAAAA GGTAACACTA	360
	TCATTTATGC AATACGGGCGC ATTACCCAGA GTTGCATGGT	400

(2) INFORMATION FOR SEQ ID NO: 3705:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 478 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3705:

55

5 TGACGGGGAC CCGCACAAGC GGTGGAGCAT GTGGTTTAAT TCGAAGCAAC GCGAaGaACC 120
 TTACCAAATC TTGaCATCCT TTGaCAACTC TAGaGATAGA GCTTTCCCCT TCGGGGGTAC 180
 10 AAAGTGACAG GTGGTGCATG GTTGTCTGCA GCTCGTGTCTG TGAGATGTTG GGTTAAGTCC 240
 CGCAACGAGC GCAACCCTTA AGCTTAGTTG CCATCATTAA GTTGGGCACT CTAAGTTGAC 300
 TGCCGGTGAC AAACCGGAGG AAGGTGGGGA TGACGTCAA TCATCATGCC CCTTATGATT 360
 TGGGgCTACA CACGTGCTAC AATGGACAAT ACAAAGGGCA GCGAAACCGT GAGTCAAGCA 420
 AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGACTAC ATGAAGCT 478

15 (2) INFORMATION FOR SEQ ID NO: 3706:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3706:

ATCTTAAGTC TTTGGTGAAC CGTTTTGTAG AATTAAATAA TATTACAGAG CCGCTAGCAG 60
 TAACGATCCA AACGAATTTA CCACCATCAC GTGGATTAGG ATCGAGTGCA GCTGTCGCGA 120
 30 TTGCTTTTGT TCGTGCAAGT TATGATTTTT TAGGGAAATC ATTAACGAAA GAAGAACTCA 180
 TTGAAAAGGC TAATTGGGCA GAGCAAATTG CACATGGTAA ACCAAGTGGT ATTGATACGC 240
 AAACGATTGT ATCAGGCAAA CCAGTTTGGT TCCAAAAGG TCATGCTGAA ACGTTGAAAn 300
 35 CTCAAAGTTT AGACGGCTAT ATGGTTGTTA TAGAnACTGG TGTGAAAGGT TCACCAAGAC 360
 AAGCAGTAGA AGATGTTCCA TAACTTTGG TGAGGACCCT 400

40 (2) INFORMATION FOR SEQ ID NO: 3707:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3707:

50 GTCGAACTGC CGACACATGG AGCTTCAATC CATTGCTCTA CCAACTGAGC TACTGAACCA 60
 TAATAAAAAT GTAATnnTGG CGGTCTCGAC GGAATCGAA CCCGCGATCT CCTGCGTGAC 120
 AGGCAGGCGT GTTAACCGCT AACTACGAG ACCTATAAAA TATTGCGGGA GGCGGATTTG 180

55

TAAAAAATAA TGGCGGAGGA AGAGGGATTG GAACCCCCGC GGCCCGTTAA GGCCCTGTCTG 300
 GTTTTCAAGA CCGATCCCTT CAGCCGGACT TGGGTATTCC TCCATTATTA TAGGTAAATC 360
 5 GCTATTAATT ATAAAATTAA ATGGCGGTCT CGACGGGAAT 400

(2) INFORMATION FOR SEQ ID NO: 3708:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3708:

GTTCGCCCAT TAAAGCGGTA CCAnGCTGGG TTCAGAACGT CGTGAGCAnG TTCGGTCCCT 60
 20 ATCnGGGGTG GCGGTAGGAA ATTTGAGAGG AGCTGTCCTT AGTACGAGAG GACCGGGATG 120
 GACATACCTC TGGTGTACCA GTTGTCGTGC CAACGGCATA GCTGGGTAGC TATGTGTGGA 180
 CGGGATAAGT GCTGAAACAT CTAAGCATGA AGCCCCCTC AAGATGAGAT TTCCCAACTT 240
 25 CGGTTATAAG ATCCCTCAAA GATGATGAGG TTAATAGGTT CGAGGTGGAA GCATGGTGAC 300
 ATGTGGAGCT GACGAATACT AATCGATCGA AGACTTAATC AAAATAAATG TTTTGCGAAC 360
 AAAATCCACT TTTACTTACT ATCTAGTTTT GAATGTATAA 400

(2) INFORMATION FOR SEQ ID NO: 3709:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3709:

AATTTTATGG GCCCTTTATG GACTTTATAT TmCCTAAAAT ACTATTAAGA AGTCCTGAAA 60
 AATTCACATT AGCAGTTGGA TTGTTCAACT TTATTAAATGA TAAGTATGCA AATAATTTCA 120
 45 CAGTGTTTGC AGCAGGGGCA ATTATGATTG CAGTACCTAT AGCAATCGTA TTCTTGTTCT 180
 TGCAACGCTA TTTAGTATCA GGTTTAACAA CAGGTGCGAC AAAAGGTTAG TTTGAAATTr 240
 50 GGAGTGGGGC AGAATTGATA AAGAACCACT AATGACGATA AAGATTAAAA GGAGGACGTT 300
 ATGATGACGA TTAAAGTTGG AATCATTGGG TGTGGTGGTA TTGCGAATGG CAAGCACATG 360
 CCAAGTTTAC AAAAAGTTGA AAATGTTGAA ATGATCGCAT TTGTGACGTG GACTTTGCGAA 420

(2) INFORMATION FOR SEQ ID NO: 3710:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3710:

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AGTGCTCTAC CAAGCTGAGC TACTTCCCGT ATAATTAACG CGCCCGATAG GAGTCGAACC      60
CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT      120
TTATTGAAAA TGGTGCCGAG GACCCGAATC GAACCGGTAC GTGATCACTC ACCGCAGgAT      180
TTTAAGTCCT GTGCGTCTGC CAGTTCGGCC ACCCCGGCAC TATAAAAATG GAGCAGAAGA      240
CGGGATTTCGA ACCCGCGACC CCAACCTTGG CAAGGTTGTa TTCTACCGCT GAACTACTTC      300
TGCATATGCG GGTGAAGGGA GTCGAACCCC CACGCCGTAA GeTkAGaTCC TgAAGTCTAG      360
TGCGTCTGCC AATTCCGCCA CACCCGCAAA TGGTGAGCCA TAGAGGATTC GAACCTCTGG      420
ACCCTCTGGA TTGAAAAGTh CAGATGCTCT GACCAACTGG AGCTAATGGC TCTTCCCATG      480
GTGGCCGGCC AGAAGGACTT GGAACCCCCA ACCTGATGGA TTTACAATTC AGTTGGCTCT      540
AACCAATTTG AGCTAAGGC                                         559

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(2) INFORMATION FOR SEQ ID NO: 3711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3711:

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AACCTTTTAG GAGCTAGCCG TCGAAGGTGG GACAAATGAT TGGGGTGAAG TCGTAACAAG      60
GTAGCCGTAT CGGAAGGTGC GGCTGGATCA CCTCCTTTCT AAGGATATAT TCGGAACATC      120
TTCTTCAGAA GATGCGGAAT AACGTGACAT ATTGTATTCA GTTTTGAATG TTTGTTCAAT      180
CAAATTAATG GGCCTATAGC TCAGCTGGTT AGAGCGCACG CCTGATAAGC GTGAGGTCCG      240
TGGTTCGAGT CCACCTAGGC CCACCATTAA TTTAATACCT ATTTGGGGGC TTAGCTCAGC      300
TGGGAGAGCG CCTGCTTTGC ACGCAGGAGG TCAGCGGTTG GATCCCGCTA GTCTCCACCA      360
TTATTTGTAC ATTTGAAAAC TAGATAAGTA AGTAAAATAT                                         400

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3712:

TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG 60
 CGAnnTCATG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GCCTGAAACC nnGTGATCTA 120
 CCCTTGGTCA GGTGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTGA 180
 AAAGTGAGCG GATGAACTGA GGGTAGCGGA GAAATTCCAA TCGAACCTGG AAATAGCTGG 240
 TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGG ATTATTGGAG GTAGAGCACT 300
 GTTTGGACGA GGGGCCCCTC TCGGGTTACC GAATTCAGAC AAACCTCCGAA TGCCAATTTA 360
 ATTTAACTTG GGGAGTCAGA ACATTGGGTG ATAAGGTCCG 400

(2) INFORMATION FOR SEQ ID NO: 3713:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3713:

TTTTAAAGTC TGATGTGAAA GCCCACGGCT CAACCGTGAA GGGTCATTGG AAACCTGGAAA 60
 ACTTGAGTGC AGAAGAGGAA AGTGGAATTC CATGTGTAGC GGTGAAATGC GCAGAGATAT 120
 GGAGGAACAC CAGTGGCGAA GGCGACTTTC TGGTCTGTAA CTGACGCTGA TGTGCGAAAC 180
 GTGGGGATCA nACAGGATTA GATACCGGT AGTCCACGCC GTAAACGATG AGTGCTAAAG 240
 TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGTAAACGCA TTnAAGCACT CCGnCTGGGG 300
 AGTACGnCCG CAAGTTGGAA ACTTCAAAGG AATTGACGGG GGACCCGCAC AAGCGTTGGG 360
 AGCATGTGGT TTAATTTCTGA AGCAACGGAG AGGAACCTGA 400

(2) INFORMATION FOR SEQ ID NO: 3714:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3714:

5 AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60
 TGTGGATTAA TATTATGCCT GGCAACGTTT TACTCTAGCG GAACGTAAnT CGACTACCAT 120
 CGACGCTAAG GAGCTTAACT TCTGTGTTTC GCATGGGAAC AGGTGTGACC TCCTTGCTAT 180
 10 AGTCACCAGA CATATGAATG TAATTTATAC ATTCAAAnT AGATAGTAAG TAAAAGTGAT 240
 TTTGCTTCGC AAAACATTTA TTTTGATTAA GTCTTCGATC GATTAGTATT CGTCAGCTCC 300
 cAtGTCACCA TGCTTCCACC TCGAACCTAT TAACCTCATC ATCTTTGAGG GATCTTATAA 360
 15 CCGAAGTTGG GAAATCTCAT CTGAGGGGG GCTTCATGTC TTAGCATTTC AGTCACTTAT 420
 GCCCG 425

(2) INFORMATION FOR SEQ ID NO: 3715:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3715:

30 GTCCCTGCTG TTCCTATCAT ATAAATGATA GATTCAAATA GATTGTAGG TTTGTCATGC 60
 CCAGTTACAA GTTGCGTTAT CGTAGACACT AACATTAATA TGAAGGTAA TGTGCTGTT 120
 AATAAACTCA TACCAAATCC TGGCATCTCT TGATCCGTAA ATTCTTTTTG TGCACCTAAC 180
 35 GCTGAAATAT CGCCTTCTCG TGTATACGCA GACGGAATCA TTTTTGTGC ACTTTGTTAA 240
 ATATAGCCCC TGCAATGAGT GTACTGGAAT GGCAATAATC ATACCATACA GTAATACATC 300
 TCCAACATTT GCCTTTAATT CTTTTCGAG ACTACCGGTC CTGGGATGTG GTGGTAAAAA 360
 40 GCCATGTGTC ACTGATAAAG CTGTTACCAT AnGTAGTCCT 400

(2) INFORMATION FOR SEQ ID NO: 3716:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3716:

55 TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG TTTTGCTTGG TAAAATCTAT 60

5 GCAATATCAC TTTAACCAAA AAATATTGA ATGTTAAATA AACATTCAAA ACTGAATACA 180
 ATATGTCACA TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA 240
 10 GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG 300
 TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTAATCCACC GGnTTCGGGT GTTACAAACT 360
 GTTCGTGGTG TGACGGGGCG GTGTGTTACA AGACCCGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3717:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3717:

AAAGGACGAC ATTAGACGAA TCATCTGGAA AGATAATTCA AAGAAGGTAA TAATCCTGTA 60
 25 GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGGTACGAC GGAGCACGTG AAATTCCGTC 120
 GGAATCTGGG AGGACCATCT CCTAAGGCTA AATACTCTCT AGTGACCGAT AGTGAACCAG 180
 TACCGTGAGG AAAGGTGAAA AGCACCCCGG AAnGAGTTGA AATAGAACCT GAAACCGTGT 240
 30 GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG CCTTTTGTAG AATGAACCGG 300
 CGAGTTACGA TTTGATGCAA GGTAAAGCAG TAAATGTGGA GCCGTAGCA_n AAnnTGTCT 360
 GAATAGGGCG TTTAGTATTT TGGTCGTAGC CCGAGAACCA 400

35 (2) INFORMATION FOR SEQ ID NO: 3718:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3718:

TAATTCATCT GCAGCATCTG GTTGATTTAA GCTTTCACGT AAACACATCG CTAAAGATAG 60
 AATCATTCCA AATGGATTGG CAACGTTTTT ACCTGCAATA TCTGGTGCTG ATCCATGAAT 120
 50 AGGCTCATAC AATCTTGGAC CATCGTTACT AAAACTAGCA GAAGGTGATA AACCAAGTGA 180
 ACCAGGAATC ACTGAAGCTT CATCACTTAA AATATCGCCA AATAAGTTTT CACATACGAT 240
 GACGTCAAAT TGTTTTGG_n TTTGTGATTA AATGCATACT ACAAGCATCA ACAAATAAGT 300

55

TTTACTAGAA GCTAATACAT TTCCTTATCA ACGGATGTnA

400

(2) INFORMATION FOR SEQ ID NO: 3719:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3719:

ATTTAAAAC TGCCTGGCAAC GTTCTACTCT AGCGGAAnTA AGTnGAGCTA CCATCGACGC 60
 TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC 120
 CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT 180
 TCGCAAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG TATTCGTCAG CTCCACATGT 240
 CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT TGAGGGATCT TATAACCGAA 300
 GTTGGGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA CTTATCCCGT 360
 CCACACATAG CTACCCAGCT AGCCGTGGC ACGACAAnGG 400

(2) INFORMATION FOR SEQ ID NO: 3720:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3720:

CGTTACACCT TCCAATAAAT TTGCTGTTGC TGGATAAGGA GAAATATTGA TATATTGTCT 60
 TAAATTACTA TAATGCCAAT TTAAGTCTGG ATGATTTGTT AAGACACCAA TAGGATTATC 120
 TTTTATAACC ACTTCACCCT CTTTAAATGA AACTTCGACT GTATGTCCAG TTGCATCGGA 180
 AACATGATAA TGCAATGGCG GAACTTCACC GATGTCATTT AAATATACAG CTACAACATG 240
 TATTTGGGAT GCTTGTGTT TCATATCTTC AATGCTTGTT GTATATCCCA AAATCCATGT 300
 CACAATTTCA TTTTGGGTAA TATTCATCGC GTCCGCTTTG TGTGTTGGAT CCATATGGAA 360
 CTATAACCTC GGGAAATATT GTGGTTGAAA TGGGCACGCC 400

(2) INFORMATION FOR SEQ ID NO: 3721:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3721:

	AGTCAGTTTA TAGCGATTGC TGGACTGACA GTACTTGTGC CATTATTGCC AATTTATATG	60
10	GCATCACTAC AAAATCTATC AGTCGTAGAA ATACAGTTGT nGAGTGGTAT AGCGATTGCT	120
	GCTCCAGCTG TAACGACGAT GATAGCTTCG CCGATATGGG GGAAGCTAGG TGATAAGATC	180
	AGCCGAAAAT GGATGGTGTT AAGAGCGTTA CTTGGTTTGG CGGTATGCTT ATTTTAAATG	240
15	GCATTGTGTA CGACACCATT ACAGTTTGTA CTTGTGGAGG TTATTGCAGG GACTATTTGG	300
	TGGTGTGTTT GATGCATCAA GTGCGTTTGC GAGTGCAGAA GCGCCACTG AnAGATCGTG	360
	GGAAAGGTAT TAGGAAGACT GCAAATTnCA GTTCAGCGCA	400

20

(2) INFORMATION FOR SEQ ID NO: 3722:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3722:

	TCTAAAAGTT GAACTACTCC CGCATAAACC TGGAGGCGGC AACCGGATTT GAACCGGTGA	60
	TAAAGGTTTT GCAGACCTCT GCCTTACCAC TTGGCTATGC CGCCAATAAC TGGGCTAGCT	120
35	GGATTCGAAC CAACGAGTGA CGGATAAAGT CCGTTGCCTT ACCGCTTGGC TATAGCCCAT	180
	TAATAATAAG GCGGCTGAA GGGGATCGAA CCCTCGAATG TCGGAACCAC AATCCGATGT	240
	GTTAACCACT TCACCACAGC CGCCATGGCA GGGGCAGTAG GAATCGAACC CACACCAAAG	300
40	GTTTTGGAGA CCTCTATTCT ACCnTTGAAC TATGCCCCTA TTAAATGAT AAATGGAGGG	360
	GGGCAGATTC GAACTGCCGA ACCCGAGGGG CGGATTTTAC	400

45

(2) INFORMATION FOR SEQ ID NO: 3723:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3723:

55

GGTTCAAGTC CTCTGGCCCG CACCATTThT GGAGGGGTAG CGAATGGCTA AACGCGGCGG 120
 ACTGTAAATC CGCTCCTTCG GGTTCGGCAG TTCGAATCTG CCCCCCTCCA TTTATTATTT 180
 5 TTAATAGGGG CATAGTTCAA CGGTAGAATA GAGGTCTCCA AAACCTTTGG TGTGGGTTTCG 240
 ATTCCTACTG CCCCTGCCAT GCGGGCTGTG GTGAAGTGGT TAACACATCG GATTGTGGTT 300
 10 CCGACATTCG AGGGTTCGAT CCCCTTCAGC CGCCTTATTA TTAATGGGCT ATAGCCAAGC 360
 GGTAAGGCAA CGGACTTTGA CTCCGTCCT CGTTGGTTTCG 400

(2) INFORMATION FOR SEQ ID NO: 3724:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3724:

CACTTTAGCA AATGGTGACA AAGTCCGTAT TGCTACAATT TTTGACTTAA TGGCAAGTCA 60
 25 ATATGGCGTG CGTCGTTTTG ATCATAAATT AGAATCAAAA GGATACGACG ATGCAGAATC 120
 AAAATATACA CCTGCTTGGC AAGAAGCCAT TTCAGGCGTA AAACAAAGTG TThGTCATTC 180
 30 AAGTAGCGAA AGAATTTGCG CAAAACGCTA TCGATACTGA AGGGCGTTCA ATGATTATCA 240
 TGGGTGCGGG TATTAACCAT TGGTTTAACT CAGATACGAT TTATCGTTCC AATCTTAAAC 300
 TTAGTTATGT TATGTGGCTG TCAGGTGTGA ATGGTGGCGG TTGGGGCTCA CTATGTGGGG 360
 35 ACAAGAAAAA TGTCGTCCGA TTGAAGGATG GAGTACTGTC 400

(2) INFORMATION FOR SEQ ID NO: 3725:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3725:

CGCTATCTGA ATCTGAATCG CTATCTGAAT CTGAGTCGTT GTCTGAGTCC GAATCGCTAT 60
 50 CTGAATCTGA GTCGCTATCT GAGTCTGAGT CGCTATCTGA ATCTGAGTCG CTGTCTGAAT 120
 CTGAATCACT GTCTGAGTCT GAGTCGCTGT CTGAGTCTGA ATCGCTGTCA GAATCTGAGT 180
 CGCTATCTGA GTCTGAATCT GAATCACTGT CTGAGTCCGA ATCGCTATCT GAATCTGAAT 240

55

CCGAGTCTGA ATCGCTGTCT GAGTCTGAGT CGCTGTCTGA ATCTGAATCG CTATCTGAGT 360
 CTGAGTCGCT GTckGAATgC GCTGTCTGAA TCTGAGTCGC TATGCTGAAT GCTGAGTnCG 420
 5 CTATGTGAGT CTGAATGCGC TGTGCAGAAT CTGAGTGC GC TCATCTGATG TTTCTT 476

(2) INFORMATION FOR SEQ ID NO: 3726:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3726:

ATACGACCAC TGTTTAATGC GTCCATTAAA TCTGGCCAAT TATTGAATTT AACTAATTCT 60
 20 AGTTTATATT TCGGATGATT GTATTGTGAT AATAATTTTT TAGTCATCAT CAAATTAGCT 120
 GAATGTGTAA TCGGCAAATA TCCAATTTTA ATCACTTGCT GATTTTGGGC ATTTT TAGAC 180
 CGTTCTTTAG ACGTCCTTTG CCAATCACAT CCTGTAATTA TAAAGATTCC AATGATGACG 240
 25 ATTATGCTTA ACCTTTTCAT CGTCACTCAC TCCTTATAAA TAATATTCAG GTTCAACTTG 300
 ATGATGATTC AATGCAAnGT TTCCATAATT TCATTACGAA TCTTAAGTAG GTGGCTATCA 360
 TTACGGACTG CGTGGATGTG AnGCTGTAAA TTCCATAnTG 400
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(2) INFORMATION FOR SEQ ID NO: 3727:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3727:

ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCTGAAC CCAGCTCGCG TACCGCTTTA 60
 ATGGGCGAAC AGCAAACCCT TGGGACCGAC TACAGCCCCA GGATGCGATG AGCCGACATC 120
 45 GAGGTGCCAA ACCTCCCCGT CGATGTGAAC TCTTGGGGGA GATAAGCCTG TTATCCCCGG 180
 GGTAGCTTTT ATCCGTTGAG CGATGGCCCT TCCATGCGGA ACCACCGGAT CACTAAGTCC 240
 GTCTTTCGAC CCTGCTCGAC TTGTAGGTCT CGCAGTCAAG CTCCCTTATG CCTTTACACT 300
 50 CTATGAATGA TTTCCAACCA TTCTGAGGGA ACTTTGAGCG CCTCCGTTnC CTTT TAGGAG 360
 GCGAACGGCC CCAGTTCAAA CTGCCCGCCT GAACACTGTC 400

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3728:

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10  TTGAAAAGTC ATATCAAAGC GCACATGTTT TTAAGCGTCG TCGAACACCT ATCGTGAAAG      60
    GTGTGTCATT TGAGTGTCCA ATCGGTGCCA CGATTGCGAT TATCGGAGAA AGTGGTAGCG      120
15  GTAAATCGAC GTTGAGTCTA TTGATATTAG GTATTGAGAA ACCGGATAAA GGTGTGTGTA      180
    CCTTAAATGA TCAACCGATG CATAAGAAGA AAGTGAGACG TCATCAAATT GGTGCTGTAT      240
    TTCAAGATTA TACGTCATCA TTACATCCAT TTCAGACTGT TAGAGAAATC TTATTGAAG      300
20  TGATGTGTCA ATGTGATGGA CAACCTAAAG AAGTTATGGA AGTCCAAGCA ATTACATTGT      360
    TGAAGAAGT CCGTCTATCT AAGGCATACA TGGGATAAAT      400
  
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(2) INFORMATION FOR SEQ ID NO: 3729:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3729:

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35  ATCGAACCCC CGACCTCACG GGTATGAACC GTACGCTCTA GCCAGCTGAG CTACACCGCC      60
    TTATATAGTT TGTAATAAAT ATGGTGGAGA CTAGCGGGAT CGAACCGCTG ACCTCCTGCG      120
    TGCAAAAGC CGCTCTCCCA GCTGAGCTAA GCCCCATAA TAATTACAGT ATATCGGGAA      180
40  GACAGGTTTC AACCTGCGAC CCCTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC      240
    TTCCCGTATA ATTAACGCGC CCGATAGGAG TCGAACCCAT AACCTCTGA TCCGTAGTCA      300
    AACGCTCTAT CCAATTGAGC TACGGGCGCA TATGTTTTTA TTGAAAATGG TGCCGAGGAC      360
45  CGGAATCGAA CCGTAGTGA ATCACTCACC GCAGATTTTA      400
  
```

(2) INFORMATION FOR SEQ ID NO: 3730:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3730:

5 ATCTCTGGAT CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT 60
 CATCGGCTTC TAGTGCCAAG GCATCCACCG TCGGCCCTTA ATAACTTAAT CTATGTTTCC 120
 ACCATTTTAA TAAGTCAAAC GTTAACATGA AGTTACGTTT TTTTATAAAA AGATTTAAAC 180
 10 GCGTTATTAA TCTTGTGAGT GTTCTTTTGA AACTAGCGA TTATTTCTTA TGAATTCAAG 240
 CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT TTAATTACTT 300
 ATCTAGTTT CAATGTACAA ATAATGGTGG AGACTAGCGG GATCGAACCG CTGACCTCCT 360
 15 GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC 400

(2) INFORMATION FOR SEQ ID NO: 3731:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 401 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3731:

TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG 60
 30 TGGAGAATGA CGGGTTCGAA CCGCCGACCC TCTGCTTGTA AGGCAGATGC TCTCCAGCT 120
 GAGCTAATTC TCCGATTTAA AACTGCCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTC 180
 GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCTG CATGGGAACA GGTGTGACCT 240
 35 CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA TTCAAAACTA GATAGTAAGT 300
 AAAAGTGATT TTGCTTCGCA AAACATTAT TTTGATTAA GTCTTCGATC GATTAGTATT 360
 CGTCAGCTCC ACATGTCACC ATGCTTCCAC CTCGAACCTA T 401

40

(2) INFORMATION FOR SEQ ID NO: 3732:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 397 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3732:

50 CATTATTAAC GGCTATGGTT TAACTGAAGC ACCTCTTGTA CTTGTTAATA CACCGGAAAA 60
 TTCAAAACGT AAGCCAATGA GTATTGGTAA AGCAGTCATG TTCGTTGATG CACGTATCCT 120

55

AAATGTCACG CCAGGATATT GGAATAAACC AGCAGAGACT GCCAAAGCAT TTCATGGTCG 240
 ATATTTATTA ACTGGTGA CT TAGCGAGATG GACAACGATG GCGATATATT TATTATTGAC 300
 5 CGCAAAaAG AaTTAATCAT AACTGGTGGc GAAAATGTCT TACCATCCGa gTCGAAAtGC 360
 TTaCtGaGCA TCCACTAGTA GACCGGTGTG TGGTCGT 397

(2) INFORMATION FOR SEQ ID NO: 3733:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3733:

20 AAGTAACAAT CGTTCACCGT CGTGATGAGT TACGTGCACA GCGTATTTTA CAAGATAGAG 60
 CATTCAAAAA TGATAAAATC GACTTTATTT GGAGTCATAC TTTGAAATCA ATTAATGAAA 120
 AAGACGGCAA AGTGGGTTCT GTGACATTAA CGTCTACAAA AGATGGTTCA GAAGAAACAC 180
 25 ACGAGGCTGA TGGTGTATTC ATCTATATTG GTATGAAACC ATTAACAGCG CCATTTAAAG 240
 ACTTAGGTAT TACAAATGAT GTTGTTATA TTGTAACAAA AGATGATATG ACAACATCAG 300
 TACCAGGTAT TTTTGCAGCA GGnGATGTTT GCGACAAAGG TTACGCCAAA TTGTCACTGC 360
 30 CACGGCGATG GTAGTATGCC AGCGCAAGTG CCACGGAATG 400

(2) INFORMATION FOR SEQ ID NO: 3734:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3734:

GCCGTTTACT GTGGCTTCGA TTCGTAGCTT CGCAGAAGCT AACCACTCCT CTTAACCTTC 60
 45 CAGCACCGGG CAGGCGTCAG CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT 120
 TTGATAAACA GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGCGTTAA CCCTAAAGAG 180
 CACCCCTTCT CCCGAAGTTA CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG 240
 50 CTCACCTTAG AATTCTCATC TTGACTACCT GTGTCGGTTT GCGGTACGGG CACCTATTTT 300
 CTATCTAGAG GCTTTTCTCG GCAGTGTGAA ATCAACGAaT CGAAGACACA ATGTCTTCTC 360

TAGACGTGCA ATCCAATCGG CAACGCTTCG CCTAATCCTA ACTGGCGGTC CCCCCCnAT 480

(2) INFORMATION FOR SEQ ID NO: 3735:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3735:

CGATCCCTTC AGCCGGACTT GGGTATTCTT CCAAATTAT ATGGACCTTG CAGACTCGAA 60
 CCTGCGACCG AACGGTTATG AGCCGTTAGC TCTAACCAAC TGAGCTAAAG GTCCTAAATA 120
 TAATTTTACA ACTAATAAAT AGTGGCGGTG GAGGGGATCG AACCCCGAC CTCACGGGTA 180
 TGAACCGTAC GCTCTAGCCA GCTGAGCTAC ACCGCCTTAT ATAGTTTGTA AATAATATGG 240
 TGGAGACTAG CGGGATCGAA CCGCTGGACC TCCTGCGTGC AAACAGnCGC TCTCCAGCT 300
 GAGCTnAAGC CCCATAATA ATTACAGTAT ATCGGAAGA CAGGATTCGA ACCTGCGACC 360
 CCTTGGTCCC CAAACCAAGT GGTTTnACCA AGTTGAGCTA 400

(2) INFORMATION FOR SEQ ID NO: 3736:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3736:

TGAGCCCGAC GAGCTACCGA ACTGCTCCAT CCCGCGATAA TAAAAAATAA TGGCGGAGGA 60
 AGAGGGATTG GAACCCCGC GGCCCGTTAA GGCCCTGTCG GTTTTCAAGA CCGATCCCTT 120
 CAGCCGGACT TGGGTATTCC TCCATTATTA TAGGTAAATC GCTATTAAAT ATAAAAATTAA 180
 ATGGCGGTCT CGACGGGAAT CGAACCCGCG ATCTCCTGCG TGACAGGCAG GCGTGTTAAC 240
 CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTCGAACCC CCGCGAGCCG 300
 TTAAGCCCCT GTCGGTTTTT AAGACCGATT CCTTCAGCCG GACTTGGGTA nTCnTCCAAA 360
 ATTATATGGA CTTGTCAGGA CTCGAACTGC GAnCGAACGG 400

(2) INFORMATION FOR SEQ ID NO: 3737:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3737:

	TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC	60
10	AAGTGCTCTA CCAAGCTGAG CTACTTCCCG TATAATTAAC GCGCCCGATA GGAGTCGAAC	120
	CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTT	180
	TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGGTA CGTGATCACT CACCGCAGGA	240
15	TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT GGAGCAGAAG	300
	ACGGGATTCTG AACCCGCGAC CCAACCTTG GCAAGTTGT ATTCTACCGC TGAACACTT	360
20	CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA	400

(2) INFORMATION FOR SEQ ID NO: 3738:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3738:

	AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG CAGATGCTCT CCCAGCTGAG	60
	CTAATTCTCC GATTTAAAC TGCCTGGCAA CGTTCTACTC TAGCGGAAGT AATCGGAnCT	120
35	ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG TGACCTCCTT	180
	GCTATAGTCA CCAGACATAT GAATGTAATT TATACATTCA AACTAGATA GTAAGTAAAA	240
	GTGATTTTGC TTCGCAAACA TTTATTTTGA TTAAGTCTTC GATCGATTAG TATTCGTCAG	300
40	CTCCACATGT CACCATGCTT CCACCTCGAA CCTATTAACC TCATCATCTT TGAGGGATCT	360
	TATAACCGAA GTTGGGAAAT CTCATCTTGG AGGGGGGCTT	400

45

(2) INFORMATION FOR SEQ ID NO: 3739:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3739:

55

CACCACCCGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAAA CCGACATCTT 120
 TAATTAATTG CThTGCACGT TTTCTATCAA ATTTATCATT ACGTGCAAGT GATGGGAATA 180
 5 TCATGTTATC TTCAATCGTT TCACCAAACA AGTCACTTTG CTGCATCAAA TAACTGATTC 240
 GTTGACGCAA TTCTTCCGGG TCATAATCAT TATAGGGTTT ACCTTTAAAA TAAAGTTCTC 300
 CACTAGTTGG ACTAAACAAA TTACATAThT GCTTTTGAAA TGTACTTTTA CCACTACCTG 360
 10 ATGGACCTAT AATGGCAATA CTCTCGCCTT TATCTACTTT 400

(2) INFORMATION FOR SEQ ID NO: 3740:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 413 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3740:

ATCGCTTGCT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAGCTCT ACTAAACTCG 60
 25 TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTCGCCAAG CCATTTTCT 120
 TTGTGTTTAC TTTTATTTT GACGTTTtag ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180
 TGCGGCTCAT CGCATCCaTT TTTTGCCTGG CAACGTTCTA CTCTAGCGGA AnTAATTGGC 240
 30 TACCATCGAC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTTCT 300
 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACGTTTG CGCTCTTTTC TCGTTTCGTC 360
 AGATtCAAAC GTTTTCACTT CGCCAAGCCA tTTTTctTTG TGTTTGCTTT TnA 413
 35

(2) INFORMATION FOR SEQ ID NO: 3741:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3741:

CTTAGATGCT TTCAGCACTT ATCCCGTCCA CACATAGCTA CCCAGCTATG CCGTTGGCAC 60
 GACAACTGGT ACACCAGAGG TATGTCCATC CCGGTCTCTT CGTACTAAGG ACAGCTCCTC 120
 50 TCAAATTTCC TACGCCCACG ACGGATAGGG ACCGAACTGT CTCACGACGT TCTGAACCCA 180
 GCTCGCGTAC CGCTTTAATG GGCGAACAGC CCAACCCTTG GGACCGACTA CAGCCCCAGG 240

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TAAGCTGTTA TCCCCGGGGT AGCTTTTATC CGTTGAGCGA TGGCCCTTCC ATGCGGAACC 360
 ACCGGATCA_n TAAGTCCGTC TnTCGACCCT GntGGACTTG 400

5 (2) INFORMATION FOR SEQ ID NO: 3742:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3742:

GTTTTGAATG TATAAATTAC ATTTCATATGT CTGGTGACTA TAGCAAGGAG GTCACACCTG 60
 TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTT 120
 20 CGCTAGAGTA GAACGTTGCC AGGCAGTTTT AAATCGGAGA ATTAGCTCAG CTGGGGAGAG
 CATCTGCCTT ACAAGCAGAG GGTCCGCGGT TCGAACCCGT CATTCTCCAC CATTATTCTT 240
 TACATATTGC CGGCCTAGCT CAATTGGTAG AGCAACTGGA CTTGTAATCA GTAGGTTGGG 300
 25 GGTTC AAGTC CTCTGGCCGG CACCATGGGA AGAGCCATTA GCTCAGTTGG TAGAGCATCT 360
 GACTTTTAAA TCAGAGGGTT CAGAGGTTnC GAATCCGCTA 400

(2) INFORMATION FOR SEQ ID NO: 3743:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3743:

40 TCGCAATAAC CGCATCAAAT GTATTGCCTA AAAAGGCTGG ATTTTCCAAT GTGTCATCAT 60
 TACGGATCTC GAAGTTCTCA TAACGCACAT CATGTAATAA CATATTCATG CGTGCTAAGT 120
 TGTATGTAGT ATTGTTACGT TCTTGTCGGA AATAACGATA CACTTGCCTT TCTTTACCAA 180
 45 CACGTAACAA CAATGAACCG GAACCACATG TTGGGTCGTA CACGTGACGT AATTTATCTT 240
 TACCGTCTGT GACAATCTTC GCCAGTATCT TAGATACTTG TTGTGGTGTA TAGAACTCGC 300
 CTGCTTTTTT ACCCGCTGTC GCCGCAAAGC GCCCGATTAG GAATTCATAT GCATCACCTA 360
 50 ACATATCAAT TTCCATGGTC ACTGTGAACG AATGGGTAAG 400

(2) INFORMATION FOR SEQ ID NO: 3744:

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(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3744:

10	CTACTGATTA CAAGTCAGTT GCTCTACCAA TTGAGCTAGG CCGGCAATAT GTAAGAATAA	60
	ATGGTGGAGA ATGACGGGTT CGAACCGCCG ACCCTCTGCT TGTAAGGCAG ATGCTCTCCC	120
	AGCTGAGCTA ATTCTCCGAT TTA AAAACTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA	180
15	GTTCGACTAC CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG	240
	ACCTCCTTGC TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT	300
	AAGTAAAGT GATTTGCTTC GCAAAACATT ATTTGATTAA GTCCTCGATC GATAGTATCG	360
20	TCAGCTCCAC ATGTCACCAT GCTTCCanCT CGnACCTATT	400

(2) INFORMATION FOR SEQ ID NO: 3745:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3745:

	CATAAGTAAA CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT	60
35	AAAAAGATTT AAACGCGTTA TTAATCTTGT GAGTGTTCCT TCGAACACTA GCGATTATTT	120
	CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACCTCG GTTTTGCTTG GTAAAATCTA	180
	TATTTTACTT ACTTATCTAG TTTTCAATGT ACAATTTCTT TTTAGTCAAG CGCTCGCATA	240
40	CTGCTTTATT nTCAAAAAAT CAAATGCTCA TTTACAAAAG TAAACTCCGC TTTAATTTTC	300
	TTAATGCATT GTCTAACAAC CGCTTGCTTT AAAAAGAATA GATTGnCAAG CGCTCGCATA	360
	AGCAATATCA CTThAACCAA AAAATA	386

45

(2) INFORMATION FOR SEQ ID NO: 3746:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 677 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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AAGGTGAAAA GCACCCCGGA AGGATGTTGA AATAGAACCT GAAACCGTGT GCTTACAAGT 60
 AGTCAGAGCC CGTTAATGGG TGATGGCGTG CCTTTTGTAG AATGAACCGG CGAGTTACGA 120
 5 TTTGATGCAA GGTTAAGCAG TAAATGTGGA GCCGTAGCAk AACanGGTCT GAATAGGGCG 180
 TTTAGTATTT GGTCGTACCG AnaACCAGGT GATCTACCCT TGGTCAGGTT GAAGTTCAGG 240
 10 TAACACTGAA TGGAGGACCG AACCGACTTA CGTTGAAAAG TGAGCGGATG AACTGAGGGT 300
 AGCGGAGAAA TTCCAATCGA ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGc 360
 TAGCCTCAAG TGATGATTAT TGGAGGTAGA GCACTGTTTG GaCGAgGGGC CCCTCTCGGG 420
 15 tTACCAATTc AGACAAACTC CGAATGCCAA TTAATTTAAC TTGGGgAGTC aGAACATGGG 480
 TGATAAGGTC CGTGTTTCGAA AGGGAAACAG CCCAGACCAC CAGCTAAGGT CCCAAAATAT 540
 ATGTTAAGTG GAAAAGGATG TGGCGTTGCC AGACAACTGA GGATGTTGGC TTAGAAGCAG 600
 20 CCATCATTTT AAAGAGTGCg TAATAGCTCA CTAGTCGAAG TGACACTGCG CCGAAAATGT 660
 GACCGGGCnT AAACnAT 677

(2) INFORMATION FOR SEQ ID NO: 3747:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3747:

35 GTCCAATGAT TCATATGCTT TATTATCAGG GTATTGCCTT TGAATCGCAT GCACAAAATA 60
 TGATGCTCAT TCATGAAAAT GGTGGCCTA CACGTATTGC CTTAAAAGAT TTCCATGATG 120
 40 GTGTTTCGTTT TAAGCGTGAc ATTTAAGTGA AGCTGCTTCA CACCTGACAT TAAAGCCAAT 180
 GCCAGAAGCA CATAAAAAAG TGAATAGTAA TTCATTTATT GAAACAGATG ACGAACGTTT 240
 AGTACGCGAC TTTTACATG ATGCATTTTT CTTTATTAAT ATCGCCGAAA TCATCTTATT 300
 45 TATTGAAAAG CAATATGGTA TCGATGAGGA GCTGCAATGG cAATGGGkTa AAGGCATCAT 360
 CGAGGCGTAT CCAGrAGcAT TTCCaGAGTT kGAATaACTA TCCAACCATT CGGTTTTT 417

(2) INFORMATION FOR SEQ ID NO: 3748:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3748:

5 ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTA AAAACTGC CTGGCAACGT TCTACTCTAG 60
 CGGAACGTAA GTTCGACTAC CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG 120
 AACAGGTGTG ACCTCCTTGC TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA 180
 10 ACTAGATAGT AAGTAAAAGT GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGTCTTCG 240
 ATCGATTAGT ATTGCTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT 300
 CATCATCTTT GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGCTTCA 360
 15 TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC 400

(2) INFORMATION FOR SEQ ID NO: 3749:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3749:

25 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 60
 30 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TGTTTACTTT TTATTTTGAC 120
 GTTTTAGGCA TAAAAAAAAG AGACCTTGCG GTCTCAATGC GGCTCATCGC ATCCATTTTT 180
 TGCCTGGCAA CGTTCTACTC TAGCGGAAGT AAGTTGGGCT ACCATCGTCG CTAAAGACCT 240
 35 TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTA CTCA TTT 300
 AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 360
 GCCAAGCCAT TTTTCTTTG TGTnTACTTT TTAATTTTGA 400

(2) INFORMATION FOR SEQ ID NO: 3750:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3750:

50 ATAAAAAAA GAGACCTTGC GGTCTCAAAT GCGGCTCATC GCATCCATTT TTGCCTGGC 60
 AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC CTTTCTTGAC 120

55

TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC 240
 ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAA GAGACCTTGC 300
 5 GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGGC AACGTTCTAC TCTAGCGGAA 360
 nTAAnTTGGG CTACCATCGA CGCTAAGAAC CTTTCTTGGA 400

(2) INFORMATION FOR SEQ ID NO: 3751:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3751:

20 CACTCACCGC AGATnTTTAA GTCCTGTGCG TCTGCCAGTT CCGCCACCCC GGCACTATAA 60
 AAATGGAGCA GAAGACGGGA TTCGAACCCG CGACCCCAAC CTTGGCAAGG TTGTATTCTA 120
 CCGCTGAAC TCTTCTGCAT ATGCGGGTGA AGGGAGTCGA ACCCCCACGC CGTAAGCTnA 180
 25 GnATTCTTAA GTCTAGTGCG TCTGCCAATT CCGCCACACC CGCAAATGGT GAGCCATAGA 240
 GGATTCTGAAC CTCTGGACCC TCTGATTAAA AGTCAGATGC TCTACCAACT GGAGCTAATG 300
 GCTCTTTCCA TGGTGCCCGG CCAGAGGACT TGGAAACCCC AACCTACTGA TTACAAGTCA 360
 30 GTTGCTCTAA CCAATTGAGC TAAGCCGGGC AATATGTTAn 400

(2) INFORMATION FOR SEQ ID NO: 3752:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3752:

45 TTAnAnAnCC GCGACATTAT AGAGCCAATC ACTAGCCTAT CTCAGAATCA CCAACGAATC 60
 CTTCAATTATT AAGGAATCTA GGCATCTTTA CGGCGTGGTT CTAATCGCAT CTTTTTCAAT 120
 CTAAGTGCGT TTGTGACAAC ACTTACTGAA CTTAGTGCCA TTGCAGCACC AGCAACCCAT 180
 50 GGCGCAAGTA AGCCCAATGC AGCTATAGGG ATACCGGCAA TATTATAGCC GAATGCCCAA 240
 AATAGATTTT GACGAATATT ACGAATGGTT GcTTTACTTG cATAAATGGC TTTAGGaATA 300
 AGCATCAAGT cGCCACCAAG AATAGTAATA TCAGCTGCTT CAATGGGCAA CTTCTGTTAC 360
 55

(2) INFORMATION FOR SEQ ID NO: 3753:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3753:

CCTTGCGGTC	TCAATGGCGG	CTCATCGCAT	CCATTTTTTG	CCTGGCAACG	TTCTACTCTA	60
GCGGAACGTA	AGTTGGCTAC	CATCGTCGCT	AAAGACCTTT	CTTGACTTGT	GACAATCGCT	120
TGCTTCTTTC	CTCTCCTTCG	GCTCTCGCTT	ACTCATTTAG	CTCTACTAAA	CTCGTTGCGC	180
TCTTTTCTCG	TTTCGTCAGA	TTCAAACGTT	TTCACTTCGC	CAAGCCATTT	TTCTTTGTGT	240
TTACTTTTTTA	TTTTGACGTT	TTAGACATAA	AAAAAAGAGA	CCTTGCGGTC	TCAATGCGGC	300
TCATCGCATC	CATTTTTTGC	CTGGCAACGT	TCTACTCTAG	CGGAACGTAA	GTGGCTACCA	360
TCGACGCTAA	GAACCTTTCT	TGACTGGTGA	CAAnCGCTTG			400

(2) INFORMATION FOR SEQ ID NO: 3754:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 381 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3754:

CTGAGCTAAG	CCCCCAAATA	GGTATTAAAT	TAATGGTGGG	CCTAAGTGA	CTCGnACCAC	60
CGACCTCAG	CTTATCAGGC	GTGCGCTCTA	ACCAGCTGAG	CTATAGGCC	ATTAATTTGA	120
ATGAnCAAAC	ATTCAAAACT	GAATACAATA	TGTCACGTTA	TTCCGCATCT	TCTGAAGAAG	180
ATGTTCCGAA	TATATCCTTA	GAAAGGAnGT	GATCCAGCCG	CACCTTCCGA	TACGGCTACC	240
TTGTTACGAC	TTCACCCCAA	TCATTTGTCC	CACCTTCGAC	GGCTAGCTCC	TAAAAGGTTA	300
CTCCACCGGC	TTCGGGTGTT	ACAAACTCTC	GTGGTGTGAC	GGGCGGTGTG	TACAAAACCC	360
GGGAACGTAT	TCACCGTAGC	A				381

(2) INFORMATION FOR SEQ ID NO: 3755:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3755:

5 AGCTCCCCAA AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCAAGGCAT 60
 CCCCCTGCGC CCTTAATAAC TTAATCTATG TTTCCACCAT TTTTATAAGT CAAACGTTAA 120
 CATGAAGTTA CGTTCTTTTA TAAAAAGATT TAAACGCGTT ATTAATCTTG TGAGTGTCT 180
 10 TTCGAACATA GCGGATTATT TCCTATGAAT TCAAGCTTAT TTAAACTCT TTATTCACCTC 240
 GGTTTTGCTT GGTA AAAACn ATATTTTACT TACTTATCTA GTTTTCAATG TACAATTTCT 300
 TTTTAGTCAA GCGCTCGCAT ACTGCTTTAT TTTCCATAAG CAATAnCACT TTAACCAAAA 360
 15 AATATTTGGA ATGTTnAAAT AAACATnCAA AACTGAATAC 400

(2) INFORMATION FOR SEQ ID NO: 3756:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3756:

CTACTCACAC CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA 60
 30 CGCCCTTAGA ACGCTCTCCT ACCATTGTCC AAAGGCATGC GCACAGCTTC GGTAATATGT 120
 TTAGCCCCGG TACATTTTCG GCGCATGTCA CTCGACTAGT GAGCTATTAC GCACTCTTTA 180
 AATGGATGGC TGCTTCTAAG CCAACATCCT AGTTGTCTGG GCAACGCCAC ATCCTTTTCC 240
 35 ACTTAACATA TATTTTGGGA CCTTAGCTGG TGGTCTGGGC TGTTTCCGGn GGGGnACACG 300
 GACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTCCG ATTTGTCTGA 360
 40 ATCGGTAACC CGAGAGGGCC CnTCGTCCAA ACAGTGCTCT 400

(2) INFORMATION FOR SEQ ID NO: 3757:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3757:

GGCAGATGCT CTCCCAGCTG AGCTAATTCT CCGATTAAAA ACTGCCTGGC AACGTTCTAC 60
 55

ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT 180
 TCAAAACTAG ATAGTAAGTA AAAGTGATTG TGCTTCGCAA AACATTTATT TTGATTAAGT 240
 5 CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT GCTTCCACCT CGAACCTATT 300
 AACCTCATCA TCTTTGAGGG aTCTTATAAC CGAARtTtGG GAAtCTCATC TTGAGGGGGG 360
 gCTCATGCTt AGATGCTTcA GCACTTATCC CGTCCACACA TAGCTAnCCA GCTATGCCGT 420
 10 TnGCACGACA ACTGGTACAC CAGAnGTATG TCCATCCC 458

(2) INFORMATION FOR SEQ ID NO: 3758:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3758:

AGCGCTCGCA TACTGCTTTA TTTTCAAAAA ATCAATGCT CATTTACAAA AGTAAACTCC 60
 25 GCTTTAATTT TTCTTAATGC ATTGTCTAAC AACCGCTTTC TTTAAAAAGA ATAGATTGTC 120
 AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAATAT TTGAATGTTA AATAAACATT 180
 30 CAAAACTGAA TACAATATGT CACGTTATTC CGCATCTTCT GAAGAAGATG TTCCGAATAT 240
 ATCCTTAGAA AGGAGGTGAT CCAGCCGCAC CTTCCGATAC GGCTACCTTG TTACGACTTC 300
 ACCCCAATCA TTTGTCCCAC CTTGACGGC TAGCTCCTAA AAGGTTACTC CACCGGCTTC 360
 35 GGGTGTTACA AACTCTCGTG GTGTGACGGG CGGTGTGTAC 400

(2) INFORMATION FOR SEQ ID NO: 3759:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3759:

GACTTGGGTA TTCCTCCAAA ATTATATGGA CCTTGACAGG CTCGAACCTG CGACCGAACG 60
 50 GTTATGAGCC GTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT TTTACAACTA 120
 ATAAATAGTG GCGGTGGAGG GGATCGAACC CCCGACCTCA CGGGTATGAA CCGTACGCTC 180
 TAGCCAGCTG AGCTACACCG CCTTATATAG TTTGTAAATA ATATGGTGA GACTAGCGGG 240

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TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTG CGACCCCTTG GTCCCAAACC 360
 AAGTGCTCTA CCAAGCTGAA GCTACTTTCC CGTATAATTA 400

5 (2) INFORMATION FOR SEQ ID NO: 3760:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3760:

CACTTAATGC CCGTACCACA CATAGCTACC CAGCTATGCC GTTGGCACGA CAACTGGTAC 60
 ACCAGAGGTA TGTCCATCCC GGTCTCTCG TACTAAGGAC AGCTCCTCTC AAATTTCTTA 120
 20 CGCCACGAC GGATAGGGAC CGAACTGTCT CACGACGTTT TGAACCCAGC TCGCGTACCG 180
 CTTTAATGGG CGAACAGCAA nCCCTTGGGA CCGACTACAG CCCAGGATG CGATGAGCCG 240
 ACATCGAGGT GCCAAACCTC CCCGTCGATG TGAACCTCTG GGGGAGATAA GCCTGTTATC 300
 25 CCCGGGGTAG CTTTTATnCG TTGAGCGATG GnCCTTnCAT GCGGAACACC GGATCACTAA 360
 GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCAGT 400

30 (2) INFORMATION FOR SEQ ID NO: 3761:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 623 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3761:

40 TATGTATTTT ATAATGTACA GCTCGTTGAn TcTATTTTTT CTTATATTA AGTGCCATTA 60
 ATACAAAACC TAGCTCTCGT TTAACCTTAT TTATTCCTCG AACTGACATT CGAGTGAACC 120
 CAAAATAGCC TTCATAAATC CAAAAACAGG CTCTACATCA ATTTTTCTTT GACTATAGAT 180
 45 TTTTTTCGTT TCTGGTTCAG AAAGCTTTTG ATTAATTTGG ACTTTAAAGT ATTCCCAATT 240
 ATAATTCCTC ATGATTTTCT TATTGGATTT CGAATTTGGT TTCATGCATT GATGTCTCAA 300
 AGAACATGAT GAACAGTCAT CACATTCATA TAGTTTGAAG TCTCGTTTAA AACCATATCT 360
 50 ATCATTACGG TATGCATATC TTTTAAAACC TATTCCTTTG TTATTAGGAC ATATAAATTC 420
 ATCATTAAGT TCGTCATATT TCCAATTTTA AGTGTTGAAA ATGTCACCTT TAACTTTCT 480

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AATAGCCATA TAGTTTTGCT CACTACCATA ACCGGCATCA GCTACAAATA TACTCCGGTA 600
 AATAACCGAG GGATTGTTGG AAT 623

(2) INFORMATION FOR SEQ ID NO: 3762:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 718 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3762:

ATTTTAAAAA TAGTTCCTTA AATTATATAC CCACCACATT TGGTGGAGAA CCTAAAAAAA 60
 AGCACTTCCC AAAAATGGAA AGTGCAAGTA GTGAGCCATA GAGGATTCGA ACCTCTGACC 120
 CTCTGATTAA AAGTCAGATG CTCTACCAAC TGAGCTAATG GCTCTAATGG CTGGGCCTAG 180
 CTGGATTCGA ACCAACGAGT GACGGAGTCA AAGTCCGTTG CCTTACCGCT TGGCTATAGC 240
 CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG GAGCGGATTT 300
 ACAGTCCGCC GCGTTTAGCC ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT 360
 CaAAATGGTG GaGAATGACG GGTTCGAACC GCCGACCCCTC TGCTTGTAAG GCAGATGCTC 420
 TCCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG 480
 CCGTGAAAGG GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT 540
 CGAACCTTAC GACCGATCGG TTTAACAGCC GATAGCTCTT ACCACTGGAG CTACTGTGGG 600
 ATTAATATTA TGCCTGGGCA ACGTTCTTAC TCTTAGCGGA ACGTTAAGTT CCGACTTACC 660
 ATCCGACGCT AAGGAGCTTT AACTTTCTnG TGGTTCCGGC ATGGGGGGAA CAGGTGGT 718

(2) INFORMATION FOR SEQ ID NO: 3763:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3763:

TnCACTCACC GCAGATTTTT AAGTCCTGTG CGTCTGCCAG TTCCGCCACC CCGGCACTAT 60
 AAAAATGGAG CAGAAGACGG GATTCGAACC CGCGACCCCA ACCTTGGCAA GGTTGTATTC 120
 TACCGCTGAA CTACTTCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCT 180

AGGATTCGAA CCTCTGGACC CTCTGATTAA AAGTCAGATG CTCTACCAAC TGGAGCTAAT 300
 GGCTCTTCCA TGGTGCCGGC CAGAGGACTT GGAACCCCCA ACCTACTGGA TTTACAAGTT 360
 5 CAATTGCTCT A_nCAATTTGA GCTAAGGCCG GGCAATATGT 400

(2) INFORMATION FOR SEQ ID NO: 3764:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 610 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3764:

TTAAAGTATT CCAATTATA ATTCTTCATG ATTTTCTTAT TGGATTTGGA ATTTGGTTTC 60
 20 ATGCATTGAT GTCTCAAAGA ACATGATGAA CAGTCATCAC ATTCATATAG TTTGAAGTCT 120
 CGTTTAAAAC CATATCTATC ATTACGGTAT GCATATCTTT TAAAACCTAT TCTTTTGTTA 180
 TTAGGACATA TAAATTCATT ATTAAGTTCG TCATATTTCC AATTTTGAGT GTTGAAAATG 240
 25 CCACTTTTAA ACTTTCTAGT TTTATCTTTA ATAAACATGC CATACGTAAT AAGTGGCGTT 300
 TTATTAAAAT CATCTATAAT AGCCATATAG TTTTGCTCAC TACCATAACC TGCATCAGCT 360
 ACAATATACT CTGGTAAATA ACCGAaGGaT TTTGAATCAT TGTTAAAAAT GGGATTAATG 420
 30 TTCTAGTATC TGTTGGGTTT TGAAATAGGT CATAGGATAA AACAAATTGr GAATTTGTCTG 480
 CTATTTGgTA AATTGGTATC CTGGCTTAAG TTGGGCCATT TTTCCATATG GGCCTTCCTT 540
 35 CCATTCTCCA TAAAAGTTGG CATCATGGAT CCAGATCCnG TTTTAGGAAA ACCTAATTCC 600
 AACCTTTAAG 610

(2) INFORMATION FOR SEQ ID NO: 3765:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3765:

CTTCTTGGTG CTGCATATCC CCTACAATAA TTAAACCTTT TTTCTTATTT AAAATGTGTC 60
 50 TTAATGCCGA TGCATCTATA CTTTTTTGAT AGTGCGGTAA AATCTTCATC TCAGAnGTIA 120
 ACAATTCTGT TGCATTCAAA TCAGGTGTTA ACGGATCTCT AAATGGCAAG TTA_nAAATGAA 180

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CACAATGGTC TCTTTACTAT CATCCGCAAT AGGCATATCG AACTCATAnC TTACATAATT 300
 ATTAAACATA TTTACTTGAT TAATCGCTTG TGGTGCGCCT ACAnTTCTTA ATTCAGCGGA 360
 5 CGGTCACTTG TTAAACGGT TTAAGGTATT CTACTAATTn 400

(2) INFORMATION FOR SEQ ID NO: 3766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 451 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3766:

CnTTTAACCT TTTTAAGGAA TCCTGCTAAT GCGGGTTTTG GCATTTTCGA nTnTTTTrGTA 60
 20 tCTCACGCAA tCTTGGTGGT CATTCAAGTC GTATATGGCA TCCATTAAGA CGCGAAGATC 120
 AAATGGACTA TTGATGACTT CTGGAATACC ACGATCTATA TTTAGTAATT GATAAACAGC 180
 TTCCATGGCA GTACGAACCG AATATTCTGT TGTAATACA GTGTCTCGCT CTGTTTCTGC 240
 25 AAAGTTACCA ATAAATGCTA AGTTCTGAGA TTGATGCGGG ACGACTAAAG GTCTGTGCGC 300
 GATAGCACGC GTCATGAAAT AAGATGTGAT ATATGGCATA TAAACAGGgA ATCGTATTAG 360
 ATGCATGTnT TGCTAAGTCT TCAATTTTGG TCAGTTGATA CACCTAAGTG GATACAGCCA 420
 30 TTCTTGGCAT ATTCATTAC CACTACATnC T 451

(2) INFORMATION FOR SEQ ID NO: 3767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3767:

ACACGTGAAC GTCTTCAAAT GGAAGTACGT GACGTTCACT ACTCTCACTA TGGCCGTATG 60
 45 TGTCCAATTG AACACCTGA GGGACCAAAC ATTGGATTGA TTAACTCATT ATCAAGTTAT 120
 GCACGTGTAA ATGAATTCGG CTTTATTGAA ACACCATATC GTAAAGTTGA TTTAGATACA 180
 50 CATGCTATCA CTGATCAAAT TGACTATTTA ACAGCTGACG AAGAAGATAG CTATGTTGTA 240
 GCACAAGCAA ACTCTAAATT AGATGAAAAT GGTCGTTTCA TGGATGATGA AGTTGTATGT 300
 CGTTTCCGTG GTAACAATAC AGTTATGGCT AAAGAAAAA TGGATTATAT GGATGTATCG 360

(2) INFORMATION FOR SEQ ID NO: 3768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3768:

CCTACGACCG ATCGGTAAAC AGCCGATAGC TCTACCACTG AGCTACTGTG GATTAATATT	60
ATGCCTGGCA ACGTTCTACT CTAGCGGAAn TAAGTTCGTA CTACCATCGA CGCTAAGGAG	120
CTTAAC TTCT GTGTTCGGCA TGGGAACAGG TGTGACCTCC TTGCTATAGT CACCAGACAT	180
ATGAATGTAA TTTATACATT CAAAACTAGA TAGTAAGTAA AAGTGATTTT GCTTCGCAAA	240
ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT CnGCTCCACA TGTCACCATG	300
CTTCCACCTC GAACCTATTA ACCTCATCAT CTTTGAGGGA TCTTATAACC GAAGTTGGGG	360
AAATCTCATC CTGnAGGGGG CTTCATGCTT AGATGCTTTC	400

(2) INFORMATION FOR SEQ ID NO: 3769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3769:

CTTGACCGAA GTTCTTACCT ACATCACCTA AATTAATGAC ATGTCCACCA GTCATATACT	60
CTAATCCATG GTCGCCGATA CCTTCAACGA CAACATCTAC ACCACTATTT CTAATACAGA	120
ATCTTTCTnC TGCCTACCG TTAATAAATG CCTTACCACT TGTCGCACCA TAGAATGAGA	180
CGTTACCAGC AATAATTTCA TTTTGTGCTT CTTCAAAAGG TGCTTTGACA ATGACCGTAC	240
CACCAGATAA TCCTTTACCA ACATAGTCAT TCGCATCTCC AGTATGATGA ATCATTAAAGC	300
CTTTCGGTGC ATATGCTGCA GGACTTTGGA CCAGCATGAC CATTTCGTATA AACATTAATT	360
GTATTTTTCAG GGAGGTCCTG CTTCTCCATA TTGTTTCGGA	400

(2) INFORMATION FOR SEQ ID NO: 3770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3770:

5 CATTACGTAA TTAAAGATA GTCATTAAGA GAGGnTGATA ACCATGCAAG AAGCATACAT 60
 TGTAGCTTAT GGGCGTTCAG CGCAGCGAAA CAAAGCAAGG CGCATTATTC CACGAAAGAC 120
 CTGATGATGT CGCAGCCAAA GTATTACAAG GCGTATTGAA ACGTATTGAC GGAAAATTCA 180
 10 ATAAGAATAT GATTGAAGAT GTCATTGTTG GTACGGCTTT TCCAGAAGGA TTACAAGGCC 240
 AAAACATTGC ACGAACGATT GCATTGCGTG CGGGATTATC TGACACGGTA CCGGTCAAAC 300
 AGTGGAAATCG CTA CTGCTCA TCCAGGnTTT ACAAACCATT CGCGATTGCA GGCCAATCAA 360
 15 ATTATGGCnG GTCCAAGGAG ATATACTTGT TAGCTGGTGG 400

(2) INFORMATION FOR SEQ ID NO: 3771:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3771:

ACTCTCTTGC AnTAAGGGCA GGAATGACC GATGGGATTA AAAGATCAAG CTGTTACCTG 60
 30 GGGAAGGTAT TTTCATCAAT TTCCAGAACT ATCCGATAAA GAATTTAAGA CTACACAAAA 120
 AATTAAAGAT ATTTTAACAG AACATCATAT TAGAATATTA GACTTACCAC TTGCGACTGG 180
 GCTTGTGCT GAAGTGGGAC AAGGTCTGAG TTGTATAGCT GTTCGGGCTG ACATTGATGC 240
 35 TTTACCGATT CAAGAGCTTG TTGAACAGGA TTTTAAATCT GAAAATGAAG GTGTTATGCA 300
 TCGGTGTGGT CATGATATTC ACATGGCTAG nATTTTGGCT ACAGCTGGTA AAATTAAAAG 360
 40 AGATTGAGGG CACTCTTACT GGGCGTGTTA AATCCATTG 400

(2) INFORMATION FOR SEQ ID NO: 3772:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3772:

TTTATTTTGA CGTTTTAGAC ATAAAAAAA GAGACCTTGC GGTCTCAATG CGGCTCATCG 60
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GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG 180
 CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 240
 5 GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TGTTTGCTTT TTATTTTGAC GTTTTAGACA 300
 TAAAAAAAAG AGACCTTGCG GTCTCAATGC GGCTCATCGC ATCCATTTTT TGCCTGGGCA 360
 ACGTCTACT CTAGCGGGAA CGGTAAGTTC GGACTTACCA 400

10

(2) INFORMATION FOR SEQ ID NO: 3773:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3773:

TTGATATTCC TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGGnATAGGC 60
 GACGTGCGAT TGGATTGCAC GTCTAAGCAG TAAGGCTGAG TATTAGGCAA ATCCGGTACT 120
 25 CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT TCGAGTCGTT GATTTACAC 180
 TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCGTAC CGCAAACCGA CACAGGTAGT 240
 CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA AGGAACTCGG CAAAATGACC 300
 30 CCGTAACTTC GGGAGAAGGG TGCTCTTTAA GGTTAACGCC CAGAAGAGCC GCATGGAATA 360
 GGCCCAACGA nGTTTATTCA AAAACACAGT CTCTGCTAAA 400

35

(2) INFORMATION FOR SEQ ID NO: 3774:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3774:

TACTTAGACA ATCGAAAGTG TACATTATTA AATTATCATT TCCAGTTCTA CTCTAGCGGA 60
 ACGTAAGTTG GCTACCATCC TCGCTAAGAA CCTTCTCTGA CTTGTGACAA TCGCTTGCTT 120
 CTTTCCTCTC CTTCGGCTCT CACTTACTCA TTTAGCTCTA CTAAACTCGT TCGGTTCTTT 180
 50 TCTCGTTTCG TCAGATTCAA ACGTTTTTAC TTCGCCAAGC CATTTTTCTT TGTGTTTGCT 240
 TTTTATTTTG ACGTTTTTGA CATAAAAAAA AGAGACCTTG CGGTCTCAAA TGCGGCTCAT 300

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GACGCTAAGG AGCTTAAACT TCTGTGTTTC GGCATGGGGA

400

(2) INFORMATION FOR SEQ ID NO: 3775:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3775:

CGGTTTATCA AGAATGGAAA GAGTTGTACG TGAAAGAATG TCAATTCAAG ATACTGAGTC 60
 TATCACACCT CAACAATTAA TTAATATTCG ACCTGTTATT GCATCTATTA AAGAATTCTT 120
 TGGTAGCTCT CAATTATCAC AATTCATGGA CCAAGCAAAC CCATTAGCTG AGTTAACGCA 180
 TAAACGTCGT CTATCAGCAT TAGGACCTGG TGGTTTAAAC CGTGAACGGC TCAAATGGAA 240
 GTACGTGACG TTCACTACTC TCACTATGGC CGGTGTGTCC AATTGAAACA CCTGAGGGAC 300
 CAAACATTGG ATTGATTAAC TCATTATCAG TTATGCACGT GTAAATGGAA TTCGGCTTTA 360
 TTGAAACACC ATATCGTAAA AGTTGATTTC GATACACAGC 400

(2) INFORMATION FOR SEQ ID NO: 3776:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3776:

AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG 60
 TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATATA 120
 GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA 180
 CTCTGCTTTA AAATAATTTA ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT 240
 AAACGCGTTA TTAATCTTGT GAGTGTTCCT TCGAACHTAG GCGATTATTT CTTATGGAAT 300
 TCAAGCTTAT TTAAACTCTT TTATTCATC GGTTCCTTGCCT GGGTAAATC TAAATTTTAC 360
 TTACHTATCT AGGTTTTCAA TGTACAAATA ATGGTGGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3777:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3777:

AATTATAAAA TTAAATGGCG GTCTCGACGG GAATCGAACC CGCGATCTCC TCGGTGACAG 60
GCAGGCGTGT TAACnCTAC ACTACGAGAC CATTAGTAAA ACGGAGGAAG AGGGATTCTGA 120
ACCCCCGCGA GCGGTAAAGC CCCTGTCGGT TTTCAAGACC GATCCCTTCA GCCGGAATTG 180
GGTATTCCTC CAAAATTATA TGGACCTTGC AGGACTCGAA CCTGCGACCG AACGGTTATG 240
AGCCGTTAGC TCTAACCAAC TGAGCTAAAG GTCCTAAATA TAATTTTACA ACTAATAAAT 300
AGTGGCGGTG GAGGGGATCG AACCCCCGAC CTCACGGGTA TGAACCGTAC GCTCTAGCCA 360
GCTGAGCTAC ACCGCCTTAT ATAGTTTGTA AATAATATGG 400

20

(2) INFORMATION FOR SEQ ID NO: 3778:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3778:

CAAATCCTGC ACCATCAGAA AGTGGGGCAG ATGTTCTGTC AGTCATAGTG CCGTCAGCTT 60
TAAATACTGT ACGTAATTTG GCTAATGCCT CCATCGTGGT GTCAGGGCGT ATAAATTCAT 120
CTTGGTCAAA GATATTTGTG TGTACTTTTG GTCCTGCGTT TGTATATTCA ACTGAGTTTA 180
CTTGTATTGG AATAATTTCA TCTTTGAACC GACCATCACG TTGTGCGTCA TAGGCACGTT 240
GaTGACTTCT GACAGCATAA GCATCTTGaT CTTCGCGTGA TACGTCAAAT TGGGATGCTA 300
CATTTTTtCAG CAGTTAAACC CATAGGATAT GACGCACCTA TATCATCAtA TTGTAAGGTT 360
GGATTGTTTG TGGGCTTCGT TnGCCACCnn TTGGTACGGC 400

45

(2) INFORMATION FOR SEQ ID NO: 3779:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3779:

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CAATCTAAAT CGTTCAAAT TGGCACAACG ACAATAAGG CTTCAACACG AATATATTCT 120
 CTCGGTTGAA ACCTTACTTA TTCATTTATT TTTTATAAAT TAGTGACATA AACTGTATT 180
 5 AGCATCTGCA CGATCGGTTG AAATATATGT TACATTTTCT TGCTGCTTAA TAAATGCATC 240
 ATAGTAATCA TATTGCGACG AATGATATGT GCCATTGAT GTATCATTTG GGTTTAGCAA 300
 ACAGCCATAA CCTTCGTCAT ATAAATGTTT ACnGAGCATA AGGGGCGTCA TGTTTTAGAA 360
 10 CCACCTTACC TACATAAAAT TnGCCTCCAT AGGGATCATA 400

(2) INFORMATION FOR SEQ ID NO: 3780:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3780:

ATGGnCGGTC TCGACGGGAA TCGCAACCCG CGATCTCCTG CGTGACACn CAGGCGTGTT 60
 25 AACCGCTACA CTACGAGACC ATTAGTAAAA CGGAGGAAGA GGGATTGAA CCCCCGCGAG 120
 CCGTTAAGCC CCTGTCGGTT TTCAAGACCG ATCCCTTCAG CCGGACTTGG GTATTCCTCC 180
 AAAATTATAT GGACCTTGCA GGA CTGCGACCGA ACGGTTATGA GCCGTTAGCT 240
 30 CTAACCAACT GAGCTAAAGG TCCTAAATAT AATTTTACAA CTAATAAATA GTGGCGGTGG 300
 AGGGGATCGA ACCCCCGACC TCACGGGTAT GAACCGTACG CTCTAGCCAG CTGAGCTACA 360
 35 CCGCCTTATA TAGTTTGTAATAAATATGGT GGAGACTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3781:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3781:

AACCACATCT TTATCAAGTT TCATATTCGG AATACCATAC ATTAATAAAC CGCCTGATTC 60
 TCTAGCACGT TCATAAATAG TTA CTGATA TCCTAGTAGA TTAAGTTCTT CAGCAGCAGC 120
 50 TAATCCTGCT GGACCGCTTC CAACGATTGC CACTTTTTCA TCTCTACGGC GACTCGGAAC 180
 TTTCGGCGCT ACCCAACCAT TTTCAAAAGC TTCATCAATA ATTGTGCGTT CAATACCTTT 240

55

TACACGCCCT GTAAAGTCAG GAAAGTTATT TGTTTCGCTT AAGCGTCATA AGCAGTTTTA 360
 AAATCTTGAT GATACACCAA GTCGTCCAnT CAGGATGGAG 400

5 (2) INFORMATION FOR SEQ ID NO: 3782:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3782:

15 ACATGATGCG TGTGGTATTG GTTTTTATGC GAATATGGAT AATAAAAGGT CTCACGACAT 60
 CATTGATAAA TCGCTTGAAA TGTTGCGACG CTTAGATCAC AGGGGCGGGG TCGGCGCAGA 120
 20 TGGCATCACT GGTGATGGCG CAGGTATTAT GACTGAAATA CCTTTTGCAT TTTTCAAACA 180
 ACATGTAACG GACTTTGATA TCCCAGGTGA AGGTGAATAT GCCGTGGGGT TATTTTTTTC 240
 CAAAGAACGC ATTTTAGGTT CTGAACATGA AGTAGTTTTT AAAAAATATT TTGGAAGGCG 300
 25 AnGGGTTATC AATTCTTGGT TAACGTAATG TACCAGTTAA TAAAAGATGC CATTGCCTAA 360
 ACCATGTAGC AGATACGATG GCCAGTCATT CCACCAAGTG 400

(2) INFORMATION FOR SEQ ID NO: 3783:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3783:

40 AATCGGGTGA TGTTGGACGA TGATACGCAG GGAACGTTGC GTTATTCGTA TATGAAATAT 60
 TGGATAACTG TTTTAACAAT GATGGTAGAG ATATTTTCATC ATTTGTAACA TCGTCAATTT 120
 TGATATTGTG ATGATTTAAC ATAACGACAT CATCGATATT GAATTGGTAT GAAAAACCTG 180
 45 CTGTTGCTGA ATCTGTTAAT TTGGCTCCAA TATTTAAAAT TAAATCGCTG TTGTCCACAT 240
 AATCTCGTAT TTTATCTTCG GCAATTTTCC CATCGTAAAT ACCCATATAA TATGGATTTT 300
 CCTCATTAAG AGCACCTTTT CCTAATGAAA GTTGTGCTAC TGGGTATCTG TGTTTGAnTT 360
 50 ACAAATCTT CnAAGTCCTG GATGGAGGTG AAAACTGTTA 400

(2) INFORMATION FOR SEQ ID NO: 3784:

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- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3784:

10 GGTACTAAGA TGTTTCAGTT CTCCGGGTGT GCCTTCTGAT ATGCTATGTA TTCACATATC 60
 GATAACATGA CATAACTCAT GCTGGGTTTC CCCATTCCGA AATCTCTGGA TCAAAGCTTA 120
 CTTACAGCTC CCCAAAGCAT ATCGTCGTTA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180
 15 GGCATCCACC GTGCGCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA 240
 CGCTCACATA CGGCTTCGTT TTCATTATTT TAAATGCTCA TTTACATAAG TAAACTCTGC 300
 TTTAAAATAA TTAACTCAT TGTCTGCAAA ACGTTTCTT TTATAAAAAG AATTTAAACG 360
 20 CGTTAATGAA GCTGTGAGTG TTCCTTCGAA CACGAGnnGA 400

(2) INFORMATION FOR SEQ ID NO: 3785:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3785:

TACTGGAATG ACATCAGATA CATGTGCACC ACCAATCCAT TTCTTTTCAC CATTGATAAC 60
 35 CCAAGTATCG CCTTGnCGTT CAGCGACTGT TTCAAGACCT CCCGCAACGT CCGAACCGTG 120
 TTCTGGTTCA GTTAAAGCAA AGCATGTACG CAGTTCATGT GACTGTAATT TAGGTACATA 180
 TTTGCAATT TGTTCCTTGC TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTTGGTG 240
 40 AACACCGAGT AGGGTAGCTA AGGAAATATC AAATCGCGCG AGTAGGTAAG ACATGAAAAA 300
 CTGAAATAGT TGACTIONGCA TTTTGCGGTT TGGACGATCC TTGTAAAGTA ATGGATTGTT 360
 AAAATAATTT AATTCTCCCA GTCTTTAAAT AGTCCTCGGG 400

45

(2) INFORMATION FOR SEQ ID NO: 3786:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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TCATTTGACG AATTTTCATTG TTATTCAAAA TTCTATCTAA TCGTGCTTTT TCAACATTTA 60
 ATATCTTACC TCGTAATGGT AAAATCGCCT GCGTTCTAGA GTCACGACCA GATTTTGTAG 120
 5 ACCCCCCGGC AGAGTCCCCT TCGACTAAGA AAATCTCACA TTCTTCAGGA CTTTACTAG 180
 AGCAATCGGC TAATTTACCT GGAAGCTTGC TACATCTAAC GCTGATTTAC GACGTGTTAC 240
 TTCACGCGCT TTTTTCGCAG CAACACGTGC ACGGCCCCGC ATAATACCTT TTTCAACCAC 300
 10 TGTACGTGCG ACTTGTGGGA TTTTCATATA AAAATCGTTC AAAGTGCTCT GAGAATAATT 360
 TATCTACAAC TTGACGCACT TCAGAATTAC CTAATTTTGT 400

15 (2) INFORMATION FOR SEQ ID NO: 3787:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3787:

25 TCTCTTCCCG TTTGCTCGC CGCTACTAAG GGAATCGAAn TTTCTTTCTC TTCCTCCGGG 60
 TACTAAGATG TTTGAGTTCT CCGGGTGTGC CTTCTGATAT GCTATGTATT CACATATCGA 120
 TAACATGACA TAACTCATGC TGGGTTTCCC CATTTCGAAA TCTCTGGATC AAAGCTTACT 180
 30 TACAGCTCCC CAAAGCATAT CGTCGTTAGT AACGTCCTTC ATCGGCTTCT AGTGCCAAGG 240
 CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTTAT AAGTCAAACG 300
 TTAACATGAA GTTACGTTCT TTTATAAAAA GATTAAACG CGTTATTAAT CTTGTGAGTG 360
 35 TTCTTTTCGGA CACTAGCGAT TATTTCTnAT GATnCAAGCT 400

(2) INFORMATION FOR SEQ ID NO: 3788:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3788:

ATTCTCTGCT TTCATCTCAT TTGGTGACTA ATACCCTGAT TTTGTCCAAG TAAATGCTTC 60
 50 ATAAAGTATT CTTGACCTTT TGCAGAACTT GAAATTAAGT TTGAACGCCA TATATAATGA 120
 TTTTGATGA TTCTTTTTC AATCAGGATC TCTATTGCAA ATTGTGTTTG TnTTGATTTTC 180

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TCTTCTGCAA ACAACAAACT ATTTTATTATA AATTGTGGAT ATGATGGTAA CCAACCAAGT 300
 CTAGCTGCTA AnACATTATA ATCAGCTGGA TGTTGATGCT TTAACCTCTC TGTTTTAGCT 360
 5 AATGGAGATT TTAAACGATC TACATTTGAC TCTTCATAAT 400

(2) INFORMATION FOR SEQ ID NO: 3789:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3789:

CGGTTTCTTA ATTATGAACG CAACTATGAA TGGCTTATTA ACTATCACGG GCACATTGGC 60
 20 AAAAGATCAG CTTGCACAAA ATGGACAAGG CATGGTGCTC GGTATACAAA CGGTTGAAAC 120
 CGGTGTTTTT GGCGGGATTA TCACAGGTAT TATGACCGCA ATACTTCACA ACAAATATCA 180
 CAAAGTGGTA TTACCACCGT ATTTAGGTTT CTTTGGTGGC TCTAGATTTG TCCCTATTGT 240
 25 CACAGCATTT GCCGCAATCT TTTTAGGTGT ATTGATGTTT TTCATTTGGC CAAGCATACA 300
 nGCCGGCATT TATCATGTTG GTGGGATTTG TAACGAAAAC AGGTGCCATC GGTACTnTTG 360
 TTTATGGGTT CATCTTTAGG ATTGTTAGGT CCACTCGGTT 400

30 (2) INFORMATION FOR SEQ ID NO: 3790:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 716 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3790:

ATAATGGACT GTGCCGnGTA ATAATATnGn TCTCTAAAAG TTGTATTTTA AAAATAGTTC 60
 TTAAATTAT ATACCCACCA CATTTGGTGA KGAACCTAAA AAAAGCACT TCCC AAAAAT 120
 45 GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAAGTCA 180
 GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC TAGCTGGATT CGAACCAACG 240
 AGTGACGGAT CAAAnGTCCG TTGCCTTACC GCTTGGCTAT AGCCaATATA TAGATGGTGG 300
 50 AGGGGGGCAG ATTCGAACTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC 360
 ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG 420

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CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGTGnTCTT 540
 AACCGtTGAC CAAGGAGCCA TGGCTCaCcA GGTAgGACTC GAACCTACGA CCGATCGGTT 600
 5 TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGGATTA ATATTATGCC TGGCAACGTT 660
 CTACTCTAGC GGAACATAAG TnGAACThA CCATCGACGC TAAAGGAGCT TAACTT 716

(2) INFORMATION FOR SEQ ID NO: 3791:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3791:

20 TGTCATGACG TTATTTGAAG ATATCGCGCA AGTCTTTTAA AAGGTAACAC TATCATTTAT 60
 GCAATACGGC GCATTACCAG AGTTGCATGG TCAAAATATA TTGTTGTCAT TTGAAGATGG 120
 ACGTGTACAA AAATGCGTGT TACGTGATCA TGATACTGTC AGAATTTATA AACCATGGCT 180
 25 AACAGCACAT CAGCTTTCAT TGCCGAAGTA TGTCGTCAGA GAAGATACAC CTAATACGCT 240
 AATTAATGAG GATTTGGAAA CATCTTTGTC nTGATTTTCA AACATTAGCT GTGATCGGTA 300
 AATCTATATG CCATTATTGA TGCAATTCCA AGATTTATTT GGTGTGAAGT GnAGCATGAA 360
 30 CTTATGTCGT TGTAAAACA AATTTTGAAA AAAGGAAGTG 400

(2) INFORMATION FOR SEQ ID NO: 3792:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 425 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3792:

TTTTCACACA ATACATGGAC ACCATGGTTC AATGCTTCTA TAGAAAGATC AGCATGGAAT 60
 45 TTATTAGGTG TACAAATGAC CACCGCATCA ACAAGTTTAA ACAGCTCGCT AGGTGTCTCA 120
 ACTGCATGAG GTATATTAAA GCGCTTCGCA ACATCAATCA TCTGCACTGT ATTAATATCT 180
 TGTACTGCAA CTAATGAGAC TGTGTCTTTG AGTTTCAGCA ATGCTGGAAT ATGACGGTCT 240
 50 TGTGCAATAC CACCAACACC TATCACACCA ACTTTTAATT TTGTCATGAT GTGCCTCCTT 300
 ACGTATGAT GTtATTCAAA GTAAATTGCT TTGCCTGATT TkGCAGACTG ATaAATyGCT 360

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TACCA

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(2) INFORMATION FOR SEQ ID NO: 3793:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3793:

GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC TAGCTGGATT CGAACCAACG 60
 AGTGACGGAG nAAAGGTCCG TTGCCTTACC GCTTGGCTAT AGCCCAATAT ATAGATGGTG 120
 GAGGGGGGCA GATTGGAAGT GCCGAACCCG AAGGAGCGGA TTTACAGTCC GCCGCGTTTA 180
 GCCACTTCGC TACCCCTCCA GCTTATTCAT ATAATTTAAT AATCAAAATG GTGGAGAATG 240
 ACGGGTTCGA ACCGCCGACC CTCTGCTTGT AAGGCAGATG CTCTCCCAGC TGAGCTAATT 300
 CTCCAAAATA ATGACTCCTA CGGGACTCGA ACCCGTGTTA CCGCCGTGAA AGGGCGGTGT 360
 CTTAACCGCT TTGACCAAGG AGCCATGGCT CCACAGGTAG 400

(2) INFORMATION FOR SEQ ID NO: 3794:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3794:

ATCAGCAGGG TTGAAAGTAC CTGCTGCAAC AGTAATACCA TTATTAGTTC CAGCAATACC 60
 TGCTACAGTT GCTGCAGATG CTTCTTTCAC CCATGGACTC GTATTATTGC GACGTGTAAA 120
 TGTnTCACAA CGTTACCATT ACGTTTAATA ACTAATTTAT CAGCGTATGT CGTTACGTTA 180
 CCGGCATGTG TATTCAGTGT TTGGTTTGCT CCAGGTGCAA TTGTAATCGC TCCTGCCGCT 240
 GTTTCAGTCA CAGTTGGTTT CGCTGGTTGC ACATCTTTTA CTACAAATTT CGCTGGTAAA 300
 GATGTTGCAA AAGTATGTCC GTTATAGATG ACGTCCATAT TTTGCGTTAA CGACTTTAGC 360
 CACATTCGGT TTATTCATAG CGGACCAGTT TCGTCCATT 400

(2) INFORMATION FOR SEQ ID NO: 3795:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3795:

	GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACAA	60
10	TGGTAGGAGA GCGTTCTAAG GCGGTTGAAG CATGATCGTA AGGACATGTG GAGCGCTTAG	120
	AAGTGAGAAT GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT	180
	AAGGTTTCCA GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCCCTAAGC TGAGGCCGAC	240
15	AGGCGTAGGC GATGGATAAC AGGTTGATAT TCCTGTACCA CCTATAATCG TTTAATCGAT	300
	GGGGGGACGC AGTAGGATAG GCGAACGTGC CATTTGATTG CACGTCTAAA GCAGTAAAGC	360
20	TGAGTATTAG GCnAATCCGG TACTCGTTnA AGGCTGAACT	400

(2) INFORMATION FOR SEQ ID NO: 3796:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3796:

	GCACATGTTG CCATgCTTGA GCTAAATTAC CTTGCATCAT TGCTAGCTTT TCTTGTATTA	60
	ACTGATATTT ACTAATTGGT TTGCCGAATT GCTTACGCTC AGTGACATAA TCTAATGTGG	120
35	CACGTAAAGC GCCACCATAC CACCTGTAGC CATATAAGCA ACGsCTGCTC TCGTTGAATA	180
	AAGAATTTTG GCAATATCTT TAAAGCTTGT TATGTTTTGT AAGCGATCCG CTTTCATCTAC	240
40	TTTGACATTA GTTAATTTAA TTAGGGCGTT AGGAACAATG CGAAGTGCGA TTTTATTATC	300
	AATGACTTCA ATATCGACGC CATCTTGTTT TGGTCTGACT ACAAAGCAAT GGGGTTTGCC	360
	AGTTTCnGTT ATTTACTGCG AATACTGGGG GGGnGnGGTT	400

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(2) INFORMATION FOR SEQ ID NO: 3797:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3797:

GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAAGTG ACGCTGATGT GCGAAACGTG 120
 GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT AAACGATGAG TGCTAAGTGT 180
 5 TAGGGGGTTT CCGCCCCTTA GTGCTGCAGC TAACGCATTA AGCACTCCGC CTGGGGAGTA 240
 CGACCGCAAG TTGAACTCA AAGGAATTGA CGGGGACCCG CACAACGGTG GGAGCATGTG 300
 GTTTAATTCG AAGCAACGnA GAGAACCTTA CCAATCTTTG ACATCCTTTT GACTCTAG 360
 10 GAGATAGAGC CTTCCCTTCG GGGGGACnAA GTGACAGTTG 400

(2) INFORMATION FOR SEQ ID NO: 3798:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3798:

CACAAAACAA GCCAAGCAAA ACAACGCAT ATAACGTAAC AACACATGGA AACGGCCAAG 60
 25 TATCATATGG CGCTCGCCCA ACACAAAACA AGCCAAGCAA AACAAATGCA TACAACGTAA 120
 CAACACATGC AAACGGTCAA GTGTCATACG GAGCTCGCCC GACATACAAG AAGCCAAGTA 180
 AAACAAATGC ATACAATGTA ACAACACATG CAGATGGTAC TGCGACATAT GGGCCTAGAG 240
 30 TAACAAAATA AGTTTGTAAC TCTATCCAAA GACATACAGT CAATACAAA CATTACGTAT 300
 CTTTACAACA GTAATCATGG CATTCTATGG ATGCTTCTAA CTGGAATTAA AGCATCGGAA 360
 35 CAATCGGGAn GCATATTTCT AAAATTATTT ATTCCATTAT 400

(2) INFORMATION FOR SEQ ID NO: 3799:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3799:

CTTCGCCGAT ATGGGGGAAG CTAGGTGATA AGATCAGCCG AAAATGGATG GTGTTAAGAG 60
 50 CGTTACTTGG TTTGGCGGTA TGCTTATTTT TAATGGCATT GTGTACGACA CCATTACAGT 120
 TTGTACTTGT GAGGTTATTG CAGGGACTAT TTGGTGGTGT TGTTGATGCA TCAAGTGGT 180
 TTGCGAGTGC AGAGGCGCCA CTGAAGGATC GTGGAAAGGT ATTAGGAAGA CTGCAAAGTT 240

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TTTtAGTGCG TtACTGATGA GTATTGCCGT TATTACTTTT ATTGTCTGTh TTTTCGGTGC 360
 CATTAAAAATG ATTGAAACGA CACATATGGC CAAAnnCACA 400

5 (2) INFORMATION FOR SEQ ID NO: 3800:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3800:

GGAATCTATT ATATTAGATG TAAAAAATTT CGCGCAAAAT GTGTTAGGTA AAGGTGTCAT 60
 TGTCGTCAAT GATGTGCCTG GCTTTGTGCG AAATAGAGTC GGCACGCAAA CAATGAATGA 120
 20 TATTATGTAT CGCGCCGAGC AACACAAGAT AAGCATTGTA GATGTGGATG CTTTAACTGG 180
 GCAAGCGATT GGTCGTCCTA AAACAGGTAC ATATGCGCTA TCTGACCTAG TCGGTTTAGA 240
 TATTGCAGTG TCTGTAAATT AAAGGCATGC AACAACTACC TGAAGAAACA CCTTATTTTC 300
 25 ATGATGTCAA AATGTAAATA CGTTGTTTGA CCATGGGCGC ACTCGGACGT TAAnnCGnAA 360
 ACCAAGGGTT TTTACCAAAA AGGGTTAAAG GGnAACTTAA 400

30 (2) INFORMATION FOR SEQ ID NO: 3801:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3801:

40 TGCAGGCGTT TCTGGTCTGC ATAGTTTACG CATACGACCT GCGCGATCCT TATCTGGTAA 60
 TAAATTGTAA AACGATAGTT CCCGTTGTTC CTAATAGTTG TATTCTATCT GACGCATAAT 120
 GTGAAAAATA ACCTGCCATC TCTAAGCCCG GTCTTGATAT ATCAGCATTT TTAATTGGCT 180
 45 TCGATAGTCC TTCTTCACCA GCGATTAAAT CTAACTTTAA TGTTTCAACT AGTTTTTCTG 240
 TCGTTAACAT GGGTTCACCT CAATTGTATT TACCCTACTC TTACATCTCT TCTTATCATA 300
 50 TCAAAAATAT AACACCAATC TACATTGAAA AGCTAAAnTA AATATTAATG TTCATTATTG 360
 TTAThATTTT ACAAGTCAAT ATCATCATAA TTTATTGCTG 400

(2) INFORMATION FOR SEQ ID NO: 3802:

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(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3802:

10 TTTCACCTTTT GAACCATGCG GTTCAAAATG ATTATCCGGT ATTAGCTCCG GTTTCCTCGAA 60
 GTTATCCCAG TCTTATAGGT AGGTTATCCA CGTGTTACTC ACCCGTCCGC CGCTAACATC 120
 AGAGAAGCAA GCTTCTCGTC CGTTCGCTCG ACTTGCATGT ATTAGGCACG CCGCCAGCGT 180
 15 TCATCCTGAG CCAGGATCAA ACTCTCCATA AAAATTATGA TGTTTGATTA GCTCATAAAT 240
 ACTAAATAAT GTTTGTAAC TATAGTTACG TTTTTTGAA TTAACGTTGA CATATTGTCA 300
 TTCAGTTTTT AATGTTCAIT TTTCTTACCG ACAAGAATTA ATTATACATT TTATTAACAT 360
 20 TTAAGTCAAT AACTTTnTTT ATCCTGTCCA TTTnATTTTT 400

(2) INFORMATION FOR SEQ ID NO: 3803:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3803:

TAGTCACCAG ACATATGAAT GTAATTTATA CATTCAAAAC TAGATAGTAA GTAAAAGTGA 60
 35 TTTTGCTTCG CAAAACATTT ATTTTGATTA AGTCTTCGAT CGATTAGTAT TCGTCAGCTC 120
 CACATGTCAC CATGCTTCCA CCTCGAACCT ATTAACCTCA TCATCTTTGA GGGATCTTAT 180
 AACC GAAGTT GGGAAATCTC ATCTTGAGGG GGGCTTCATG CTTAGATGCT TTCAGCACTT 240
 40 ATCCCGTCCA CACATAGCTA CCCAGCTATG CCGTTGGCAC GACAACTGGT ACACCAGAGG 300
 TATGTCCATC CCGGTCCTCT CGTACTAAGG ACAGCTCCTn TCAAATTTCC TACGnCCAnG 360
 45 ACGGATAGGG ACCGAACTGT TTTCACGACG GTnCTGAACC 400

(2) INFORMATION FOR SEQ ID NO: 3804:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 457 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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AGTnCACTCA CnCCAGATGT TTAAGTCCTG TGGCTCTGCC AGTTCCGCCA CCCCggCACT 60
 ATAAAAATGG AGCAGAAGAC GGGATTTCGAA CCCGCGACCC CAACCTTGGC AAGGTTGTAT 120
 5 TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 180
 TTAGwATCCT AAGTCTAGTG CGTCTGCCAA TTCCGCCACA CCGCAAATG GTGAGCCATA 240
 GAGGATTCTGA ACCTCTGACC CTCTGATTAA AAGTCAGATG CTCTACCAAC TGAGCTAATG 300
 10 GCTCTTCCAT GGTGCCGGCC AGAGGACTTG AACCCCCAAC CTACTGATTA CAAGTCAGTT 360
 GCTCTtACCA ATTGaGCTAG GCCGGCAATA TGTaAGAATA AATGGTGGAG AATGACGGGT 420
 15 TTCGAAACCG CCGnACCCTC TGGCTTGTTA AGGGCAG 457

(2) INFORMATION FOR SEQ ID NO: 3805:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3805:

ACTTTTTTATT TTGACGTTTT AGACATAAAA AAAGCTCAG GTCTCAACTT GCCTGGCAAC 60
 GTTCTACTCT AGCGGAACGT AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 120
 30 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 180
 CTCGTTGCGC TCTTTTCTCG TTTCGTGAGA TTCAAACGTT TTCATTTCGC CAAGCCATTT 240
 35 TTCTTTGTGT TTACTTTTTTA TnTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGCGGTC 300
 TCAATGCGGC TCATCGCATC CATnTTTTGC CGGGCAACGT TCTACTCTTA GCGGAACGTA 360
 AGTTGGCTAC CATCGTCGCT AAAGACCTTT TTGGACTGTG 400

40 (2) INFORMATION FOR SEQ ID NO: 3806:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3806:

GTTATGAAAG TCGCGCTTAA AATGCGTTAA TGTGACAAGG ATAATTCAAC ATCGTTTCAT 60
 TTTACTGAGT CATTGCACTT ATCATACACA TTATATTIAG CATGAGTTAT ATTACTAAAA 120

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TCATTGGCTT AATATTTACA GCGCTTGGTA TTGCAGGTGC CGTATTACCT TTA CTGCCAA 240
 CGACCCCTTT TTTACTCGTA GCAGTTTTTT GCTTTGCTCG AAGTTCAGAT CGCTTTTACA 300
 5 ATTGGGCnnA TTAATCAAAA AATTTATAAA GAATATGTAG AAAACCTTTn TTTGACATCG 360
 AGGCTACACG CTACAACAGA AAATTGAAAA TTTAATTAGC 400

(2) INFORMATION FOR SEQ ID NO: 3807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3807:

20 AGGAGAACAT GCTGTTACAT TTGGAGAGCC TGCTATTGCA GTGACCGTTT AACGCAGGTA 60
 AAATCAAAGT TTTAATAGAA GCCTTAGAGA GCGGGA ACTA TTCGTCTATT AAAAGCGATG 120
 TTTACGATGG TATGTTATAT GATGCGCCTG ACCATCTTAA GTCTTTGGTG AACCGTTTTG 180
 25 TAGAATTAAA TAATATTACA GAGCCGCTAG CAGTGAACGA TCCAAACGAA TTTACCACCA 240
 TCACGTGGAT TAGGATCGAG TGCCAGCTGT CGCGGTTGCT TTTGTTCTGT CAAGTTATGG 300
 ATTTTTTAGG GnAAATCATT AACGAAAGnA AGAACTCATT GGAAAAGGCT nATTGGGCCA 360
 30 GAAGCAAATT GCCACATGGT AAAACCAA 388

(2) INFORMATION FOR SEQ ID NO: 3808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3808:

ATGCGCAGAG TATATGGAGG AACACCAGTG TCGAAGCGCA CTTTCTGGTC TGTA ACTGAC 60
 45 GCTGATGTGC GAAACGTGkG GGATCAAACA GGATTAGATA CCCTGGTAGT CCACGCCGTA 120
 AACGATGAGT GCTAAGTGTT AGGGGGTTTC CGCCCTTAG TGCTGCAGCT AACGCATTAA 180
 GCACTCCGCC TGGGGAGTAC GACCGCAAGT TgAAAACTCA AAGGrATTGA CGGGGACCCG 240
 50 CAcAAGCGTG GGAGCATGTG GtTTAATTCG AaGCAACGnn GAGGAACCTT ACCAAATCTT 300
 GACATCCTTT GACAACTCTA GAGATAGAGC CTTCCCCTTC nGGGAACAAA TGACAGGTGG 360

ACCCTTAAGC TTATTTGCCA TCATTAA

447

(2) INFORMATION FOR SEQ ID NO: 3809:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3809:

15 CCAACTGAGC TACTGAACCA TAATAAAAT GTAATGACTG GCGGTCTCGA CGGGAATCGA 60
 ACCCGCGATC TCCTGCGTGA CAGGCAGGCG TGTTAACCGC TACACTACGA GACCTATAAA 120
 ATATTGCGGG AGGCGGATTT GAACCACCGA CCTTCGGGTT ATGAGCCCGA CGAGCTACCG 180
 20 AACTGCTCCA TCCGCGGATA ATAAAAAATA ATGGCGGAGG AAGAGGGATT CGAACCCCCG 240
 CGGCCCGTTA AGGCCCTGTC GGTTTTCAAG ACCGATCCCT TCAGCCGGAC TTGGGTATTC 300
 CTCCATTATT ATAGGTAAAT CGCTATTAAT TATAAAATTA AATGGCGGTC TCGACGGGAA 360
 25 TCGAACCCGC GATCTCCTGC GTGACAGGCA GGCCTGTTAA 400

(2) INFORMATION FOR SEQ ID NO: 3810:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3810:

TGCTTGGTAA AATCTATATT TTACTTACTT ATCTAGTTTT CAATGTACAA ATAATGGTGG 60
 40 GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT AACCAGCTGA 120
 GCTATAGGCC CATTTTTTTG AATGTAAAT AAACATTCAA AACTGAATAC AATATGTCAC 180
 GTTATTCCGC ATCTTCTGAA GAAGATGTTT CGAATATATC CTTAGAAAGG AGGTGATCCA 240
 45 GCCGCACCTT CCGATACGGC TACCTTGTTA CGACTTCACC CCAATCATTT GTCCACCTT 300
 CGACGGCTAG CTCCTAAAAG GTTACTCCAC CGGCTTCGGG TGTACAAAC TCTCGTGGTG 360
 TGACGGGCGG TGTGTACAAG ACCCGGGAAC GATTTCACCG 400

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(2) INFORMATION FOR SEQ ID NO: 3811:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3811:

	GCTTCATGCT TAGATGCTTT CAGCACTTAT CCCGTCCACA CATAGCTACC CAGCTATGCC	60
10	GTTGGCACGA CAACTGGTAC ACCAGAGGTA TGTCCATCCC GGTCTCTCG TACTAAGGAC	120
	AGCTCCTCTC AAATTTCTTA CGCCCACGAC GGATAGGGAC CGAACTGTCT CACGACGTTC	180
	TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCTTGGG ACCGACTACA	240
15	GCCCCAGGAT GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCCTCGAT GTGGAATCT	300
	TGGGGGAGAT AAGCCTGTTA TnCCCGGGGT AGCTTTTATC CGTTGAGCGA TGGnnCTTCC	360
	ATGCGGGAAC CACCGGGATT	380

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(2) INFORMATION FOR SEQ ID NO: 3812:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 386 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3812:

	GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTGAG GGGGGCTTCA TGCTTAGATG	60
	CTTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTAGC ACGACAACTG	120
35	GTACACCAGA GGTATGTCCA TCCCGGTCCT CTCGTACTAA GGACAGCTCC TCTCAAATTT	180
	CCTACGCCCCA CGACGGATAG GGACCGAACT GTCTCAGGAC GTTCTGAACC CAGCTCGCGT	240
	ACCGCTTTAA TGGGCGAACA GCAACCCCTT GGGACCGACT ACAGCCCCAG GATGCGATGA	300
40	GCCGACATCG AGGTGCCAAA CCTCCCCGTC GnTGTGAACT CTTGGGGGAG ATAAGCTGTT	360
	ATCCCCGGGT GAGnTTTnTC CGTTGA	386

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(2) INFORMATION FOR SEQ ID NO: 3813:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
50	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3813:

CTTGGTACTT CTGGTGTGG TGGCGTTGGT GTTCCGGCT CACTTGGTAC TTCTGGTGTG 120
 GGTGGCGTTG GTGGCACGAT TGGAGGTGTT GTATCTTCTT CAATCGTTTG TTGACCTTCA 180
 5 TTTTGGCCGC TTACTIONTGG AAGTGTATCT TCTTCAAAGT CAACACTATT GTGTCCACCG 240
 AATTGATAAC TTGGTTTATC TTTATTGTGA TCTTCTTCAA TAATTTCAGT GTGCTTATTG 300
 AATCCGTGAA TATGTGGCAC nTGGTCGAAG TCGATATCAA TGATGTTACC GCCATGTTCA 360
 10 TACTTAGGTT TGTCTTTTTT TGTAnCTTCC TCGAATGACT 400

(2) INFORMATION FOR SEQ ID NO: 3814:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3814:

TAATTGGGCT ACCATCGTCG CTAAAGACCT TTCTTGACTT GTGACAATCG CTGCTTCTT 60
 25 TCCTCTCCTT CGGCTCTCGC TTACTIONT AGCTChACTA AACTCGTTGC GChCTTTTTCT 120
 CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTCTTTGT GTTACTTTT 180
 TATTTTGACG TTTTAGGCAT AAAAAAAGA GACCTTGCGG TCTCAATGCG GTCATCGCA 240
 30 TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGGCT ACCATCGTCG 300
 CTAAAGACCT TTCTTGACTT GTGACAATCG CTGCTTCTT TCCTCTCCTT CGGCTCTCGC 360
 35 TTACTIONT AGCTCTACTA AACTCGGTGC GCTTTTTCT 400

(2) INFORMATION FOR SEQ ID NO: 3815:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3815:

TTCTTTCATA TGATTTTTTA GATTTTAGTA AGTCAATAAA GCCAATTTT TCCAACGATT 60
 GAATGTAACG TTGATTGATA AATGTATTTT TTGGTAAATC ACCACCCGCT AAAATTGTGG 120
 50 CGATATTTAA GGCAATATGA TAATCATGGT CGCTAATAAA ATGACCCCGT CTTTGCGCAT 180
 CTAATTGTCC TTGGATCAAT GCTTTGAAGT CTTACCTAA AGCGATATAT TGATGTCTAG 240

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GTGTGCTGT ATTGAAAATA ATCGTATCTG GTATCACGTA AATnACCATA ACGACGTGCC 360
 TCCAAAGGCA TTTGGTAnGA GCCTTCGGCA ATGCCGATAA 400

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(2) INFORMATION FOR SEQ ID NO: 3816:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3816:

CCAATATTTA TATTAATGAA AATAAGATGT TATATTCATT GTTAATTTAA CACATAGTAA 60
 GAnAAACAGT CATAAATTGA TTTCTAATTG AAATCATCTT ATGACTGCTT TTTATTATAC 120
 TTTACATTTT TCGTTTCGTC AGATTCAAAC GTTTTCACCT CGCCAAGCCA TCTTTCTTTG 180
 TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTTGCGGT CTCAATGCGG 240
 CTCATCGCAT CCACTTTTTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA GTCGGACTAC 300
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG GAACAGGTGT GACCTCCTTG 360
 GCTATAGTCA CCAGACATAT GAATGTAAAT TCATACATTC 400

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(2) INFORMATION FOR SEQ ID NO: 3817:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3817:

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TGTATTGTT CAAAATCATG ATCAAGATCA GTATATCGGG GGGnATTATG AAGCGATGCA 60
 TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120
 ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180
 GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240
 TACCGAACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300
 TCATGATAAT TTCTTTGAAT TAGGTGGCCA TTCATTAAAA GCAACGTTAT GGnTGAATC 360
 GGATAGAGGC ATCTACTGGG GAAACGATTA CCAATTGGGG 400

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(2) INFORMATION FOR SEQ ID NO: 3818:

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(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3818:

10 TCGGAATCTG GGAGGACCAT CTCCTAAGGC TAAATACTCT CTAGTGACCG ATAGTGAACC 60
 AGTACCGTGA GGAGAAGGTG AAAAGCACCC CGGAAGGAAG TTGAAATAGA ACCTGAAACC 120
 GTGTGCTTAC AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA 180
 15 CCGGCGAGTT ACGATTTGAT GCAAGGTTAA GCAGTAAATG TGGAGCCGTA GCAnAACATG 240
 TTCTGAATAG GCGGTTTAGT ATTTGGTCGT AGCCGnAAAC CAGGTGATCT ACCCTTGGTC 300
 CAGGTTGAAG TTCAGGTAAC ACTGGAATGG AGGACCGAAC CGACTTACGT TTGAAAAGTG 360
 20 AGCGGATGAA CTGAAGGTAG CGGAGAAATT CCAATCGAA 400

(2) INFORMATION FOR SEQ ID NO: 3819:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3819:

CAACGAGAGA CTCGGTGAAG TCATAGTACC TGTGAAGATG CAGGTTACCC GCGACAGGAC 60
 35 GGAAAGACCC CGTGGAGCTT TACTGTAGCC TGATATTGAA ATTCGGCACA GCTTGTACAG 120
 GATAGGTAGG AGCCTTTGAA ACGTGAGCGC TAnTTACGTG GAGGCGCTGG TGGGATACTA 180
 CCCTAGCTGT GTTGGCTTTC TAACCCGCAC CACTTATCGT GGTGGGAGAC AGTTTCAGGC 240
 40 GGGCAGTTTG ACTGGGGCGG TCGCCTCCTA AAAGGTAACG GAGGCGCTCA AAGGTTCCCT 300
 CAGAATGGTT GGAAATCATT CATAGAGTGT AAAGGCATAA GGGACTTGAC TCGAGACCT 360
 45 ACAAGTCGAG CAGGTCCAAA AACGGACnTA GTGATnCGGT 400

(2) INFORMATION FOR SEQ ID NO: 3820:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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TGGCTCGAAC CACCGACCTC ACGCTTATCA GGCCTCGCTC TAACCAGCTG AGCTATAGGC 60
 CATTAATTTG AATGAACAAA CATTCAAAAC TGAATACAAT ATGTCACGTT ATTCCGCATC 120
 5 TTCTGAAGAA GATGTTCCGA ATATATCCTT AGAAAGGAGG TGATCCAGCC GCACCTTCCG 180
 ATACGGCTAC CTTGTTACGA CTTACCCCCA ATCATTGTGTC CCACCTTCGA CGGCTAGCTC 240
 10 CTAAGAGGTT ACTCCACCGG CTTGGGTGT TACAACTCT CGTGGTGTGA CGGGCGGTGT 300
 GTACAAGACC CGGGAACGTT ATTCACCGTA GCATGCTGAT CTACGATTAC TAnCGATTCC 360
 AGCTTCATGT AGTCGAGTTT GCAGACTACA ATnCGAACTG 400

15 (2) INFORMATION FOR SEQ ID NO: 3821:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3821:

TATTAAATTA ATGGTGGGCC TAAnTGGACT CGAACCACCG ACCTCACGCT TATCAGGCGT 60
 GCGCTCTAAC CAGCTGAGCT ATAGGCCCAT TAATTTGAAT GAACAAACAT TCAAACTGA 120
 ATACAATATG TCACGTTATT CCGCATCTTC TGAAGAAGAT GTTCCGAATA TATCCTTAGA 180
 30 AAGGAGGTGA TCCAGCCGCA CCTTCCGATA CGGCTACCTT GTTACGACTT CACCCCAATC 240
 ATTTGTCCCA CCTTCGACGG CTAGCTCCTA AAAGGTTACT CCACCGGCTT CGGGTGTTC 300
 35 AAAGTCTCGT GGTGTGACGG GCGGTGTGTA CAAGACCCGG GAACGTATTC ACCGTAGCAT 360
 GCTGATCTAC GATTACTnAG CnTTCCAGC TTCCATGnTA 400

(2) INFORMATION FOR SEQ ID NO: 3822:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3822:

50 TCTACCAACT GAGCTAATGG CTCTAATGGC TGGGCTAGCT GGATTCTGAAC CAACGAGTGA 60
 CGGATAAAGT CCGTTGCCTT ACCGCTTGGC TATAGCCCAA TATATAGATG GnGGAGGGGG 120
 GCAGATTCTGA ACTGCCGAAC CCGAAGAGCG GATTACAGT CCGCCGCGTT TACCACTTCG 180

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GAACCGCCGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCCA GCTGAGCTAA TTCTCCAAAA 300
 TAATGACTCC TACGGACTCG AACCCGTGTT ACCGCCGTGA AAGGGCGGTG TCTTAACCGC 360
 5 TTGACCAAGG AGCCATGCTC CACAGTAGGA TTCGAACTAA 400

(2) INFORMATION FOR SEQ ID NO: 3823:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3823:

AACTTGCCCTC TTTAGGTACA GCATGAGGCC CTAGGAAAGT ATGTTTCATG TCTAAATCAT 60
 20 ATTTCTCAGC TAAACGATTA GACACTTTCA ATTGCTTCAG TTCATTTTCT CTATCTAATC 120
 CATAACCACT CTTACTTTCA ACTGCAnGCA CGCCGTGTTT AATCATAGTA AGCAAATCAT 180
 GCTCTGCTTT TTTAAACAAG TCATCTTCGG ATGTTTCTCT AGTAGCATT ACGGTAGATA 240
 25 ATATGCCACC ACCCATTCT AATATTTCAA GGTAAGACTT ACCTGGACGT TTTAATGACA 300
 TCTCATGTTT TCGAGATCCA CCAAATGThA AATGGGGTAT GTGGCATCTA CTAAGCCGGG 360
 GGACACTAnC TTTCCCACTA GGCATCAATC G 391

(2) INFORMATION FOR SEQ ID NO: 3824:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3824:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT CTCTGGATCA 60
 AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120
 45 GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA 180
 ACGCGTTATT AATCTTGTGG AGTGTCTTTT CGAACACTGA GCGATTATTT CTTATGAATT 240
 CAAGCTTATT TAAAACTCTT TATTCACCTG GTTTTGCTTG GTAAAATCTA TATTTTACTT 300
 50 AChTATCTAG TTTTCAATGT ACAATTCTTT TTAGTCAAGC GCTCGCATAA GCAATATCAC 360
 TTTGAACCAA AAAAGATTGG AAGGTGAAAT AAACATTCAA 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3825:

10 ATCGATAACA TGACATAACT CATGCTGGGT TTCCCCATTC GGAAATCTCT GGATCAAAGC 60
 TTACTTACAG CTCCCCAAAG CATATCGTCG TTAGTAACGT CCTTCATCGG CTTCTAGTGC 120
 15 CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT TTCCATCCTA CAGGAAACGC 180
 GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG AATTCAAGCT 240
 TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA TCTATATnTT ACTTACTTAT 300
 20 CTAGTTTICA ATGTACAATT TCTTTTtagt CAAGCGCTCG CATAAGCAAT ATCACTTTAA 360
 CCAAAAAATA TTTGAATGTn AAATAAACAT TCAAAACTGA 400

(2) INFORMATION FOR SEQ ID NO: 3826:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3826:

35 TCACTCACCG CAGATTTTTTA AGTCCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA 60
 AAAATGGAGC AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT 120
 ACCGCTGAAC TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGnCT 180
 40 TAGATCCTAA GTCTAGTGCG TCTGCCAATT CCGCCACACC CGCAAATGGT GAGCCATAGA 240
 GGATTGGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT CTACCAACTG AGCTAATGGC 300
 TCTTCCATGG TGCCGGCCAG AGGATTTGAA CCCCCAACCT TATTGGTTAC AAGTCAGTTG 360
 45 CTCTTACCAA TTGAGCTAGG nCGGCAATAT GTTAAGATTA 400

(2) INFORMATION FOR SEQ ID NO: 3827:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3827:

AGTGGTGGAA TGGTCTTAAA AGTTGGTGGT CTAACCTTAG AGAAGACCAA AAGAAGAAAA 60
 5 GTGATAAATA CGCTAAAGAA CAAGAAGAAA CAGCTCGTAG AACAGAGAA AATATAAAGA 120
 AATGGTTTGG AAATGCTTGG GACGGCGTAA AACTAAAAC TGGTGAAGCC TTTAGTAAAA 180
 TGGGCAGAAA TGCTAATCAT TTTGGCGGCG AAATGAAAAA AATGTGGAGT GGAATCAAAG 240
 10 GAATTCCAAG CAAATTAAGT TCAAGTTGGA GCTCAGCCAA AAGTTCTGTA GGATATCACA 300
 CTAAGGCTAT AGCTAATTAG TACTGGTAAA ATGGTTTGGG AAAGCTTGGC CAATCTGTTA 360
 15 AATTCGACTA CAGGAAGTAT TTACATTCAA ACTAGGCAAA 400

(2) INFORMATION FOR SEQ ID NO: 3828:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3828:

TCTCAGTTCC AGTGTGGCCG ATCACCCTCT CAGGTCGGCT ATGCATCGTT GCCTTGGTAA 60
 GCCGTTACCT TACCAACTAG CTAATGCAGC GCGGATCCAT CTATAAGTGA CAGCAAGACC 120
 30 GTCTTTCACT TTTGAACCAT GCGGTTCAAA ATATTATCCG GTATTAGCTA CGGTTTCCCG 180
 AAGTTATCCC AGTCTTATAG GTAGGTTATC CACGTGTTAC TCACCCGTCC GCCGCTAACA 240
 35 TCAGAGAAGC AAGCTTCTCG TCCGTTGCTG CACTTGCAT GTATTAGGCA CGCCGCCAGC 300
 GTTCATCCTG AGCCAGGATC AACTCTCCA TAAAAATTAT GATGTTGANT AGCTCATAAA 360
 TACTAAATAA TGTGTGTAAT TATAGTACGT TTTTGAAAT 400

40 (2) INFORMATION FOR SEQ ID NO: 3829:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3829:

50 CAAGCGCCAT GACATCATAA CTTTCTTGCA CAAGATATGT GAACGGCGGT GTTGATCCTA 60
 GATTCGTGGC ATGCATACGC AAACCATTTT CTTCAATTAC TTCACCAAGG CGTTTAAAAAT 120

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ATTGATAAAA CCTTGATGTG TTTCGTGTCA ATGACATACC ATATCGACTA GGTACCTTTT 240
 TAGAATGTTG ATTAATCACA ACAAATATCA TGGCAAGGTC ATCTTCAAAA TGATTGATT 300
 5 CAAGTGGGAr sGGCATATGA CGTCTCATCA CtATACCCTt TnTnCCCATT CTGCAAATnC 360
 ACCCATAAAT ACTACGGGAC GGAGAACCCG TACCCATTTC 400

(2) INFORMATION FOR SEQ ID NO: 3830:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3830:

20 GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTCACATAT 60
 CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCCG AAATCTCTGG ATCAAAGCTT 120
 ACTTACAGCT CCCCAAAGCA TATCnCGTTA GTAACGTCCT TCATCGGCTT CTAGTGCCAA 180
 25 GGATCCACCG TCGGCCCTTA ATAACCTAAT CTATGTTTCC ACCATTTTTA TAAGTCAAAC 240
 GCTCACATAC GGCTTCGTTT TCATTATTTT AAATGCTCAT TTACATAAGT AAACCTCTGCT 300
 TTAAAATAAT TTAACCTATT GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTAAACGCG 360
 30 TTATTAATCT TGTGAGTGGT CCTTCGAACA CTAGCGATnA 400

(2) INFORMATION FOR SEQ ID NO: 3831:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3831:

AAATGCGGCT CATCGCATCC ATTTTTTGCC TGGCAACGTT CTA CTCTAGC GGAACGTAAG 60
 45 TTGGCTACCA TCGTCGCTAA AGACCTTTCT TGA CTGTGTA CAATCGCTTG CTTCTTTCTT 120
 CTCCTTCGGC TCTCGCTTAC TCATTAGCT CTA CTAACT CGTTGCGCTC TTTTCTCGTT 180
 TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTGTGTTT ACTTTTTATT 240
 50 TTGACGTTTT AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA 300
 TTTTTGCTT GGGCAACGTT CTA CTCTAGC GGAACGTAAT TGGGCTACCA TCGACGCTAA 360

(2) INFORMATION FOR SEQ ID NO: 3832:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3832:

AGCTTATTTT AAAACGTCGT TTATTCACCTC TGGTTTTGCT TGGTAAAATC TATATTTTAC 60
 TTACTTATCT AGTTTTCAAT GTACAATTTT TTTTATAGTCA AGCGCTCGCA TAAGCAATAT 120
 CACTTTAACC AAAAAATATT TGAATGTAA ATAAACATTC AAAACTGAAT ACAATATGTC 180
 ACATTATTCC GCATCTTCTG AAGAAGATGT TCCGAATATA TCCTTAGAAA GGAGGTGATC 240
 CAGCCGCACC TTCCGATACG GCTACCTTGT TACGACTTCA CCCCATCAT TTGTCCCACC 300
 TTCGACGGCT AGCTCCTAAA AGGTTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG 360
 TGTGACGGGC GGTGTGTACA AGACCCGGGA ACGTATTTCA 400

(2) INFORMATION FOR SEQ ID NO: 3833:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3833:

TTTTCTTCTG GTAAAATATC TGCAATAACA GTATCTATGC CTACTTGTTT TGCAATGGCT 60
 TGAGCAGTGT TTTTATTATC GCCAGTTAAC ATGGCAACTT CAATGCCCAT ATCATGCAAT 120
 TGTATTATAG CATCTTTGGC ATGATCTTTG ACAGTATCTG CCACTGCnAT GATACCAGTT 180
 AATGAATAAT TAACAGCAAT GAGCATAGCA GTTTTACCAT CTCGTTTCATA ATGTGTTAAA 240
 TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG CCATTAATnT ACGGGTTACC 300
 AACCAATATA TGGTGATGAT CAATCCGTGG CTTCAATACC ATGGCCAGGT ACCGCTThAA 360
 AGTTGTTGTC TCAGTTAATA TTAATTGCTT TCCTTTTGCA 400

(2) INFORMATION FOR SEQ ID NO: 3834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3834:

5 AAATTATATG GACCTTGCAG GACTCGAACC TCGACCGAA CGGTTATGAG CCGTTAGCTC 60
 TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TnGCGGnnGA 120
 GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 180
 10 CGCCTTATAT AGTTTGTAAA TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC 240
 TGCGTGCAAA GCAGGCGCTC TCCCAGCTGA GCTAAGCCCC CATAATAATT ACAGTATATC 300
 GGGAAGACAG GATTCTGAACC TCGACCCCCT TGGTCCCAA CCAAGTGCTC TACCAAGCTG 360
 15 AGCTACTTCC CGTATAATTA ACGCGCCCGA TAGGAGTCGA 400

(2) INFORMATION FOR SEQ ID NO: 3835:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3835:

AATAACAATT GCGCCACTAA AACTCAAAAT TTCCACCACC AACATCCAAA TTATCAACAT 60
 30 CGCAACATAA CCAAATGTTA TAATAAATCT ATTACACAAA GAGATAAATT ACTTATGCAA 120
 AGGCGGAGGA ATCACATGTC TATTACTGAA AAACAACGTC AGCAACAAGC TGAATTACAT 180
 AAAAAATTAT GGTGATTGTC GAATGATTTA AGAGGGAACA TGGATGCGAG TGAATTCGGT 240
 35 AATTACATTT TAGGCTTGAT TTTCTATCGC TTCTTATCTG AAAAAGCCGA ACAAGnATAT 300
 GCAGATGCCT TGTCAGGTGA AGACATCACG TATCnAGAAG CGTGGGCAGA TGAAGAATAT 360
 40 CGTGAAGACT TnAAAAGCAG GAATTAATTG GTTCAAGTCG 400

(2) INFORMATION FOR SEQ ID NO: 3836:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3836:

50 CTAATCGCAT CTTTTTCAAT CTAAGTGGCT TTGTGACAAA CTTACTGAAC TTAGTGCCAT 60

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ATTATAGCCG AATGCCCAAA ATAGATTTTG ACGAATATTA CGAATGGTTG CTTTACTTGC 180
 ATAAATGGCT TTAGGAATAA GCATCAAGTC GCCACCAAGA ATAGTAATAT CAGCTGCTTC 240
 5 AATGGCAACT TCTGTACCTG TACCAATGGC GATACCGATA TCAGCTTTAA CTAAATGCAG 300
 GTGCATCATT TACACCGTCA CCAACCATCG CAACCTTCTT ACCTGTTGGC TGTAGTTTCG 360
 10 CAATTGTGGC AGCTTTTTnC TTCCGnGAA AATATCnGGC 400

(2) INFORMATION FOR SEQ ID NO: 3837:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3837:

AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC CCCTCCAGCT TATTCATATA 60
 ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC GCCGACCCTC TGCTTGTAAG 120
 25 GCAGATGCTC TCCCAGCTGA GCTAATTCTC CAAAATAATG ACTCCTACGG GACTCGAACC 180
 CGTGTTACCG CCGTGAAAGG GCGTGTCTTA ACCGCTTGA CCAAGGAGCC ATGGCTCAAC 240
 30 AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 300
 TGTGGGATTA ATATTATGCC TGGCAACGTT CTACTCTAGC GGAAGTAAn TCGGACTACC 360
 ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGG 400

35 (2) INFORMATION FOR SEQ ID NO: 3838:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3838:

AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC TACTAAACTC 60
 GTTGCCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA GCCATTTTTC 120
 50 TTTGTGTTTA TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180
 ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG AAGTAATTGG 240
 GCTACCATCG ACGCTAAGAA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 300

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TCAGATCCAA ACGTTTTTCAn TCGnCCAAGC CAATTTCCT

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(2) INFORMATION FOR SEQ ID NO: 3839:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 416 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3839:

15	TTACGGCCGC CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGTAGAcrc GACTCCTCTT	60
	AACCTTCCAG CACCGGGCAG GCGTCACCCT gATAcATCAC CTTACGGTTT AGCAGAGACC	120
	TGTGTTTTTG ATAAACAGTC GCTTGGGCCT ATTCACTGCG GCTCTTCTGG GCGTTAACCC	180
20	TAAAGAGCAC CCCTTCTCCC GAAGTTACGG GGTCATTTTG CCGAGTTCCT TAACGAGAGT	240
	TCGCTCGCTC ACCTTAGAAT TCTCATCTTG ACTACCTGTG TCGGTTTGCG GTAGGGcACC	300
	TATTTTCTAT CTAGAGGCTT TTCTCGGCAG TGTGAAATCA ACGACTcGAg GACACAATGT	360
25	CTTCTCCCCA TCACAGtTCA GCCTTgAACG rGTaCCGGAT TTGnCTAATG ATTCAG	416

(2) INFORMATION FOR SEQ ID NO: 3840:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3840:

40	AAGTTAGGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT	60
	TCCTCTCCTT CGGCTCTCGC TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT	120
	CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTACTTTT	180
45	TATTTTGACG TTTTAGACAT AAAAAAGAG ACCTCACGGT CTCAAACTTG CCTGGCAACG	240
	TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT	300
	GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA	360
50	CTCGTTGGnG CTCTTTTCTT CGGTTTnGTC AGAnTTCAAA	400

(2) INFORMATION FOR SEQ ID NO: 3841:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3841:

	CGCGACTGAn GAATACAATG nCTACGATAA CTAAACCCAA TCAATCTTTT CATTCTATCA	60
10	ATTCTTTTCA AAATCTTCAC TATATATCAT TAATGTCTAC GTATGAATCT AGCTAGAACA	120
	TTCCCTAGCG TTTGAATCAC TTGGACAATA ATGACTAATA CAATAACGGT AATAATAATG	180
	ACCGTCGTAT CAAATCTTTG ATAACCATAC ACTAAAGCTA AGTCTCCTAT ACCACCACCG	240
15	CCAACAGCTC CTGCCATCGC CGTACTTCCA ATAAGTCCAA TAATCGCAGT GGTAATTGCT	300
	AATACTAACG AACCTAAAGC TTCAGGAATT AAAAAATATC TAATGATTG TAGTGGTGAA	360
	GCGCCCATCG CTTTCGCCGC TTCAATAATC CCCTCGTCTA	400

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(2) INFORMATION FOR SEQ ID NO: 3842:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3842:

	TCGCGATTTCG CGTGTTCAGA AATCATCGGC ATCGCGTCAT TCAATGATTC ATATGCATCT	60
	AAAGCAATAG AAGATAATGT GTCTGGCACA TATACCCATG CCAACGTATC AGTAGACGTA	120
35	TGATGTTCTG CTACCGCAA AACAGTTGTC TCTGGAATAT ACACACCTGA TTGTTTTAAT	180
	CCTTGTCTGA CATTGGACG ATTACATATC ATCGCTAATA ACTTAGCATT AAAACCGCTT	240
	GATGCGCCAC CACAAGCCCC ACATTCAAGT GATGCATGAT GTGGATTATT GTGAGAATGA	300
40	CTAGCATGAC CTGCTAACAC AACGAACGGC GCAAATGCTT CGGkTAAATC CATCAATTC	360
	AACGCTgTAA CGCGAATCAA TTGCTCTGCT CAGTAAATCC	400

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(2) INFORMATION FOR SEQ ID NO: 3843:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3843:

5 GCCAACATCC TAGTTGTCTG GGCAACGCCA CATCCTTTTC CACTTAACAT ATATTTTGGG 120
 ACCTTAGCTG GTGGTCTGGG CTGTTTCCCh GTCGAACACG GACCTTATCA CCCATGTTCT 180
 GACTCCCAAG TTAAATTAAT TGGACATTCG GAGTTTGTCT GAATTCGGTA ACCCGAGAGG 240
 GGCCCCCTCGT CCAAACAGTG CTCTACCTCC AATAATCATC ACTTGAGGCT AGCCCTAAAG 300
 10 CTATTTCCGA GAGAACCAGC TATTTCCAGG TTCGATTGGG AATTCTCCGC TAACCTCAGT 360
 TCATCCGnTC ACTTTCAACG TAAnTCGGGT CGGGTCTCCA 400

(2) INFORMATION FOR SEQ ID NO: 3844:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 469 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3844:

25 ACTTTTACTT GCTGCGCCTC CAGCCAAACC TGCTGTTCCA GCACCGATCG CTGCACCTTT 60
 TTTGCCATTA TGATGATCTT TAGACTTATC TTGAGACGCT TTATCCTCAG TCGAGTTATT 120
 CGCCTTGCCA GAATTACTTT TGTTTTGAGC GTCATTTGAA TGTTCCTTAG CTTTAGAAGC 180
 30 AGCCATTGCA CCAGCTGCAC CTGCAACACC TGCTGTTCCA GCACCAATAG CTGCTGCTTT 240
 TTTACCATTA TGATGTTCTT TAGGTTTCATC TTGATCTTGT TTTACAGAAT CATTATCATG 300
 TTCATTTTTT GATGTTTCTG ATTGGTTAGC ACCTGTTGTA AAATATGGTT TAGGTTGCTG 360
 35 AGATTGTTCA GCTTCACTCT TATCAGAAAC TGTTGAATGC TCAGTGTTAT TTTCTGCATT 420
 TTTAATAGTA TCGTGTTTAn CCATTGTCCT CGAATGGGTT CnGGATGTG 469

(2) INFORMATION FOR SEQ ID NO: 3845:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3845:

50 GCTTCACTAC CAAGTAAGA AGTTGCTGAA ACTCCTGCAG CACCTGCAnC AGTAACATTA 60
 GAAGGCGACT TCCCAGAAAC AACTGAAAAA ATCCCTGCTA TCGGTAGAGC AATTGCGnAA 120
 CATGnTTTA ACTCTAAGCA TACTGCACCT CATGTAACAT TAATGGATGA AATTGATGTT 180

55

TTAACATTCT TACCTTATGT TGTAAAGCA CTTGTTTCTG CATTGAAAAA ATACCCAGCA 300
 CTTAACACTT CATTCAATGA AGAAGCTGGT GAAATCGTTC ATAAACATTA CTGGGAATAT 360
 5 CCGTATTGCA GCAGACACTG ATAGAGGATT ATTAGTACCT 400

(2) INFORMATION FOR SEQ ID NO: 3846:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3846:

TTAAGCTACC ATCCTCGCTA AGAACCTTTC TTGACTTGTG ACAATCGCTT GCTTCTTTCC 60
 20 TCTCCTTCGG CTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTTCTCGT 120
 TTCGTCAGAT TCAAACGTTT TCACTTCGCC AAGCCATTTT TCTTTGTGTT TACTTTTAT 180
 TTTGACGTTT TAGACATAAA AAAAGAGACC TCACGGTCTC AACTTGCCTG GCAACGTTCT 240
 25 ACTCTAGCGG AACGTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTCTT GACTTGTGAC 300
 AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTACT CATTAGCTC TACTAAACTC 360
 GTTGGCGCTC TTTTCTCGGT TCGTCAGATT CAAACGGTTT 400

30

(2) INFORMATION FOR SEQ ID NO: 3847:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3847:

ATCGTCAACT TATTATTAGA CGATGTACAA GTTACATTAG ACAAAAAAGG TATTACGATG 60
 GACGTTTCTC AAGATGCGAA AGATTGGTTA ATTGAAGAAG GCTATGATGA AGAATTAGGT 120
 45 GCACGTCCAT TAAGACGTAT TGTGAACAG CAAGTACGTG ACAAATTAC AGATTACTAT 180
 TTAGATCATA CAGACGTAA ACATGTGGAT ATAGATGTTG AGGGATAACG AATTAGTCGT 240
 50 AAAAGGTAAA TAACGACACT TTAACATATC GCGCATCAA AATGAGCATC AGGTCGCCCT 300
 TGCCTGTGGC TCATTTTTTT GAATTATTTT CCTGGGAAAA TGATTCGCTG TGTGCTGTTT 360
 TGTTCACACA ACAATCACGA TTGAATGTGC ACATGTGACC 400

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3848:

```

TTTAAAACTC TTTATTCACT CGGTTTGTCT TGGTAAAATC TATATTTTAC TTACTTATCT      60
AGTTTTCAAT GTACAAATAA TGGTGGGCCT AAGTGGACTC GAACCACCGA CCTCACGCTT      120
ATCAGGCGTG CGCTCTAACC AGCTGAGCTA TAGGCCCATC TTTTGAATG TTAAATAAAC      180
ATTCAAACT GAATACAATA TGTCACGTTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA      240
TATATCCTTA GAAAGGAGGT GATCCAGCCG CACCTTTCG ATACGGCTAC CTGGGTnACG      300
ACTTCACCCC AATCATTTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTACTIONACC      360
GGCTTCGGGn GTTACAACT CTCGTGGGTG TGACnGGCGG      400

```

(2) INFORMATION FOR SEQ ID NO: 3849:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3849:

```

GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC      60
TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT      120
TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT      180
TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGGCATA      240
AAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT CCATTTTTTG CCTGGCAACG      300
TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTGACTTGT      360
GACAATCGCT TGCTTCTTTC CTnTCCTTCG GCTCTCGCTT      400

```

(2) INFORMATION FOR SEQ ID NO: 3850:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 463 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3850:

5 GTCTACTAAT GTTACAACCA CACCTGATTa ATTGCTTTTT TAGCAGTAAT TGCCACATCT 60
 GTGTGACGAT AATGATATGC GACAGTTAAT AATTTGTGAT TTTTATTAGC CGCTTCAATC 120
 ATGCGATCAC ACTCTTCCGT CGTCATCGCC ATTGGCTTTT CACACAATAC ATGGACACCA 180
 10 TGGTTCAATG CTTCTATAGA AAGATCAGCA TGAATTTAT TAGGTGTACA AATGACCACC 240
 GCATCAACAA GTTTAAACAG CTCGCTAGGT GTCTCAACTG CATGAGGTAT ATTAAAGCGC 300
 TTCGCAACAT CAATCATCTG CACTGTATTA ATATCTTGTA CTGCAACTAA TGAGACTGTG 360
 15 TCTTTGAGTT TCAGCAATGC TGAATATGA CGGTCTTGTC CAATACCACC AACAACTATG 420
 CACACCAACT TTAAaTTTG TnCATGATGT GCCnGCTTnA CCG 463

(2) INFORMATION FOR SEQ ID NO: 3851:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 628 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3851:

30 TATGCTCTAA TGCTGGGCTT AGTGGATTTC ACCAACGAGT GACGnAGTCA AAGTChGTTG 60
 CTTTACGCTT GGCTATAGCC CCAATATATA GATGTTGGAG GGGGCAGATT CGAACTGCCG 120
 AACCcGAAGG AGCGGATTTA CAGTCGCGCcG CGTTTAGCCA CTTGCTACC CCTCCAGCTT 180
 35 ATTCATATAA TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCTCT 240
 GCTTGTAAGG CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG 300
 ACTCGAACCC GTGTTACCGC CGTGAAAGGG CGtGTcTTAA CCGCTTGACC AAGGAGCCAT 360
 40 GGCTCaCAGG TAGGACTCGA ACCTACGACC GATCGGTAA CAGCCGATAG CTCTACCACT 420
 GAGCTACTGT GGaTTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTtCG 480
 GACTrACCAT CGACGCTgAA GGAGCTTAAa CTTCTGTGTT CgGCATGGGa ACAGGTGTGA 540
 45 CCTCCTTGCT ATAGTCACCA GACATATGGA ATGTGAATTT GATGACATTG CAAAAnTAGn 600
 TTAGTAAGTA AAAGTGGATT TTGGnTTn 628

(2) INFORMATION FOR SEQ ID NO: 3852:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3852:

5 TAAAGATTTA AAAGTAGCTG TTATTGGnAC AGGTCGAATT GGCCGTGTAG TAGCCGATAT 60
 ATTTGCCAAT GGTATCAAAA GTGATGTGGT CGCATACGAC CGTTTCCTAA TGCTAAAATT 120
 GCAACGTATG TCGATTACAA AGATACGATT GAGGAAGCGG TTGAAGGTGC TGATATCGTG 180
 10 ACATTACATG TACCTGCAAC GAAATATAAT CATTATCTAT TTAATGCTGA ATTATTTAAA 240
 CATTTTAAAA AGGGCGCnTA TTTGTCAATT GTGCGAGAGG TTCTTTAGTA GGATACTAAG 300
 GCGTTATTAG ACGCATTAGA CAATGGTGTG ATTAAAGGTG CAGCACTTgn TTACGTATGG 360
 15 ATTTGGAACG GCAAACTTTT TCCCAAGTGG TCCAAAGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3853:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3853:

TCTTAAACAT TAGCCACAGC TAATTGTGAC TTAAAAATAG GAATACATGA GTAAAACTCA 60
 30 TCATAAGAAA TACTAATTTC TATAGAAAAA GTATTACTTT ATCGTTGTCC CACCCCAACT 120
 TGCACATTAT TGTAAGCTGA CTTTCCGCCA GCTTCTGTGT TGGGGCCCCG CCAACTTGCA 180
 CATTATTGTA AGCTGACTTT TCGTCACTTG CTGTGTTGGG GCCCCGCCAA CTGTCACATT 240
 35 ATTGTAAGCT GACTTTTCGT CACTTnCTGT GTTGGGGCCC CGCCAACTTG CATTGTCTGT 300
 AGAAATTGGG AATCCAATTT CTGCTATGTT GGGGCCCA CA CCCCAACTnC GCATTGCCTG 360
 TAGAATTTCT TTTCGAAATT CTCTGTGTG GGGGCCCA 400

(2) INFORMATION FOR SEQ ID NO: 3854:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3854:

50 GTGCAATCTG CGTTAACAAA TGTAATCGT GTCAATGAGC GATTAACGCA AGCAATTAAT 60

55

5 GAAATCAATA nATCAGTAAC TACTGATGGT ATGACACAAT CATCAATCCA AGCATATGAA 180
 AATGCTAAAC GTGCGGGTCA AACAGAATCA ACAAATGCAC AAAATGTTAT TAACAATGGT 240
 5 GATGCGACTG ACCAACAAAT TGCCGCAGAA AAAACAAAAG TAGAAGAAAA ATATAATAGC 300
 TTAAACAAG CAATTGCTGG ATTAnCTCCA GACTTGGCAC CATTACAAAC TGCAAAAnCT 360
 CAGTTGCAAA TGnTATTGTC AGCCACGAGT ACGGCTGGTA 400

10

(2) INFORMATION FOR SEQ ID NO: 3855:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3855:

TGTGTGAAAA ACCAATGGCT GAAAACGACA GCAGAAGCTC AAAAAATGAT AGATACAGCT 60
 AAATCAACAG GTAAAAAATT AACAATAGGT TATCAAAATC GTTCCGAGC AGATAGTCAA 120
 25 TTTTACATC AAGCAGCGCA ACGTGGCGAC TTAGGAGACA TTTACTTCGG AAAGGCACAT 180
 GCCATTCGTC GTCGAGCAGT ACCAACATGG GGTGTCTTTC TAGACGTAGT AAGCTCAAGG 240
 TGGAGGACCA TTAATCGATA TCGGTACACA CGCTTTAGAT TTAACGTTAT GGATGATGGA 300
 30 TAnTTATGGA ACCAGAATCA GTGATGGGTT TCAACATTCC ATAAATTnAA TAAACAGCCT 360
 CATGCGGGCA AACGCTTGGG GTTTCAGGnG TTCCAGATGG 400

35

(2) INFORMATION FOR SEQ ID NO: 3856:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3856:

45 CGTTCTCAAT AGAATGATTT AAATCTTCGA TTTCTTTATC TAAATGACTA CCAATTAAAT 60
 CTATTTCTTC TATTGTTAAA TCGCTATCTC CATCTTCTTT TATCTCTGGT ATTATTTTTT 120
 CTTCAACTAA GTCACGATAT AATGTTTTTG AATTTTCGTT CAATTTGAT TCGTGATTTT 180
 50 GAATACTTTT CTTCCACACA AATGTATATC TATTGGCATT AGCTTCTACT TTTGTACCAT 240
 CAATAAAAAT TGAATTATTA TCAATAAGAT TTTGCTTTAA ACATTGACTA TGGAAGTAA 300

55

TATAAGAAGG nGGTTGGAnC nTGAGCGAAC CACAnCATCC

400

(2) INFORMATION FOR SEQ ID NO: 3857:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3857:

15 GGCATACCAT GGTCAAACGC GTGATGATCA AGTAACATCA CATGTTCAAC ATATTTTTGA 60
 AGTTGTGAAT GCACATGGTA AACATTTTTG TGCATTACCA CGTGAAGATG AAGATATTGC 120
 AAAATGGCAG GCACAAGGTG TACAAACATT TATTTTAGGT GATGATCGCG GAAAAATATA 180
 20 TCGCCATTTA AGTGCATCTC TAGCGACGTC TAAACAGAAA GGGGATGAAG GCTAATGCGT 240
 AAAGTTCAAC CTGTTATTGA ACAATTAAAA GCACAATCTC ATCCAGTTTG TCATTAnATC 300
 TATGATTTAG TCGGACTGGG ACATCATTTG CAnCATATTA CATCGnCCTT GCCGAGTAAT 360
 25 TGTCAAATGT ACTATGCAAT G 381

(2) INFORMATION FOR SEQ ID NO: 3858:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3858:

GCATGAAGCC CCCCTCAAGA TGAGATTTCC CAACTTCGGT TATAAGATCC CTCAAAGATG 60
 40 ATGAGGTAA TAGGTTGAG GTGGAAGCAT GGTGACATGT GGAAGCTGAC GAATACTAAT 120
 CGATCGAAGA CTTAATCAAA ATAAATGTTT TCGACAATT CACTTTTACT TACTATCTAG 180
 TTTTGAATGT ATAAATTACA TTCATATGTC TGGTGACTAT AGCAAGGAGG TCACACCTGT 240
 45 TCCCATGCCG AACACAGAAG TTAAGCTCCT TAGCGTCGAT GGTAGTCGAA CTTACGTTCC 300
 GCTAGAGTAG AACGTTGCCA GGCAAAAAAT GGATGCCGAT GGAGCCGCAT TGAGACCGCA 360
 50 GGnCThTTTG TTTTTATGT CTAAAACGTC CAAATTAAnA 400

(2) INFORMATION FOR SEQ ID NO: 3859:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 573 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3859:

	GTTTATTAAT CGTGTCAATTA GCATCTTTAT AATTGCTTCT AATCGTATTC AAATCACCTA	60
10	ATGTTAAATC TGTTTTAACA TTATTTTGAA TTTCATTCAT GCATCTGAAT CTGAATCGCT	120
	ATCTGAATCT GAGTCGTTGT CTGAGTCCGA nTCGCTATCT GAnTCTGAGT CGCTGTCTGA	180
	ATCTGAATCG CTATCCGAGT CTGAGTCGCT ATCTGAGTCT GAGTCGCTAT CTGAATCTGA	240
15	ATCGCTGTCT GAGTCTGAAT CGCTATCTGA GTCTGAATCG CTGTCCGAAT CTGAGTCGCT	300
	ATCTGAATCT GAATCGCTAT CTGAATCTGA GTCGTTGTCT GAGTCCGAAT CGCTATCTGA	360
	ATCTGAGTCG CTATCTGAGT CTGAGTCGCT ATCTGAATCT GAGTCGCTGT CTGAATCTGA	420
20	ATCACTGTCT GAGTCTGAGT CGCTGTCTGA AGTCTGAATC GCTGTCAGAA TCTGAGTCGC	480
	CAACTGAGTC TGAATCTGAA TCACTGGTCT GAGTCCGAAT CGCnATCTGA ATCnGAATCG	540
25	CnAACCGAGT CCGAAGCCGC nAATCCGAAT CTG	573

(2) INFORMATION FOR SEQ ID NO: 3860:

(i) SEQUENCE CHARACTERISTICS:

30	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3860:

	GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG GATCGAACCG	60
40	CTGACCTCCT GCGTGCAAAG CAGGCGCTCT CCCAGCTGAG CTAAGCCCCC ATAATAATTA	120
	CAGTATATCG GGAAGACAGG ATTCGAACCT GCGACCCCTT GGTCCCAAAC CAAGTGCTCT	180
	ACCAAGCTGA GCTACTTCCC GTATAATTAA CGCGCCCGAT AGGAGTCGAA CCCATAACCT	240
45	CTTGATCCGT AGTCAAACGC TCTATCCAAT TGAGCTACGG GCGCATATGT TTTTATTGnA	300
	AAATGGTGCC GAGGnACCGG GAATCGGAAC CGGTACGGTT GATnCACTCA CCGGCAGGAT	360
	TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGnGC	400

50

(2) INFORMATION FOR SEQ ID NO: 3861:

(i) SEQUENCE CHARACTERISTICS:

55	(A) LENGTH: 400 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3861:

5 TGTTGCGACT AAACCATTAC CTATCGCACA TATGACGAAA CCAATGATAA CTGCAATGAC 60
 ATATTGTGAT GCCAATAATT GAGTCATGCT AATAATAGTG ATGCCGATGA CAGGGAACAA 120
 CGGACCAATG ATGAGCATCA ATTTGCCACC GAAACGTAAT GTTGCTTTTTT CACCTAAACG 180
 10 AATCATCGCA ACTGCCACAA TGGCATATGG CAATGTAACA nGTCCAGATT GCGCACTGAT 240
 AAACCAAGGT GTGTTTGAGC ATATATGAAA AAGACCACTG TTACGCCTAG ACCGCTATTT 300
 AAAACAAAGT TATTTAAAAA TGCACCAATG GAACGGACGG TTGCGTAATA CTGGAGAAnt 360
 15 CAATAAAAGG TACTTCCATG TCCGACGTTC CGATGGATGG 400

(2) INFORMATION FOR SEQ ID NO: 3862:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3862:

GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGA ATTAGGGATC 60
 30 GGTACTTTAT ATGAAGACGT GCTGCTTCCA TTAAATGAGT GATGCGATTT TGGCATGAAG 120
 GTCACCTTAA ATGTACATTG TTGTAATAAA ATTGCCTATA AATTTTTAGC ACATAAAATA 180
 AGAGGAGCCA ACCATTGTGA GACTATAACA ACGGTTGGCT CTTAATTGT AAAAAGAAAA 240
 35 CCATACGCTA TCGGTATGGT TCAGAAAAGG TCTACCATTG TCACCAAAAA TGCATCTCTA 300
 CGTGCTAGAA TAAATATTGG TCAGCCAACC AAAATAATCC ACACGGGGAG ATGCTATTTA 360
 ATGTCTCCT GACACCAACA GTTAGCACCA TACAAAATGG 400

40 (2) INFORMATION FOR SEQ ID NO: 3863:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3863:

TCGGCAAGCC ATTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAA 60

55

CTAGCGGAAC GTAAGTTGGC TACCATCGAC GCTAAGAACC TTTCTTGACT TGTGACAATC 180
 GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG 240
 5 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG 300
 TGTTCGCTTT TTATTTTGAC GTTTTAGACA TAAAAAAAAG AGACCTTGCG GTCTCAAATG 360
 10 CGGCTCATCG CATnCATnT TGCCGGCAAC GTTCTACTCT 400

(2) INFORMATION FOR SEQ ID NO: 3864:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3864:

GTACTATAGA ATTAAAGAAT TATAAAAATA TAATCCTGAT TAGCTTGTTG TCAAGTCATC 60
 GTTCATAATG AAGATATCAC GTTCAATTGT ATTGTTTGTT TATGGGAAAT GAATTAATGT 120
 25 AATAGTATAT GTATGCGGTT ACATAAAAAG CGAACATCTA ACCTGATATT TAAATGAACC 180
 TGACGCTCAA TCAACTAATT TACAACCGTA TTTTATAAT CAACCATAAA GGAGGAGATA 240
 30 GAAATGAAT AGTGCAAAAT TGATTGATCA CACTTTATTG AAGCCTGAGT CAACACGTAC 300
 GCAAATCGAT CCAAATCATC GATGAAGCGA AGCATACCAT TTAAATCTG TATGTGTGAA 360
 TCCAACGCAT GTTAAAnGTG CCAGCAGAGC GACTAGCTGG 400

(2) INFORMATION FOR SEQ ID NO: 3865:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3865:

GCAGCACGTC TTCATATAAA GTACCGATCC CTAATTCAAC GCATGTAGTA CCACATCTTC 60
 AAAGCTTGAT AGTTCCCATG CGCACACCAC GTTTCATACT AGCTATGCGA GCTCAACTTG 120
 50 GTTCATAAAC TCTTTAATAT AAGTCAATGT TTCAACCATC GCTGGTGGTC TTGGCACATG 180
 TCCTTCTGCC ATTTGATAAA ATGTTTCATG CGTGGCACCT TTAACTCTA GTTGGTCCGC 240
 TAAATAATAC GCATGATGAA TACCAACTTG CTGGTCTTTC CCTCCATGTA CAATTAATAT 300

TTTTTTCGGA TGACCAATCA TTCTTCGTAG CATGCCTCTT

400

(2) INFORMATION FOR SEQ ID NO: 3866:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3866:

AAGTCAATAA CTTTTTTTAT CTTGTCCATT TTATTTTTTA ACCAAAATTT GATTAAAAAA 60
 CTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTCGA nCTACCATCG ACGCTAAGGA 120
 GCTTAACTTC TGTGTTCCGC ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA 180
 TATGAATGTA ATTTATACAT TCAAACTAG ATAGTAAGTA AAAGTGATTT TGCTTCGCAA 240
 AACATTTATT TTGATTAAGT CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT 300
 GCTTCCACCT CGGAACCTAT TAACCTCATC ATCTTTGGAG GGGATCTTAT AACCGGAGGT 360
 TGGGGnAAAT CTCATCTTGA GGGGGGGCTT CCAGGCTTAG 400

(2) INFORMATION FOR SEQ ID NO: 3867:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3867:

CACCTATAAT CGTTTTAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT GnCGATTGGA 60
 TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC 120
 TGTGATGGGG AGAAGACATT GTGTCTTCGA GGTCTTGAT TTCACACTGC CGAGAAAAGC 180
 CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC AGGTAGTCAA GATGAGAATT 240
 CTAAGGTGAG CGAGCGAACT CTCGTTAAGG AACTCGGCAA AATGACCCCG TAACTTCGGG 300
 AAGAAGGGTG CTCTTTAAGG TTAACGCCCA GAAGAGCCGC ATGAATAGGC CCAAGCGACT 360
 GTTTAnTCAA AACACAGTCT CTGCTAAACC TAAGGATGTA 400

(2) INFORMATION FOR SEQ ID NO: 3868:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3868:

	TTCTTTGGAA ATAGTAACGT TGAAGTTGTA CTCACTGGTG ATACATTGA TCACTGTTTA	60
10	GCTGAAGCTT TAACTTATAC AAGTGAACAT CAAATGAnCT TTATAGATCC ATTCAATAAT	120
	GTTCATACAA TTTCTGGACA AGGTACGCTT GCTAAAGAAA TGCTAGAACA AGCAAAGTCT	180
	GACAATGTTA ACTTTGATTA TCTATTTGCC GCAATTGGTG GTGGCGGTTT AATTTCAGGT	240
15	ATTAGTACTT ACTTTAAAAC CTATTCACCT ACCACGnAAA TTATAGGTGT TGAACCTTCA	300
	GGTGCCAAGT AGTATGTGAT GGAATCTGTT GTGAAATATT CAGGTAGTCA CATTGCCCTA	360
	AnTCGATAAA TTGTGGACG GTG	383

20

(2) INFORMATION FOR SEQ ID NO: 3869:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3869:

	CTAAGCTTAA GGGTTGCGCT CGTTGCGGGA CTTAACCCAA CATCTCACGA CACGAGCTGA	60
	CGACAACCAC CACCTGTCAC TTTGTCCCC GAAGAAGnGC TCTATCTCTA GATTGTCAAA	120
35	GGATGTCAAG ATTTGGTAAG GTTCTTCGCG TTGCTTCGAA TTAAACCACA TGCTCCACCG	180
	nTTGTGCGGT TCCCCGTCAA TTCCTTTGAG TTTCAACCTT GCGGTCGTAC TCCCCAGGCG	240
	GAGTGCTTAA TGC GTTAnTG CCAGCACTAA GGGGCGGAAA CCCCCTAACA CTTAGCACTC	300
40	ATCGTTTACG GCGTGGAATA CCAGGGTATC TAATCTGTT TGATCCCCAC GGTTTCGCAC	360
	ATCAGCGTCA TTTACAGACC AGAAAGTCGn CTTCGGCAAT	400

45

(2) INFORMATION FOR SEQ ID NO: 3870:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3870:

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GTGTGCCTTC TGATATGCTA TGTATTCACA TATCGATAAC ATGACATAAC TCATGCTGGG 120
 TTTCCCCATT CGGAAATCTC TGGATCAAAG CTTACTTACA GCTCCCCAAA GCATATCGTC 180
 5 GTTAGTAACG TCCTTCATCG GCTTCTAGTG CCAAGGCATC CACCGTGCGC CCTTAATAAC 240
 TTAATCTATG TTTCCATCCT ACAGGAAACG CGTTATTAAT CTTGTGAGTG TTCTTTGAA 300
 CATGAGCGAT TATTTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC ACTCGGTTTT 360
 10 GCTTGGTAAA AGCnnGn 377

(2) INFORMATION FOR SEQ ID NO: 3871:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3871:

ATAACGTTGC CCCTCCCATG TATATCCTAC CCAAACATGA CCATCTTGTA ACATCACTTC 60
 25 TGTATAATCA CAATACCCAC CAGGTTGGAA CTGATAACCC ACTGGACAAG ATAAGAATGG 120
 CCCCACTTTT CTTACTGTGA TTGGTTGATT GCCGTTTGTG AATCTAGCAC TTTCTTCCAT 180
 GTAGTAAGTA CCATATTTAT TACGTTTCCA TGCACTTGCA ACTGGTTTAA CTGTATTACT 240
 30 TGAAGCGCTT GACTCATTAG AGACAGTGGC AACCGGTATT TTACCATCCA TGTACGCCCT 300
 AAATCTGCTT GATAAAGTAG TCTTTTAAAGT TGCAACCGCT TGTCTTCTGG GCAATAGACC 360
 35 GCGAGTTACn GGGGTCCAAA CCnTGGTGT AAAAnCGAAC 400

(2) INFORMATION FOR SEQ ID NO: 3872:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3872:

CGCTACACTA CGAGACCATT AGTAAAACGC AGGAAGAGGG ATTCTGAACCC CCGCGAGCCG 60
 TTAAGCCCCT GTCGGTTTTT AAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120
 50 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG TTATGAGCCG TTAGCTCTAA 180
 CCAACTGAGC TAAAGGTCCT AAATATAATT TTACAACTAA TAAATAGTGG CCGTGGAGGG 240

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GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG GGATCGAACC GCTGTACCTC 360
 CTGCGTGCAA ACGGGCGCTC TTCCCAGCTG nAGCTAAAGC 400

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(2) INFORMATION FOR SEQ ID NO: 3873:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 584 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3873:

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ACAGCTCACG GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 60
 CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCTTCG 120
 GTCTCGCTTA CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTCTCGTT TCGTCAGATT 180
 CAAnnGTTTT CatTCGCCAA GCCATTTTTTC TTTGTGTTTA CTTTTTATTT TGACGTTTTA 240
 GGCATAAAAA AAAGAGACCT TCGGGTCTCA AnTGCGGCTC ATCGCATCCA TTTTTTGCCT 300
 GGCAACGTTT TACTCTAGCG GAAnTAAGTT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 360
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 420
 TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTT ACTTCGCCAA 480
 GCCATTTTTT TTTGTGTTTA CTThTnATTT TGACGTTTTA GACATAAAAA AAAGAGACCT 540
 TCGGTCCCAA ATCGGGCTC ATCGCATCCA TTTTTTGCCT GGGC 584

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(2) INFORMATION FOR SEQ ID NO: 3874:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3874:

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TTTGCTGGC AACGTTCTAC TCTAGCGGAA CGTAAntTGG CTACCATCGT CGCTAAAGAC 60
 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT 120
 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180
 TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAA 240
 GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300

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GCTTGCTTCT TTCCTCTTCT TCGGCTCTCG CTTACTCATT

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(2) INFORMATION FOR SEQ ID NO: 3875:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3875:

TCTGCTAATT TAAAAATGAT ATTTTCTATC TTTTCTTTAT TATTAACGTC TAATGCACTG 60
 GTCGATTCAT CTAATAAAAG AATATCCGGT GTATACATCA GTTGCGCGC TATAGCAATT 120
 CTTTGCCGCT CACCACCCGA CATATTTTCC ACTTCCGAAC TTAATTGATA ATGTCCCAAA 180
 CCGACATCTT TAATTAATTG CTTTGACAGT TTTCTATCAA ATTTATCATT ACGTGCAAGT 240
 GATGGGAATA TCATGTTATC TTCAATCCGT CACCAAACAA GTCACTTTGC TGCATCAAAT 300
 AACTGATTCTG TTGACGCCAA TTCTTCCGGG GCATAATnCA TATAGGGGTT ACCTTAAAAA 360
 TAAAGGTCCT CCACTAGTTG GCCTAnACnA ATTACATAAn 400

(2) INFORMATION FOR SEQ ID NO: 3876:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3876:

AGATAGACTT TCTGGTGAAG ATACACGTGA AGGTATGACA GCAATTATAT CTATCAAACA 60
 TGGTGATCCT CAATTGGAAG GTCAAACGAA GACAAAATTA GGTAATTCTG AAGTGCGTCA 120
 AGTTGTAGAT AAATTATTCT CAGAGCACTT TGAACGATT TTATATGAAA ATCCACAAGT 180
 CGCACGTACA GTGGTTGAAA AAGGTATTAT GGCGGCACTG CACGTnTTGC TCGGAAAAAA 240
 GCGCGTGAAG TAACACGTCC GTAAATCAGC GTTAGATGTA GCAAGCCTTC CAGGTAAATT 300
 AGCCGATTGC TCTAGTAAAA GTCCTGAAGA ATGTGAGATT TCTTAGTCGA AGGGGCTCTG 360
 CCGGGGGGTC TACAAAATCT GGTCGTGACT CTAGACCGCA 400

(2) INFORMATION FOR SEQ ID NO: 3877:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3877:

	ACCAATTTCT CCTTTGTATC CGCCATCTTT AAATAATTTT ACTGCTCTAG CATGAGCCAC	60
10	CATCATGTTA TGTGATTGGA ATACTTTTTC AAAATCATAT TTAATACCTG GAGGGAATTT	120
	ACCTACTAAA TATTGACCAT CACCAATAGG TCCAATTTCA TTGAATGTAG TCCAATATTT	180
	TACTTCTGGG AATTCTTTAA AACAATATTC AGCATAATCT ACAAAGTAGT CAATCGTTTT	240
15	ACGnTTTGA AATCGCCAT CTTTGGTGGT ACACCTCTGG GnGTATCAAA ATGnTGCAAT	300
	GTTACAAATG GTTCAACATG ACGGTTTATG GnCACTCTGC AAATAACCTT ATGGTAATAC	360
	TCAACACCTT AGGGGTTAAC TTCGGCCATA TCCCTTTTGG	400

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(2) INFORMATION FOR SEQ ID NO: 3878:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3878:

	ATTAAAGCAG TTTCTGGATC TGGTAAAAAT GGTCGTATTA CAAAAGAAGA TG TAGATGCA	60
	TACTTAAATG GTGGTGCACC AACAGCTTCA AATGAATCAG CTGCTTCACT AACAAGTGAA	120
35	GAAGTTGCTG AAACCTCTGC AGCACCTGCh GCAGTTAACA TTAGAAGGCG ACTTCCCAGA	180
	AACAACCTGGA AAAAAATCCCT GGCTATGCGT AGAGCAATTG CGAnAACATG GGTTTAACTC	240
40	TAAGCATACT GCACCTCATG TAACATTAAT GGATGAAATT GGATGTTCAA GCATTATGGG	300
	GATCACCGTA AGAAATTTAA AGAAATCGCG GCTGAACAAG GTACTAAGTT AACATTCTTA	360
	CCTTATGTTG TTAAnGCACT GTTTTCGGCA TGGnAAAAAT	400

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(2) INFORMATION FOR SEQ ID NO: 3879:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3879:

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TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 120
 TGCGGCTCAT CGCATCCATT TTTTGCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG 180
 5 GCTACCATCG ACGCTAAGAA CCTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTT 240
 CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TGCGCTCTTT TCTCGTTTCG 300
 TCAGATTCAA ACGTTTCACT TCGCAAGCCA TTTTCTTTG TGTTGCTTTT ATTTGACGTT 360
 10 TAGACATAAA AnAAGAnCCT TGCGGnCTCA ATGCGGCCAT 400

(2) INFORMATION FOR SEQ ID NO: 3880:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3880:

TAGGTGTAAA TCCTGCGATT CGATCTGGAC CATATTTTTT TATTGTATAC AGTAATTGTG 60
 25 CTGCGATTAT CTCTGTAACG TCTTTCCAAT TTGAACGCAC GTGCCCTCCC ATACCTCGGG 120
 CTTGCTTATA TTGTTTGGCT TTGTCTTCAT TTTCAACAAT AGACGCCCAT GCAGCAACGC 180
 GATTACCATT GTTTTCTTCT AATGCTTCAG TCCATAAATC CCAGAGTTTT CCACGAATAT 240
 30 ATGGATATTG ATTCGAAGCG GACTGTATCA TACCAAGAGA ATGACGCACT CGTGGACATC 300
 CTCTCGGTCA TATTCAGGCA TATCCGGACA CAACTTGGAT AGCAGTTGTG ATTTCCCAGG 360
 35 AATCACACCA TTTCACAAAC TTCCAGACAT GGCTGACAGT 400

(2) INFORMATION FOR SEQ ID NO: 3881:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3881:

TGAGTAGCGA AAGACGGGTG AGAATCCCGT CCACCGATTG ACTAAGGTTT CCAGAGGAAG 60
 50 GCTCGTCCGC TCTGGGTTAG TCGGGTCTA AGCTGAGGCC GACAGnGTAG GCGATGGATA 120
 ACAGTTGAT ATTCCTGTAC CACCTATAAT CGTTTTAATC GATGGGGGGA CGCAGTAGGA 180
 TAGGCGAACG TGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC 240

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TCACACTGCC GAGAAAAGCC TCTAAGATAA GAAAATTAGG TGCCCGTACC GCAAACCGAC 360

ACAGGTAGTC CAAGATGGAG AnTCTnAAGG TGGAGCGAGC 400

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(2) INFORMATION FOR SEQ ID NO: 3882:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 609 base pairs

(B) TYPE: nucleic acid

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(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3882:

CATCCCCAAC TTGCACATTA TTGTAAGCTG ACTTTTCGTC ACTTCTGTGT TGGGGCCCTC 60

ACCCCAACTC GCATTGCCTG TAGAATTTCT TTTCGAAATT CTCTGTGTTG GGGCCCCTGA 120

20

CTAGAATTGA AAAAAGCTTG TTACAAGCGC ATTTTCGTTT AGTCAACTAC TGCCAATATA 180

ACTTCGTAGA GCATAGAATA TTGATTTATG TCCCAGCCTG AGTTAATTTT CTATAAAAGT 240

ATATTTAATT TCGGTTTATA CCGTCAAAC TCACTTTAGC TTTGTCAAAC CCTTTTCTAT 300

25

TAAGTTTTCA GAAATAAACC TATCTTAAAA TATAAAAAA TCGAGAATTC GTAGTTTAAT 360

AACGAAATTC TCGTTCTTAT CCTTTTGaAT aTACTCAATT TTCCACAAAA ACAACAAGT 420

AGTATATCTG TTCTAGCTAC TAGAATGACA TACTACTTGT TATTAAAATA CTTAACTAAA 480

30

CTTTATTAGT TATCTTTnTT CTCTATATT CTACGTGGAC TGACGCTTTT CAnGAATGTC 540

AGATTcATAA TCTTCTTGGT TGGACTCCTG GATATATTCT TGGTAAGCGG ATGGTTTATT 600

35

CGGAGTCAA 609

(2) INFORMATION FOR SEQ ID NO: 3883:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 394 base pairs

40

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3883:

ATATATTGGC GGACATAACG ATGTACTAGC AGGTGTCGTA ACCGTCAAAG ATGAATCACT 60

CGCGCAACAG TTGTTTGATT TTCACAACAT GACTGGCGCA ACACTTTCAC CAATAGATAG 120

50

TTATTTGTTG TTACGTGGAC TTAAACTTT GCATTTACGC ATTGAGCGTG CGCAATCAAA 180

CGCTAGAAAA CTTGCTAAAA AATGTCAGTC ACTTCAAGCA ATTGACGAAt ACTaTATAGC 240

55

GAAAATTTAG ACATTTGcAT TTTTGCAGAA AGTTTAGGAg GTACKGAAAC ATTAGTGACC 360
 TTCCCTTACA CCCAAACACt GTTGATATGC CAGT 394

5 (2) INFORMATION FOR SEQ ID NO: 3884:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3884:

CGATTAATGA ATTAACAGAA TACGGACCAG AAACGATAAC ACCAGGTCAT CGAGACGAAT 60
 TTGATCCGAA GTTACCAACA GGAGAGAAAG AGGAAGTTCC AGGTAAACCA GGAATTAAAGA 120
 20 ATCCAGAAAC AGGAGACGTG TTAGACCACC GGTGATTAG CGTAACAAA TATGGACCTG 180
 TAAAAGGAGA CTCGATTGTA GAAAAAGAAG AAATTCCATT CAAGAAAGAA CGTAAATTTA 240
 ATCCTGATTT AGCACCAGGG ACAGAAAAAG TAACAAGAGA AGGACAAAAA GGTGAGAAGA 300
 25 CAATAACGAC GCCAACACTA AAAAnTCCAT TAACTGGAGA ATTATTAGTA AAGGTGATCG 360
 AAAGAGGAAT CACAAAAGTT CChTTTATGA TTAACAGATA 400

(2) INFORMATION FOR SEQ ID NO: 3885:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3885:

40 TGAGCGGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG 60
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120
 CTAAGTGGAC TCGAACCACC GACCTCACGC TTATCAGGCG TCGCTCTAA CCAGCTGAGC 180
 45 TATAGGCCCA TTTTTTTGAA TGTAAATAA ACATTCAAAA CTGGAATACA ATATGTCACG 240
 TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG 300
 CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 360
 50 GACGGCTAGC TCCCAAAAGG GTACTnCCAn CGGGnTTCGG 400

(2) INFORMATION FOR SEQ ID NO: 3886:

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- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3886:

10 TACGGTAGGT GGCAAGCAGT TATCCnGGAA TTATTGGGCG TAAAGCGCGC GTAGGGGTTT 60
 TTTTAAGTCT GATGTGAAAG CCCACGGCTC AACCGTGGAG GGTCATTGGA AACTGGAATn 120
 CTTGAGTGCA GAAGAGGAAA GTGGAATTCC ATGTGTAGCG GTGAAATGCG CAGAGATATG 180
 15 GAGGAACACC AGTGGCGAAG GCGACTTTCT GGTCTGTAAC TGACGCTGAT GTGCGAAACG 240
 TGGGGATCAA ACAGGATTAG ATACCCTGGT AGTCCACGCC GTAAACGATG AGTGCTAAGT 300
 GTTAGGGGGT TTCCGCCCCT TTAGTGCTGC AGCTAACGCA TTTAAGCACT CCGCCTGGGG 360
 20 GAGTTACGAC CGCAAAGTTT GGAAACTCAA AGGGAATTGG 400

(2) INFORMATION FOR SEQ ID NO: 3887:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3887:

35 ATTTTTTAAT TTTTCATGCAA ATTTTTAAGC ACCATATAAT GCCTACCAA TTTCAATAAT 60
 CTTTGTTGCC GTTTAAATAA TGTGAATGTC AATAAATTCT CCAAACCTAGT CGAAAATAAA 120
 GGGAGTnGGA CATAAATCCC TAAAAAACA GCAGTAAGAT AATTTTCAAT TAGAAAATAT 180
 40 CTTACTGCTG TTCTCTATTT ATACAATACT TCGTATTGAA TGGCTTCGCT TTCCnAGGGT 240
 GCCGTCTCAG CCTCGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAATACT 300
 ACGTATTAAC ATGGAATTTT ACTTTTACAT ACTTTAAAAA ATAAGnCACT TTGGCCAAC 360
 45 TACTACTACCA TAGGAACCCT GGTAGGAATC CCCCAAATGn 400

(2) INFORMATION FOR SEQ ID NO: 3888:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

ATACGACAAT CACAGCAATA ATAATTGCTT TAGAAAGTCG TGCCGAACTG GAACTTACAA 60
 GTCTAGTTCG AACACACACT GATGTGAGTG GTTTTATTTA TTTTAAACAT GAACAATCAG 120
 5 ATAAGTTACT AGCATTAGCA AATATTATTA AATCAAAGGG CTTGATTCA TAAAATTAAA 180
 ACAATGATTA AAATTAGACG TGTAATGTT AAATTCTAAA ACGGAAATAA CCACCATCCC 240
 10 ATTAAACCAC TTTnATnGTT CAATCACTAT ATTTACACA GCTTCATTAA TAAAACGACT 300
 TGCTTCAACC CGCTTCAACT TCAACTGGCT TCAACTTCAG CCTACTTCAT TCAATnACAA 360
 AACGAATCCG CTTATCCAA AATCAnCCAT TCTAACGCAC 400

15 (2) INFORMATION FOR SEQ ID NO: 3889:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 485 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3889:

CCATGCnAGA CGCATACATT GTaGCTTATG GgCGTTCAGC gCAGCGAAmG aAAGCAAGGC 60
 GCATTATTCC ACGAAAGACC TGATGATGTC GCAGCCAAAG TATTACAAGG CGTATTGAAA 120
 30 CGTATTGACG GAAAATTCAA TAAGAATATG ATTGAAGATG TCATTGTTGG TACGGCTTTT 180
 CCAGAAGGAT TACAAGGCCA AACATTGCA CGAACGATTG CATTGCGTGC GGGATTATCT 240
 GACACGGTAC CGGGTCAAAC AGTGAATCGC TACTGCTCAT CAGGATTACA AACCATCGCG 300
 35 ATTGCAGCCA ATCAAATTAT GGCTGGTCAA GGAGATATAC TTGTAgCTGG TGGCGTTGAA 360
 TTGATGAGTG CCGTACCAAT GGGTGGCAAC GAGCCCACAA ACAATCCaAC CTTwACAATA 420
 tGaTGATATA GGTGCGTCCA TATnCTATG GGTtTnAAnt GCTGGAAAAT GTTAGCCTnC 480
 40 CCAAT 485

(2) INFORMATION FOR SEQ ID NO: 3890:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3890:

55 AGGCAGATGC TCTCCAGCT GAGCTAATTC TCCAAAATAA TGACTCCTAC GGGACTCGAA 60

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 180
 TGTGGGATTA ATATTATGCC TGGCAACGTT CTA CTCTAGC GGAAnTGAAT TCGGACTACC 240
 5 ATCGACGCTA AGGAGCTTAA CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT 300
 ATAGTCACCA GACATATGAA TGTAATTTAT ACATTCAAAA CTAGATAGTG AAGTAAAAGT 360
 GGT TTTGc nT CGCAAAACAT TTATTTTGn 389
 10

(2) INFORMATION FOR SEQ ID NO: 3891:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3891:

CAGATGTTA AGTCCTGTGC GTCTGCCAGT TCCGCCACCC CGGCACTATA AAAATGGAGC 60
 AGAAGACGGG ATTCGAACCC GCGACCCCAA CCTTGGCAAG GTTGTATTCT ACCGCTGAAC 120
 25 TACTTCTGCA TATGCGGGTG AAGGGAGTCG AACCCCCACG CCGTAAGCTn AGATCCTAAG 180
 TCTAGTGCGT CTGCCAATTC CGCCACACCC GCAAATGGTG AGCCATAGAG GATTCTGAACC 240
 TCTGACCCTC TGATTAAAAG TCAGATGCTC TACCAACTGG AGCTAATGGC TCTTCCATGG 300
 30 TGCCGGCCAG AGGACTTGAA CCCCCAACCT ACTGGATTTA CAAGTCAGTT TGCTCTACCA 360
 ATTGGAGCTA GGGCCGGGCA ATATGGTAAG AATAAATTGG 400

(2) INFORMATION FOR SEQ ID NO: 3892:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3892:

CTCTCGGTGG TCGTGCTACA ACTGGTAAAA ATGTACATGT AGGGGCTGGC GCAGTATTAG 60
 CAGGTGTGAT TGAACCCCTT AGTGCTTCAC CGGTTATAAT CGAGGATGAT GTATTAATCG 120
 50 GTGCAAATGC AGTTATTTTA GAAGGTGTAC GTGTTGGTAA AGGTGCTATT GTTGACGCTG 180
 GCGCGATTGT GACACAAGAT GTACCAGCTG GTGCAGTTGT TGCTGGTACA CCTGCAAAAG 240
 TGATTAAGCA AGCTTCTGAA GTACAAGATA CTAAAAAAGA GATTGTAGCA GCATTAAGAA 300

55

CCACnTAAT GGTnTAGCAT TGAATAAACT TATGnnCCCC

400

(2) INFORMATION FOR SEQ ID NO: 3893:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3893:

GAATGTAGTT GTGGTAAATA CAAACGTGTT CGCTACAAAG GCATGGTCTG TGACAGATGT 60
 GGAGTTGAAG TAACTAAATC TAAAGTACGT CGTGAAAGAA TGGGTCACAT TGAAC TTGCT 120
 GCTCCAGTTT CTCACATTTG GTATTTCAAA GGTATACCAA GTCGTATGGG TATTATTACT 180
 TGACATGTCA CCAAGAGCAT TAGAAGAAGT TATTTACTTT GCTTCTTATG TGTGTAGAT 240
 CCAGGTCCAA CTGGTTTAGA AAAGAAAAC TATTATCTG AAGCTGAATT CAGAGATTAT 300
 TATGATGAAA TACCCAGGTC AATTCGTTGC CAAAATGGG TGCCAGAAGG TCATTAAAAG 360
 ATTTACTTGA AGnnGATTGA TnCTTGACGA GGGAAC TnA 400

(2) INFORMATION FOR SEQ ID NO: 3894:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 485 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3894:

CACGTGAAGT TAGAGATACT TCATTACGTG TACCTCACGG CGCTGGCGGT ATCGTTCTTG 60
 ATGTAAAAGT ATTCAATCGT GAAGAAGGCG ACGATACATT ATCACCTGGT GTAAACCAAT 120
 TAGTACGTGT ATATATCGTT CAAAACGTA AAATTCATGT TGGTGATAAG ATGTGTGGTC 180
 GACATGGTAA CAAAGGTGTC ATTTCTAAGA TTGTTCTTGA AGAAGATATG CCTTACTTAC 240
 CAGATGGACG TCCGATCGAT ATCATGTTAA ATCCTCTTGG TGTACCATCT CGTATGAACA 300
 TCGGACAAGT ATTAGAGCTA CACTTAGGTA TGGCTGCTaA AAATCTTGGT ATTCACGTTG 360
 cATCACCAGT ATTTGaCGGT GCaAACGrTG aCGATGTATG GTCAnCAATT GAAGAAGCTG 420
 GTATGGCTCG TGATGGTAAA ACTGTACTTT ATCGATGGAC GTACCAGGTG ACCCnTCCGA 480
 TAACC 485

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 507 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3895:

GAACAACATA CCTTTGTTTG TTGATTCTTC TCCACCTGTT TCAAGTAGTT CAGATTTCTT 60
 AGATTGTGGT TTTTAGTTG GTGCCACTGc TTAAACCTTT TCATTGATTT CAATAACAGG 120
 TGTACTACT TTACCTTGTT CCACTGGTTT AGAAGGCTTT TTAGGTTCTT CTTTGGCAGG 180
 TGGTACTGGT TTACCAngTT CAGCTGGTAC CTCTGGTGTG GCGGTGTTG GAGTTTCTGG 240
 CTCACTCGGC ACTTCTGGTG TCGGTGGTGT TGGTGTTCG GGTCACTTG GTACTTCTGG 300
 TGTGGTGGc GTTGGTGTG CCGGCTCACT TGGTACTTCT GGTGTCGGTG GCGTTGGtGG 360
 CACGATTGGA gGTGTGTAT CTCTTCAAT CGTTTGTGA CCTTCATTTT GGGCCGCTTA 420
 CTTTGGGAA GTGTATCTTC TTCAAAGTCA AACTAATGT GGTCCACCGG AATTGATAAC 480
 TGGGGTTAAC CTTAAATTGG AACCTCC 507

(2) INFORMATION FOR SEQ ID NO: 3896:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3896:

CTAGCGGAAG TAATTGGCTA CCATCGTCGC TAAAGACCTT nGgGACTTG TGACAATCGC 60
 TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG 120
 CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTCACTTCG CCAAGCCATT TTTCTTTGTG 180
 TTTACTTTTT ATTTGACGT TTTAGGCATA AAAAAAGAG ACCTTGCGGT CTCAATGCGG 240
 CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAAnGTA ATTGGGCTAC 300
 CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG 360
 GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC 400

(2) INFORMATION FOR SEQ ID NO: 3897:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3897:

	TTGAAGAAGA TCGCGATGAC TATACAATCA ATATCGAGTA TAATACCGAT TTATATCACT	60
10	CAGAAACAGT TCGTCACATG GGTAATCAAT GTATGATTAT GATTGATTAT ATTTTGAAGC	120
	ATCAAGATAC ACTACAAATT TGTGATATAC CAAACGGCAC GAGGAACTTC TAAATTGGGT	180
	CAATACGCAT GTTAACGATC GAATGCTTAA TGTCCCGGGA AATAAATCTA TCATAAGTTA	240
15	CTTTAATGAA GTTGTCTCAC GACAAGGTAA TCATGTTGCG CTAGTCATGA ATGAnTTGAC	300
	AATGACGTAT GAAACATTAC GCAACTATGT GGGATGCCAT TCGGCACATG CTCCTATCAA	360
	ATGGTGTGGG CAATGGTCAA CGGGTTGCCT TGGTGTACAG	400

20

(2) INFORMATION FOR SEQ ID NO: 3898:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3898:

	GAAATCAGTA TTAAAGCAGT TAATCCACAA GGGAAAGTGG TTAATACAGT TGGCTCTGGT	60
	GATAGTACAG TTGCAGGCAT GGTGGCTGGA ATTGCTTCAG GTTTAACGAT TGAAAAAGCA	120
35	TTCCAACAAG CAGTCGCATG CGGTACTGCC ACGGCATTTG ATGAGGACTT AGCAACACGG	180
	GACGCTATAG AAAAAATAAA ATCACAAGTT ACGATTAGCG TACTTGATGG GGAGTGAAAA	240
	TAATGAGAGT AACAGAGTTA TTAACAAAAG ATACAATAGC AATGGATTTA ATGGCAAATG	300
40	ACAAAAATGG TGTATTGAT GAGTTAGTAA ATCAATTAGA CCAAGCAGGT AAATTAAGTG	360
	ATGTCGCGTC ATTTAAAnGGA AGCGATTAC CATCGnGATC	400

45

(2) INFORMATION FOR SEQ ID NO: 3899:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3899:

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CTAGCGGAAC GTAAGTTAGC TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 120
 GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTACTCATT TAGCTCTACT AAACCTCGTTG 180
 5 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG 240
 TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAGA nACCTCACGG TCTCAACTTG 300
 CCTGGCAACG TTCTACTTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC TnAAAGACCT 360
 10 TTCTTGGAAT TGTGGACAAT CGGCTTGGCA nTCTTnCTC 400

(2) INFORMATION FOR SEQ ID NO: 3900:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3900:

TGCACGCGTA TCTGATGGTT GCTCAGTTGC ATCTACCCAA GGTAACCATT CCCTAAGTGA 60
 25 ATTTCTTGAA CGATTGACTA AATTGAAAAG CGCTTCTGTG TCATGAGCTT CTAAAATTTT 120
 TAATGTTATT TGTTCAATTCA CTTTCATTCC AACATACCA TCACATCCTC ATTCATTTTT 180
 CATATAATTC TGTAATTAT CATTATAATA ACATATTAAT GTTACGCATT GTATCTTAAA 240
 30 TTTGTTGTCC TTCCCCAACT TGCATTGCTT GTAGAATTC TTTTCGAAAT TCTCTATGTT 300
 GGGGCCCCGn AACTTGCAAT GTCTGTAGAA ATTACGGACC CAATTTCTCT AGGTGGGGCC 360
 CATCCCCAAC TTGCACATTA ATnGCAAGCn GACTTTCCGT 400
 35

(2) INFORMATION FOR SEQ ID NO: 3901:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3901:

TACTGCTGTT CACTTTTTAT AATACTTCTG AATGTCTTCA CTTATACTTC TAGTCACAGA 60
 TTTAAATAAT CAAAAGTGCA CATTATTAAA ATATCAATTT CACACTCAAT GCGGCTCATC 120
 50 GCATTCATTT CTGTCTCAA CGTTCTACTC TAGCGGAAGT AAGTTAGCTA CCATCCTCGC 180
 TAAGAACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT 240

55

TTTCACTTCG CCAAGCCATT TTTCCTTGGT GGTTTACCTT TTAATTTGGA CGGTTTAGAC 360
 ATnAAAAAAG GGGACCTCAC GGGCCCAACT TGGCCTGGGC 400

5

(2) INFORMATION FOR SEQ ID NO: 3902:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3902:

15

TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60
 TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT AAAGACCTTT CTGACTTGT 120
 GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT ACTCATTTAG CTCTACTAAA 180
 CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT TTTCACTTCGC CAAGCCATTT 240
 TTCTTTGTGT TTACTTTTTTA TTTTGACGTT TTAGGCATAA AAAAAAGAGA CCTTGCGGTC 300
 TCAATGCGGC TCATCGCATC CATTTTTTGC CTGGGCAACG TTCTACTCTA GCGGGAACGT 360
 AAGTTGGGCT ACCAnCGGCG GCTAAAGACC TTTCCTGGAC 400

25

(2) INFORMATION FOR SEQ ID NO: 3903:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3903:

TTGTTATAAC GAAAACCATT AATAGATTTT TATTTGGTGA TTTCAAATCA TGAGACTGGG 60
 ACAGAAATGA TGTTTTATA AAAATTATTT CGTTGTTCCA CTCTCATGAT TTTTTTGATG 120
 AAACATAATT ACATGATTGA TTGCATCATT TTGTTAAACA AGTGATTGCA AACCTGCCAT 180
 TTCACACTGA AAATTTACAT AATAAGTGAC GATATTTTAC AAGTCATATA CAAATAACAT 240
 ATATTGTTAA ATAATTTTAC CTAATCTTAA CATTAAATTT ACAATTATAA GCGATAATCT 300
 AAATATAAAG CTTATTTGAG GTGAAATAAT GGAAATGTCG GTTACAGAAG TCATTTTCTC 360
 CTTTTTAGGT GGGTTTAGGG AATTTCCnTT ACGGCCTTAA 400

50

(2) INFORMATION FOR SEQ ID NO: 3904:

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(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3904:

10 CATAAGACAT AATCGCTAGT GTTCGAAAGA GCACTCACAA GATTAATAAC GCGTTTCCTG 60
 TAGGATGGAA ACATAGATTA AGTTATTAAG GGCGCACGGT GGATGCCTTG GCACTAGAAG 120
 CCGATGAAGG ACGTTACTAA CGACGATATG CTTTGGGGAG CTGTAAGTAA GCTTTGATCC 180
 15 AGAGATTTCG GAATGGGGAA ACCCAGCATG AGTTATGTCA TGTTATCGAT ATGTGAATAC 240
 ATAGCATATC AGAAGGCACA CCCGAGAnC TGAACATCT TAGTACCCGG AGGAAGAGAA 300
 AGAAAATTCG ATTCCCTTAG TAGCGGCGAG CGAAACGGGA AGAGCCCCAA CCAnCAAGCT 360
 20 TGCTTGTTGG GGTGTAGGG CACTCTATAC GGAGTTACAA 400

(2) INFORMATION FOR SEQ ID NO: 3905:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3905:

AACTAACATT ACAACATGCA TGTGAACAAT TAAAAACATA TTTTAAGTAG GTGAATGAAA 60
 35 TGgTAAATGA ACAAATCATT GATATTTTcAG GTCCGTTAAA GGGCGAAATA GAAGTGCCGG 120
 GCGATAAGTC AATGACACAC CGTGCAATCA TGTGGCGTC GCTAGCTGAA GGTGTATCTA 180
 CTATATATAA GCCACTACTT GGCGAaTtCG TCGTACgATG GaCATTtTTCC gACTGTTAGG 240
 40 TGTAGAAATC AAAGAAGATG ATGAAAAATT AGTTGTGACT TCCCCAGGAT ATCAATCTTT 300
 TAACACGCCA CATCAAGTnT TGTnTACAGG TAATTCGGG TACGACAACA CGATTGATAG 360
 TTTGGTTAAT GGGTTAAGTA TTGAAAGTGT TTTGTCCGG 399

45

(2) INFORMATION FOR SEQ ID NO: 3906:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

TTCTTTAAAA ATAAACGCCT ATnCGTTATC GGTGGTGGTG ATTcAGCAGT AGAAGAGGGA 60
 ACATTCTAAA CTAAATTTCG TGACAAAGTA ACAATCGTTC ACCGTCGTGA TGAGTTACGT 120
 5 GCACAGCGTA TTTTACAAGA TAGAGCATTc AAAAATGATA AAATCGACTT TATTGGAGT 180
 CATACTTTGA AATCAATTAA TGAAAAAGAC GGCAAGTGG GTTCTGTGAC ATTAACGTCT 240
 ACAAAGATG GTTCAGAAGA AACACACGAG GCTGATGGTG TATTCATCTA TATTGGTATG 300
 10 AACCATTAAC AGCGCCATTt AAnGCTTAGG TATTACnAAT GATGTTGGTT ATATTGTGAC 360
 AAAGGTGGAT TGGCCAC 377

(2) INFORMATION FOR SEQ ID NO: 3907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3907:

25 AATTAGGTAA TTCAAATAA TATTAGCGCG GGATGGAGCA GTTCGGTAGC TCGTCGGGCT 60
 CATAACCCGA AGTCGGtGGT TCAAATCCGC CTCCCcAAT ACATAGTTTT TAATTTAATA 120
 GGTCTCGTAG TGtAGCGrTT AACACGCCTG CCTGTcACGC AGAGATCGCG GGTTCGATTc 180
 30 CCGTCGAGAC CGCCATTATT ATTACCATTa CGGTTCAGTA GCTCAGTTGG TAGAGCAATG 240
 GATTGAAGCT CCATGTGTcG GCAGTTcGAC TCTGTCTGa ACCATTCTTA ATTcATGGCG 300
 GTTGTGGTGA AGTGGTTAAC ACATCGGATT GTGGTTCCGA CATTcGAGGG TTCGATCCCC 360
 35 TTCAGCCGCC CCATAATCGT TTACATTAGC GGGTGTAGTT TAATGGcAAA ACCTCAGCCT 420
 TCCAAGCTGA TGTGTGGGk TtCGrTTCCC AtCAmCCnGy TCCaTaATTT CnAAnAATTc 480
 40 CAACAGTAGC CGCAAGTnGG TA 502

(2) INFORMATION FOR SEQ ID NO: 3908:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3908:

50 AAAAAATGCA TCTCTACGTG CTAGAATAAA TATTGGTCAG CCAACCAAAA TAATCAACAC 60

5 TAAGTATCAT ATTGTCTTTG CACCTAAATA CAGAAGACAA GTGATATATG GAAAAATAAA 180
 AAAAGATATA GGGATTATAT TGCCTCAATT ATGTGAAAGA AAAGGTGTAG AGATAATTGA 240
 AGCAGAGGCA TGTAAGATC ATATCCATAT GTTAGTTAGT ATACCACCCA AACTTGGGGG 300
 TATCATCATT TGTGGGGCTA TTTAAAAGGG AAAAGTAGT TTAATGGATA TTTGGATAGA 360
 CATGGCTAAC TTAAAGTATA GATATGGGAA ATAGGAAAGT 400

(2) INFORMATION FOR SEQ ID NO: 3909:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3909:

GGTTTAACTA TTGAAGAAAA TGTGCCGACA ATTAACAAGA TAAAAAATGC GGTATATTCA 60
 GCAGATAAAG CTTTACCTAA GATTAATGAC TTTGCGAATA AAATTGTATA TTTGAATAAC 120
 25 CACCAAGCGG ATTTAGATAA ATATGCCAAT GATTTTAGAA AACTAGGAAA TTATAAAGGT 180
 GATATTTTAG ATGCTCAGAA AAAATTAAAC GAGTCAATGG TGCTATTCCG CAACTTAATG 240
 AAAAGGCTAA GTTGGATATT AGCTTTTAAA TAATTATATG CCGGAAAATT GGAAAAAGCG 300
 30 TTTAAATTTT GCAGCTGGAT GACGTGCCAC GCnGTTCCCT AAAATTAATC CAGGGCTTAA 360
 CATTGCGAGT CCAGGTATTG GntCCAAGCT AATGGGGCCG 400

(2) INFORMATION FOR SEQ ID NO: 3910:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3910:

45 TTACCCGATA TCGGAAGGT ATCCACGAAG GTGAAATTGT AAAATGGTTT GTTAAAGCTG 60
 GAGATACTAT TGAAGAAGAC GATGTTTTAG CTGAGGTACA AAACGATAAA TCAGTAGTAG 120
 AAATCCCATC ACCAGCATCT GGTACTGTAG AAGAAGTTAT GGTAGAAGAA GGTACAGTAG 180
 50 CTGTAGTTGG TGACGTTATT GTTAAAATCG ATGCACCTGA TGCAGAAGAT ATGCAATTTA 240
 AAGGTCATGA TGATGATTCA TCATCTAAAG AAGAACCTGC GAAAGAGGGA AGCGCCACAG 300

GCCATGCCTT CCAGTTACGT TAAATACGCA CGTGGAAAAG

400

(2) INFORMATION FOR SEQ ID NO: 3911:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3911:

CGTGTAnCTC AAGTTATGGG TCCTGTAATT GATGTTTCGAT TTGAACATAA CGAATTCCTA 60
 AAATTAATAA CGCCTTGGTT ATTGATGTGC CTAAAGAAGA AGGTACAATA CAACTAACAT 120
 TAGAAGTTGC GCTGCAATTA GGTGACGACG TTGTTTCGTAC AATTGCGATG GATTCAACTG 180
 ATGGTGTCCA AAGAGGCATG GATGTAAAAG ATACAGGCAA AGAAATTAGT GTACCTGTTG 240
 GTGACGAAAC ATTAGGTCGT GTATTTAATG TACTAGGTGA AACAATTGAC CTTAAAGAAG 300
 AAATTAGTGA TTCTGTTTCG CGCGATCCTA TCCATCGTTC AAGCACCAGC ATTCCGATGG 360
 AACTTTTCAA CAGAAGTTCC AAATTTTTCG GnACAGGGTA 400

(2) INFORMATION FOR SEQ ID NO: 3912:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3912:

TTGTACAAGT TGAAGAAAAA TCAACACAAC CAAAAGGTAG AAAATTCAAA GATTTCCTA 60
 GTAAATTTAA TATAGCATCA GAAGCTAAAG AAAATGAACC TATATCAGTC ATTGGTTATC 120
 CAAATCCTAA TGGAATATAA CTACAAATGT ATGAATCAAC TGGTAAAGTA TTATCAGTGA 180
 ATGGGAATAT AGTGTCTATCG GATGCAATTA TTCAGCCTGG TAGCTCTGGT TCACCTATAT 240
 TAAATAGTAA ACACGAnGCT ATTGGTGTA TCTATGCCGG TAATAAGCCA TCAGGTGAAA 300
 GCACCAGAGG GATTTGCTGT TTATTTCTCT CCTGAAATTA AGAAATTCCA TTGCAGATAA 360
 TTTAGATAAA TnATTAGAC CTAnGACATT CACCCAATCC 400

(2) INFORMATION FOR SEQ ID NO: 3913:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3913:

ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 60
 10 TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGACATAA 120
 AAAAAAGAGA CCTTGCGGTC TCAATGnGGC TCATCGCATC CATTTTTTGC CTGGCAACGT 180
 TCTACTCTAG CGGAAGTAAG TTGGCTACCA TCGACGCTAA GAACCTTTCT TGACTTGTGA 240
 15 CAATCGCTTG CTTCTTTCCT CTTCTTCGGC TCTCGCTTAC TCATTAGCT CTAATAAAGT 300
 CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AGCCATTTTT 360
 CTTTGGGGTT TGCnnTTTGA ATTTGGACGT TTTAGACATA 400

20

(2) INFORMATION FOR SEQ ID NO: 3914:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3914:

TGGAATGAGC GGATATAAGC ATCTTTAGAT AATGCACCAT CAACTAATGG ATATTTATGT 60
 CCAGTTGGAC GCCAGAAATC ATAAACGTCT TCAGTGTAAG CAACAGCATC TTCATTAAAT 120
 35 GCCAAAATGC TTGGATTATG TGCAATAACC ATCGCAACTG nGCCACACCT TGTGTTGGCT 180
 CGCCGCCTGA ATTCAATCCA TAACGTGCTG TATCTGTAGC AATAACTAAT ACTTTTTCAT 240
 TCGGTCTAGT TGCTAAATAA TCTTTAGCTA ATTGAATTGC TGGTGTGCA GCATAACAAG 300
 40 CTTCTTTCAT TTCAAAGCAG CGTGCAAAAG GTTGGnATAC CTAATAAGTT GTGGAATTTG 360
 nACAGCGGCT GCTTTACGAA TTCCAACGTC TGATTCCAGT 400

45

(2) INFORMATION FOR SEQ ID NO: 3915:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3915:

55

TCTTTATTTA TCCAGTTTCA TAGTCAATGT TTAAAGCAAA ATCTTATTGA TGGTACAAAA 120
 GTAGAAGCTA ATGCCAATAG GTATACATTT GTGTGGAAGA AAAGTATTCA AAATCACGAA 180
 5 TCGAAATTGA ACGAaAATTC AAAAACATTA TATCGTGACT TAGTTGAAGA AAAAATAATA 240
 CCAGAGATAA AAGAAGATGG AGATAGCGAT TTAACAATAG AnGAAATAGA TTTAATTGGT 300
 AGTCATTTAG ATAAAGAAAT CGAGGTTTAA ATCATTCTAT TGAGACGnGA TAGTACTCAA 360
 10 ATTAGAAACA G 371

(2) INFORMATION FOR SEQ ID NO: 3916:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3916:

ACCATGGACG ACGGTTAGGT TTATGAATGT TATTCCAAAT AGGTTTCATCT ATAAATAGC 60
 25 TTTAGTTGGA AAAGATGAGA AAAAATATAA AGATGGACCT TACGATAATA TCGATGTATT 120
 TATCGTTTTA GAAGACAATA AATATCAATT GAAAAAATAT TCTGTCGGTG GCATCACGAA 180
 GACTAATAGT AAAAAGTTA ATCACAAAGT AGAATTAAGC ATTACTAAAA AAGATAATCA 240
 30 AGGTATGATT TCACGCGATG TTTCAGAATA CATGATTACT AAGGAAGAGA TTTCTTGAA 300
 AGAGCTTGAT TTAAATTGA GAAAACAACT TATTGAAAAA CAGATCTTTA CGGTAACATG 360
 GGTTCAAGAC AATCGTATTA AATGAAAACG GGGGAATATA 400

35

(2) INFORMATION FOR SEQ ID NO: 3917:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 412 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3917:

GAGGAAATTA TTAACCTTnC GCATCGTATG GGCcTGAAG GAATAACAaC CTTTAGACCT 60
 GGAGATTGAG CTAAATACC TTCTAAGTTA TCTGCGTGTA ATTCTGGTGT GTGTACGCCA 120
 50 CCACCAAATG GGCTACGAAT TGTTACAGGT GCAGTTTTAG TACCGCCTGA ACGGAAACGA 180
 GTACGTGCAA TTTGTCCAGC AATCGCATCA AATACTTCGA ATACGAAACC TAAGAATTGT 240

55

GATTCAGCTA AAGGTGTATC GAATACTCTA TCTTCACCAA ATTCTTTTTG TAGTCCTTCA 360

GTAACACGGA AAACACCGCC GTTAACACCA ACGTCTTCAC CAnAATnAAA AC 412

5

(2) INFORMATION FOR SEQ ID NO: 3918:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

10

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3918:

ATAGATTGCT GAGTGACAAT ACTTCAGGAn TCGCATATGC AGGCCCAATA CCCATAATTT 60

TCGGGTCAAC GCCTACTGCC TTA AAACCAA CGAATCGTGC AATAGGTGTC ACGCCGAGTT 120

20

CTTTCACTTT ATCTCCAGAC ATTAAAACTA CAAATCCTGC ACCATCAGAA AGTGGGGCAG 180

ATGTTCTCTGC AGTCATAGTG CCGTCAGCTT TAAATACTGT ACGTAATTTG GCTAATGCCT 240

25

CCATCGTGGT GTCAGGGCGT ATnAAATTCA TCTTGGTCAA AGATATTTGT GTGTACTTTT 300

GGTCCTGCGT TTGTATATTC AACTGAGTTT ACTTGTATTG GGATnATTTC ATCTTTGGAA 360

CCGACCATCA CCGTGTGCGT TCATAGGCAC GTTGATGnAC 400

30

(2) INFORMATION FOR SEQ ID NO: 3919:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

35

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3919:

40

CAAGGGCAAC AAGGTGGCAA CGGCAATTAT TTAGAACAAA TTGGTCGTAA CCTTACnAAG 60

AAGCACGTGA CGGTTTATTA GATCCAGTCA TTGGTCGTGA TAAAGAAATT CAAGAAACTG 120

45

CTGAAGTTTT AAGTAGACGA ACTAAAAACA ATCCTATATT AGTTGGAGAA GCTGGTGTG 180

GTAAAACTGC GATTGTTGAA GGTTTAGCAC AGGCAATCGT TGAAGGAAAT GTACCAGCAG 240

CAATCAAAGA CAAAGAAATT ATTTCTGTAG ACATTTTCATC ATTAGAAGCT GGAACGCAAT 300

50

ATCGTGGTGC TTTTGAGGAA AATATTCCAA AATTAATCGA GGTGTTAAnc TTCACAAATG 360

CCGTACTATC TTTGATGAAn CCATCAATTA TCGGTTTCAGT 400

(2) INFORMATION FOR SEQ ID NO: 3920:

55

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3920:

10	CTTATCCCGT CCACACATAG CTACCCAGCT ATGCCGTTGG CACGACAACT GGTACACCAG	60
	AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACAGCTC CTCTCAAATT TCCTACGCCC	120
	ACGACGGATA GGGACCGAAC TGTCTCACGA CGTTCTGAAC CCAGCTCGCG TACCGCTTTA	180
15	ATGGGCGAAC AGCCAAGnCC TTGGGACCGA CTACAGCCCC AGGATGCGAT GAGCCGACAT	240
	CGAGGTGCCA AACCTCCCCG TCGATGTGAA CTCTTGGGGG AGATAAGCCT GTTATCCCCG	300
	GGGTAGCTTT TATCCGTTGA GCGATGGCCC TTCCATGCGG GAAnCAACGG ATTCACTAAA	360
20	GTCCGTCTTT TCGAACCTGG CTCGGACTTG TAGGTCTCGG	400

(2) INFORMATION FOR SEQ ID NO: 3921:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3921:

	CGGGTTGGGC AGGTATGTTG TATTACCGTT CACAGCAGCA TCACTTTGAA CAACATTTGT	60
35	TAACGGATTA TTTGGCAATT CGGTTAGTTG TCGAACAATT GCTAGTTGGT GATGAGTTTA	120
	AGTCAGTCGC TAAAGATTGT GAAAGTAGAT CGGAAAATTG GTTTAAGCAA ACTGTTGCAT	180
	CATGGTGTTA CTACAGTGGA TATGCCTAGC GATGTATTAC TACAACATGA CGTCAATGAA	240
40	ATTCAAACGT TTATTCATTT TGGCAGCAAC TATGGAATAA AAATGTATTT AAAATTTATG	300
	GCTnAATTGC CnGGGGAAAT GACATACGGG ATCTCAGTTT AAAACAAAAA TTAAAGCAGG	360
45	TCATGGAAAG TGTGGCGGGC GCCTTAGGTG TnAACCCAGT	400

(2) INFORMATION FOR SEQ ID NO: 3922:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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GTGCGCTCTA ACCAGCTGAG CTATAGGCCC ATTTTTTTGA ATGTTAAATA AACATTCAAA 60
 ACTGAATACA ATATGTCACG TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC 120
 5 TTAGAAAGGA GGTGATCCAG CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC 180
 CAATCATTG TCCCACCTTC GACGGCTAGC TCCTAAAAGG TTA CTCCACC GGCTTCGGGT 240
 GTTACAACT CTCGTGGTGT GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCACCGT 300
 10 AGCATGCTGT ATCTACGTTT ACTAGCGATT CCAGCTTCAT GTAGTCGAGT TGCAGACTAC 360
 AATnCGAACT GAGGAACAAC TTTTATGGGG TTTGnTTTGn 400

15 (2) INFORMATION FOR SEQ ID NO: 3923:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3923:

25 AGTAAGTAAA ATATAGATTT TACCAAGCAA AACCGAGTGA ATAAAGAGTT TTAAATAAGC 60
 TTGAATTCAT AAGAAATAAT CGCTAGTGTT CGAAGAACTC CACAAGATTA ATAACGCGTT 120
 30 TCCTGTAGGA TGGAACATA GATTAAGTTA TTAAGGGCGC ACGGTGGATG CCTTGCCACT 180
 AGAAGCCGAT GAAGGACGTT ACTAACGACG ATATGCTTTG GGGAGCTGTA AGTAAGCTTT 240
 GATCCAGAGA TTTCCGAATG GGGAAACCCA GCATGAGTTA TGTCATGTTA TCGATATGTG 300
 35 AATACATAGC ATATCAGAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGAGAAG 360
 AGAAAGAAAT TCGnTCCCTA GTACCGCGAn CGAAACGGGA 400

(2) INFORMATION FOR SEQ ID NO: 3924:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3924:

50 ATGCGATACG TAGCACAGCT GCAACAATCC ATGCTAGTAA AATCGGAGAC ATCTCTGTAC 60
 CTTCAAATA GCAATTGTAT TTCCGACACC GCCGTCAATT AATACTTGTT TAATGTACCG 120
 CCACCGCCAA TAATCAATAA CATCATTCGG ATTGGATAAA TCGCATTCGT CACTGATTCC 180

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5 GCTATTAGCA TGGCTGTCCC TGCTGTTCCT ATCATATAAA TGATAGATTG AAATAGATTT 300
 GTAGGGTTGT CATGCCCAGT TACAAGTTGC GTTGATCGTn GACACTAACA TTAATATGAC 360
 TGGTAATGTT GCTGTTAATA AACTCATACC AAnTCCGGGC 400

(2) INFORMATION FOR SEQ ID NO: 3925:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 525 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3925:

GGCTGGGCTA GCTGGATTG AAccAACGAG TGACGGAnAn AGGTCCGTTG CCTTACCGCT 60
 20 TGGCTATAGC CCAATATATA GATGGTGGAG GGGGGCAGAT TCGAACTGCC GAACCCGAAG 120
 AGCCGGATTT ACAGTCCGCC GCGTTTACCA CTTGCTACC CCTCCAGCTT ATTCATATAA 180
 TTTAATAATC AAAATGGTGG AGAATGACGG GTTCGAACCG CCGACCCTCT GCTTGTAAGG 240
 25 CAGATGCTCT CCCAGCTGAG CTAATTCTCC AAAATAATGA CTCCTACGGG ACTCGAACCC 300
 GTGTTACCGC CGTGaAAGGG CGTGtGCTTA ACCcTTGGAC CAAGGAGCCA TGGCTCaCAG 360
 GTAGGACTCG AACCTACGAC CGATCGGTTA AcAGCCGATA GCTCTACCAC TGGAGCTGAC 420
 30 TGTGGATTAA TATTATGCCT GGCAACGTTT TGAnnCTAGC GGAAnTGAAT TCGGACTGAC 480
 CATCGACGCh AAGGAGCTGA ACTTCTGTGT TCGGGCATGG GGAAC 525

35 (2) INFORMATION FOR SEQ ID NO: 3926:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3926:

45 TGTTATTGTT CAAAATCATG ATCAAGATCA GTATATCGTT GCTTATTATG AAGCGATGCA 60
 TACATTATCA CATAATAAGA TTAAATCACA ATTACGTATG ACCTTACCGG AGTACATGAT 120
 ACCAGTTAAT TTCATGCATA TTGAGCAAAT TCCTATTACT ATTAATGGGA AATTAGATAA 180
 50 GAAGGCATTG CCTATCATGG ACTATGTCGA TACGGATGCC TATGTAGCAC CGAGTACAGA 240
 TACCGnACAC TTGCTATGCC AAATTTTTGC AGATATTTTA CATGTGAATC AAGTAGGTAT 300

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TCCGGATAGA GGCATCCACT GGGGAACGGT TACCAATTGG

400

(2) INFORMATION FOR SEQ ID NO: 3927:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3927:

TATCGATCAA TTTCTATCGA GTTGGACAAT GCCGAACGTG ACAAAGTTTT TACCATGCAT 60

GGTTGCATTT AGCGCAACAT GACCATAGTT TTACTAAAGC ACAGCGCGCA AGTGATTAAA 120

GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT TAACTCATTT TTCAATAGAT 180

CAGGAAGACT ACCAAGCTTA TGTGAAGGA CATCTTTTGG CGTTACCGGG TTGGGCAGGT 240

ATGTTGTATT ACCGTTTACA ACAGCATCAC TTTGGAACAA CATTTGTTAA CGGATTATTT 300

GGCAATTCGG TTAGTTGTCG AACAAATTGCT AGTTGGTGGG TGAGTTTAAG TCCATCGCTA 360

AAGATGTGGA AATAGnCCGG AAAATGGTTT TAAGCAAAC 400

(2) INFORMATION FOR SEQ ID NO: 3928:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3928:

GTGCACCTAA CGCTGAAATA TCGCCTTCTC GTGTATAGCA GACGGAATCA TTTTTGTGC 60

AnTTTTGTTAA ATATAGGCCC TGCAATGAGT GTACTGGAAT GGCAATAATC ATACCATACA 120

GTAATACATC TCCAACATTT GCCTTTAATT CTTTTGCGAT GACTACCGGT CCTGGATGTG 180

GTGGTAAAAA GCCATGTGTC ACTGATAAAG CTGTTACCAT AGGTAGTCCT AGTTTAAACA 240

CTGAAACATT TCGCGTTTTT GCTACTGTAA ATACTAATGG AATCAGTAAG ACTAAACCTA 300

CTTCAAAGAA CAATGCAATA CCGACGATAA ATGCTGGCAA CAAGCATTGC CCCATTGGTA 360

CATGGTTTTT GGACCAAATT TTTGGAATCA ACGTGTCTGG 400

(2) INFORMATION FOR SEQ ID NO: 3929:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3929:

	CTCAAGGTGT TGCCTATACA GCTAAAAAAC TTAATTTAAA CGCTGTTATC TTTATGCCAG	60
10	TCACTACACC TTTACAAAAG GTAAATCAAG TAAAGTTCTT TGGAAATAGT AACGTTGAAG	120
	TTGTACTCAC TGGTGATACA TTTGATCACT GTTTAGCTGA AGCTTTAACT TATACAAGTG	180
	AACATCAAAT GAACTTTATA GATCCATTCA ATAATGTTCA TACAATTCTT GGACAAGGTA	240
15	CGCTTGCTAA AGAAATGCTA GAACAAGCAA nGTCTGACAA TGTTAACTTT GCATTATCTA	300
	TTTGCCGCAA TTGGTGGTGG CGGTTTAATT TCAGGTATTT CGTACTTACT nTTAAACCT	360
	ATTACCTAC CACGnAAATT ATAGGTGTTG AACCCnAGT	400

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(2) INFORMATION FOR SEQ ID NO: 3930:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3930:

	ATATGATCCT ATGAAGCAAT TTTATGTAGT AAGTGGTTCT AAACATGACG CCCTTATGCT	60
	CTGTGAACAT TTATATGACG AGGTTATGGC TGTTTGCTAA nCCCAAATGA TACATCGAAT	120
35	GGCACATATC ATTCGTCGCA ATATGATTAC TATGATGCAT TTATTAAGCA GCAAGAAAAT	180
	GTAACATATA TTTCAACCGA TCGTGCAGAT GCTAATACAG TGTTATGTCA CTAATTTATA	240
	AAAAATAAAT GAATAAGTAA GGTTTCAACC GAGAGAATAT ATTCGTGTTG AAGCCTTATT	300
40	TGTCGTTGTG CCAAATTTGA ACGnTTTAGA TGGCAATAAG CATGACCATA CAGATTGTGT	360
	ATTATTTCCA TGnA	374

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(2) INFORMATION FOR SEQ ID NO: 3931:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3931:

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TGCTTCTTTC GCTAGCCTCG TATGGGCATC TTTATCAATA ATATACTCGC CATGACTATC 120
 TTTCGCTTTT AAGTCAATTT CATCAAATC TTTCCACCT GTTAACGGTG CACCACTATG 180
 5 TCGTTTCCGA CCAAATGTAG CCTCTTGTTT TTCCAGCGCA GTACGATCCC ACGTTTCAAT 240
 GTGTATTTGA ATACGTCTGA CAACGCAATA AGTTCCATGT TTCGCCATC CGTCATCAAT 300
 AAACACATAA TCTTTAAGTT GATTATTCTT CCTAGGATTA ATTGTTCCAC TTAAAAATGC 360
 10 CATTAATAATT CTAGGTGTTT CCnTAnC 387

(2) INFORMATION FOR SEQ ID NO: 3932:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3932:

AAGGTAATAA TCCTGTAGTC GAAAATGTTG TCTCTCTTGA GTGGATCCTG AGTACGACGG 60
 25 AGCACGTGAA ATTCCGTCGG AATCTGGGAG GACCATCTCC TAAGGCTAAA TACTCTCTAG 120
 TGACCGATAG TGAACCAAGTA CCGTGAGGAG AAGGTGAAAA GCACCCCGGA AGGTAGnTGA 180
 AATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGG TGATGGCGTG 240
 30 CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTAAAGCAG TAAATGTGGA 300
 GCCGTAGCnG AAGnAnGTTT TGAATAGGGC GTTTAGTATT TGGTCGTAGC CGATAACCAG 360
 GTGATTCTAC CCTTTGGTCA GGTGAAGTT CAAGTAACAT 400

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(2) INFORMATION FOR SEQ ID NO: 3933:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3933:

GCGATGGTTG AAACATTGAC TTATATTAAG GAGTTTATGA ACCAAGTTGA GTCGCATAGC 60
 TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120
 50 CGTTGAATTG GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180
 CGATTTTGGC ATGAAGGTCA CCTTAAATGT ACATTGTTGT AATAAAATTG CCTATAAATT 240

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AATTGTAAAA AGAAAACCAT ACGCTATGTG nTGCCAAGGA AAAGGTTCTA CCATTGTCAC 360

nAAAAATGCA TCTCTACGTG CTAGGAATAA ATATTGGGTC 400

5

(2) INFORMATION FOR SEQ ID NO: 3934:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3934:

15

TTTGACGTTT TAGACATAAA AAAAGAGACC TTGCGGTCCA GATGGGGCTC ATCGCATCCA 60

CTTTTTGCCT GGCAACGTTT TACTCTAGCG GAAnTAATCG AACTACCATC GACGCTAAGG 120

20

AGCTTAACTT CTGTGTTCCG CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC 180

ATATGAATGT AAATTATACA TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA 240

AACATTTATT TTGATTAAGT CTTGATCGA TTAGTATTCG TCAGCTCCAC ATGTCACCAT 300

25

GGCTTCCACC TCGAACCTAT TAACCTCATC ATCTTTGAnG GATCTTATAA CCGAATTGGG 360

AAAnTCATCT GAAGGGGGCT CAGCTAGATG CTTCAAnACTT 400

(2) INFORMATION FOR SEQ ID NO: 3935:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 393 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3935:

40

TGTTCTTTTT GGGCAGTGGG ACACAAATGG ATATTTTCGG CAAAATTAT TTCGTTCGnT 60

CCCCCCCCAA CTTGGCACAC TATTGTAAGC TGACTTTTCG CCAGCTTCTG TGTGTTGGGCC 120

CCGCCAACTT GCCATTGTCT GTAGAAATTG AGGAGCTAAT TTCTCTGTGT CGGGGCTCCA 180

45

CCCCAACTTG CACACTATTG TAAGCTGACT TTCCGCCAGC CTCTGTGTTG GGGCCCCGCC 240

AACTTGCACA CTATTGTAAG CTGACTTTCC ACCAGCCTCT GTGTTGGGCC CCGACTATTT 300

TTGAAAAGAG CGTGTTACAC GGGCATGTGT TTACAGTCAA CTACTGCTAA AATAAAATTA 360

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ACGAGCTTAA GGCTTTGGnT TCTGTCCCAA GCC 393

(2) INFORMATION FOR SEQ ID NO: 3936:

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(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3936:

10 AAAAAGAAGA CAACCAAGCC CAATAATGGA CTGGCCGCGT AATAATnGTG GCTCTAAAAG 60
 TTGTATTTTA AAAATAGTTC TTAAATTAT ATACCCACCA CATTTGGTGG AGAACCTAAA 120
 AAAAAGCACT TCCCAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT TCGAACCTCT 180
 15 GACCCCTCTGA TTAAGAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA ATGGCTGGGC 240
 TAGCTGGATT CGAACCAACG AGTGACGGAh TCAAAAGTCC GTTGCCTTAC CGCTTGGCTA 300
 TAGCCCAATA TATAGATGGT GGAAGGGGGC AGATCGAACT GCCGAACCCG AGGAGCGGAT 360
 20 TTACAGTCCG CCGCGTTTtag CACTTCGCTA CCCTCCAGCT 400

(2) INFORMATION FOR SEQ ID NO: 3937:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 609 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3937:

GGTTTAACAC GCCTGCCTGT CACGCAGGAG ATCGCGGGTT CGATTCCCTG TCGAGACCGC 60
 35 CATTATTATT ACCATTACGG TTCAGTAGCT CAGTTGGTAG AGCAATGGAT TGAAGCTCCA 120
 TGTGTCGGCA GTTCGACTCT GTCCTGAACC ATTCTTAATT CATGGCGGTT GTGGTGAAgT 180
 40 GGTTAACACA TCGGATTGTG GTTCCGACAT TCGAGGGTTC GATCCCCTTC AGCCGCCCCA 240
 TAATCGTTTA CATTAGCGGG TGTAGTTTAA TGGCAAAACC TCAGCCTTCC AAGCTGATGT 300
 TGTGGGTTCG ATTCCCATCA CCCGCTCCAT TATTTTCTAT TATTCCACAG TAGCTCAGTG 360
 45 GTAGAGCTAT CGGCTGTAA CCGATCGGTC GTAGGTTTCA GTCCTACCTG TGGAGCCATG 420
 GCTCyTTGGt CAAGCGGTTA AGACACCGCC CTTTCACGGC GGTAACACGG GTTCGAGTCC 480
 CGTAGaGTyC ATACAAGCAG AAGTGnAAAT ATCGCTTCTG TTTTTTTaTT ACATAwTTAA 540
 50 TkGTTGgAGG aAGtTGTcCG AgCyGGGCCG AAGGaGCACG CCTGGAAATG TGTAAGCGTT 600
 CACAAGCTT 609

(2) INFORMATION FOR SEQ ID NO: 3938:

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(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3938:

10 TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC TACATGAAGC TGAATCGCT 60
 AGTAATCGTA GTCAGCATGC TACGGTGAAT ACGTTCCCGG GTCTTGTAACA CACCGCCCGT 120
 CACACCACGA GAGTTTGTAA CACCCGAAGC CGGTGGAGTA ACCTTTTAGG AGCTAGCCGT 180
 15 CGAAGTGGA CAAATGATTG GGGTGAAGTC GTAACAAGGT AGCCGTATCG GAAGGTGCGG 240
 CTGGATCACC TCCTTTCTAA GGATATATTC GGAACATCTT CTTCAGAAGA GCGGAATAAC 300
 GTGACATATT GTATTCAGTT TTGAATGTTT GTTCATTCAA ATTAATGGGC CTATAGCTCA 360
 20 GnGGTTAnAG CGCACCTGA TnAACGTGAA GTCGGTGGTT 400

(2) INFORMATION FOR SEQ ID NO: 3939:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3939:

AGTTTTGAAT GTATAAATTA CATTATATG TCTGGTGACT ATAGCAAGGA GGTCCACCTG 60
 35 TTCCCATGCC GAACACAGAA GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTT 120
 CGCTAGAGTA GAACGTTGCC AGGCATAATA TTAATCCACA GTAGCTCAGT GGTAGAGCTA 180
 TCGGCTGTTA ACCGATCGGT CGTAGGTTTC AGTCCTACCT GTGGAGCCAT GGCTCTTGGT 240
 40 CAAGCGGTTA AGGACACCGC CCTTTCACGG CGGTAACACG GGTTTCGAGTC CCGTAGAGTT 300
 CATTATTTTG GAGAATTAGC TCAGTAGGGA GAGCATCTGC CTTACAAGCA GAGGGTCGGC 360
 45 GGTTCGAAC CCTnCATTTT CCACCATTTG GTTATTAAAn 400

(2) INFORMATION FOR SEQ ID NO: 3940:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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ACACAACAGC TGTTTCAAAA ATGATTGGTA CAACTGCTGG TTATGTTGGT TATGATGACA 60
 ATTCAAATAC GTTAACTGAA AAAGTACGCC GTAATCCATA CTCAGTCATT CTATTTGATG 120
 5 AAATCGAAAA AGCAAATCCA CAAATTTTAA CATTGTTATT ACAAGTAATG GATGATGGTA 180
 ATTTGACTGA TGGTCAAGGT AATGTCATCA ACTTTAAAAA TACAATTATT ATTTGTACAT 240
 CAAATGCTGG CTTTGGCAAT GGCAATGACG CTGAAGAAAA AGATATTATG CACGAAATGA 300
 10 AAAAATTCTT CCGCCCTGAA TTCCTTAACC GCTTCAACGG CATCGTGAAT TnCTTACATT 360
 TAGATAAGGT GCCnTGCAGG TATCGTCCAA CTATTATTAG 400

15 (2) INFORMATION FOR SEQ ID NO: 3941:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3941:

25 ATACAATTTT AAATCTGTAT GTGTGAATCC AACACATGTT AAATATGCAG CAGAGCGnCT 60
 AGCTGATTCA GAGGTGCTCG TTTGTACGGT AATAGGATTC CCATTAGGTG CGTCGACAAC 120
 30 TGCAACGAAA GCATTTGAAA CAGAAGATGC AATTCAAAAT GGTGCAGATG AAATTGACAT 180
 GGTCAATCAAC ATCGGCGCAT TAAAAGATGG ACGTTTTGAT GATGTACAAC AAGACATTGA 240
 AGCAGTGGTT AAAGCTGCGA AAGGTCACAC AGTAAAAGTG ATTATTGAGA CGGTATTGTT 300
 35 GGACCATGAC GAAATTGTAA AAGCGAGTGA TTAACAAAAG CGGCTGGTGC GGACTTCGTT 360
 AAAAATTCA GCAGGTTTTG CCAGTGGCnG TGCGACTGCA 400

(2) INFORMATION FOR SEQ ID NO: 3942:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3942:

50 CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA 60
 TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC 120
 CATTTTTATA AGTCAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG ATTTAAACGC 180

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TATTTAAAAC TCTTTATTCA CTCGGTTTTG CTTGGTAAAA TCTATATTTT ACTTACTnAT 300
 CTAGTTTTCA ATGTACAAAT AATGGTGGAG ACTAGCGGGA TCCGAACCCG CTGACCCnAC 360
 5 CnGCGTGCAA AGCAGGCGCT CTACCCAGCT TGAGCTAAGG 400

(2) INFORMATION FOR SEQ ID NO: 3943:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3943:

CGCTACACTA CGAGACCATT AGTAAAACGG AGGAAGAGGG ATTCTGAACCC CCGCGAGCCG 60
 20 TTAAGCCCCT GTCGGTTTTT CAGACCGATC CCTTCAGCCG GACTTGGGTA TTCCTCCAAA 120
 ATTATATGGA CCTTGCAGGA CTCGAACCTG CGACCGAACG GTTATGGAGC CGTTAGCTCT 180
 GAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA 240
 25 GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC 300
 CGCCTTATAT AGTTTGTAAA TnAnnATGGT GGGAGACTAG CGGGGTTCGA ACCGCTGGAC 360
 30 CTCCTGCGTG CCAAAGCAGG CGGCTTCTAC CCAGCTGGAG 400

(2) INFORMATION FOR SEQ ID NO: 3944:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 406 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3944:

CCAAAATTGC ACCTTGTCGT TTATTCGGAA AATCAATATn GnTAGGGGGT ATAAGATGCA 60
 45 CCTACTTTAA CTGTCGCCAA CATCGCCGCA ATCATTTCAA AACTACGTTC TGTAACAAG 120
 GCAACCCGTT GACCATTGCC CACACCATTT GATAGGAGCA TGTGCGCAAT GGCATCCACA 180
 TAGTTGCGTA ATGTTTCATA CGTCATTGTC AAATCATTCa TGA TAGCGC AACATGATTA 240
 50 CCTTGTCGTG AGAAACTTCA TTAAAGTAAC TTATGATAGA TTTATTTCCC GGGACATTAA 300
 GCATTGATC GTTAACATGC GTATTGACCC AATTTAGAAG TTCCTCCGTG CCGTTTGGTA 360
 TATCACAAT TTGTAGTGTA wCtTGaTGCT TCmAAATATc AATCAn 406

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3945:

CAATGACAAC AGCAACTGAG ACAGTGTCAA ACGCTTAATA ATAATGATGT AGTGTGCAAT	60
AATACCGCAT TAAATGTACC AACTAAACA AATGAAAATG GTTCAGGAGG ACATCTAACT	120
TTAAAGGAAA TTCAAGAAGA TGTCGTCAT TCTTCAAATA AACCAGAGCT AGTTGCAATT	180
GCTGGAACCA GCATCTGAAT AGACCGAAAA AGAGAAGTTA GACGTGCGGC ACCGGCAGAT	240
CCTGAATGCC AACTCCAGCA GATCCAGCGG CTGCAGCGGT TAGGAAACGG TGGTGCACCA	300
GTTCGAATTA CAGCGCCATA TACGCCAACA ACTGATCCTA ATGCCATGAn GCCAGGACAA	360
ATGGCACCTA ACGAnGCTTG TTCATTTGAT GGACAnGGTA	400

(2) INFORMATION FOR SEQ ID NO: 3946:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3946:

CTCGCTGCGA TAAAGTACCA GTTCATAGCA ACGTTTGTnT TAATAGGnTC TGAAACGATA	60
CGTGTTGCCG GTTCTGTAAA TGAATAGACC AAAGCATCTT GCATACCAAC AACTATATTT	120
GCTGCAAATC CTCCAACAGC GGAAnATATG CCATCGTTAG TCCAGCGATA GGGTGATAGC	180
CAATTTTAAT AAAAAGCATT GCTGCAACGG CCGGCAAGAT AATTGTCGCA GCATCGCCGG	240
CTGTACTACC TAAAATACCA ATTAATATAA TAGTCGGTAA AATTAAGAAA CGTGGTGCGC	300
GATTCACAAC AGAAATCATT AACTTATCGA AGTATCCTGT TTTCTCTGCA ACACCAATAC	360
CAATCATCAC TGCTAGGTAC TAAGCCTAAT GCTGGGnACT	400

(2) INFORMATION FOR SEQ ID NO: 3947:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3947:

5 GCCGGCCAGA GGA¹CTTGGA² CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT 60
 GAGCTAGGCC GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTCG AACCGCCGAC 120
 CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT 180
 10 GGCAACGTTT TACTCTAGCG GAA¹nTAATT²C G¹nACTACCAT CGACGCTAAG GAGCTTAACT 240
 TCTGTGTTTCG GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG 300
 TAATTTATAC ATTCAAAACT AGATAGTAAG TAAAAGTGAT TTTG¹nTTTCG CAAAACATTT 360
 15 A 361

(2) INFORMATION FOR SEQ ID NO: 3948:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3948:

25 TTCCGTCAGA CCCTGACATG GTTCATGGGT TCATATTGCA TAGGACCGAA ATCTTCAAAC 60
 30 ACTACGTGCT TTGGGCAGAC TTCGCAAAAA TACGGCCTCA ACAAAGGAAT TAAGCCTCGC 120
 ATAAAGCGGA TTTGAGTAC AGGGAACCGC TACCTCCCCA CCTAGCACGG CAAGATATAT 180
 ATTACTATAT TTTAATAGTT AATTGCAAGT ATAAATCATT TATATCATTG TTTACTTTAT 240
 35 ACGACGTCTT GAGAAGTCAT TAATTTAAAT TCATTTGCAA GATGTTTTGA AATATTATAT 300
 TGAAACGGCA TTGTATTTTC TAAATACACA nTACTTCGAA CTGTTG¹nGA ATAGGCCACC 360
 GATACATCAC CAACAATTGG nA 382

(2) INFORMATION FOR SEQ ID NO: 3949:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3949:

50 GCCAAGCCAT TTTTCTTTGT GTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGA 60
 GACCTTGCGG TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGCAAC GTTCTACTCT 120

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TTGCTTCTTT CCTCTTCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA ACTCGTTGCG 240
 CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATT TTTCTTTGTG 300
 5 TTTGCTTTTT AnTTTGACGT TTTAGACATA AAAAAAGAG ACCTTGCGGn CTCAATGnGG 360
 GCTCATCGCA TCCAATTTTT GGCCTGGCAA CGGTTCTACT 400

(2) INFORMATION FOR SEQ ID NO: 3950:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3950:

20 ACTCGTTTT GCTTGGAAAA TCTATATTTA CTTACTTATC TAGTTTTCAA TGTACAATTT 60
 CTTTTTAGTC AAGCGCTCGC ATACTGCTTT ATTTTCATAA GCAATATCAC TTAAACCAAA 120
 AAATATTGA ATGTTAAATA AACATTCAAA ACTGAATACA ATATGTCACG TTATTCCGCA 180
 25 TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG CCGCACCTTC 240
 CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC GACGGCTAGC 300
 TCCTAAAAGG nTACnCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT GACGGGCGGT 360
 30 GTGTACAAGA CCCGGGAACG nATTACCG 389

(2) INFORMATION FOR SEQ ID NO: 3951:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3951:

45 AAAGCTCGAC TTGTTTACGA TGTTGAAAAA CAAGATTATG TACCTGTATC GCAACCACAA 60
 TTACCAATTT TAAATGAATT TAATAAGAC TTAGTGCATA ACCTTGATAC CATATTCAAT 120
 GCGCAAGACG AnCGGGACTA TTTTATGGG AGACATTACG TAATAATTC TATTACTCTG 180
 50 CTATCAATGT ACCTAAAGCT ACCGATGATT TCCGAGACAT AGACCGTGCG CTTGTCTGGG 240
 GGTTCAACTG GAACTTGGT CCATTCCAAT TATGGGATGC AATGGGATAC GAACGTGTTA 300
 AAACAnTGAT GGGAAGACGA ACTTGGGAGA CTTACCACAA TGGGATTAGT GAnTTAGATG 360

(2) INFORMATION FOR SEQ ID NO: 3952:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3952:

CAAAGGGCAG CGAAACCGCG AGTCCAGAGC AAATCCCAT AAGTTGTTCT CAGTTCGGAT 60
 TGTAGTCTGC AACTCGACTA CATGAAGCTG GAATCGCTAG TAATCGTAGA TCAGCATGCT 120
 ACGGTGAATA CGTTCCCGGG TCTTGACAC ACCGCCGTC ACACCACGAG AGTTTGTAAC 180
 ACCCGAAGCC GGTGGAGTAA CCTTTTAGGA GCTAGCCGTC GAAGTGGGAC AAATGATTGG 240
 GGTGAAGTCG TAACAAGGTA GCCGTATCGG AAGGTGCGGC TGGGATCACC TCCTTTCTGA 300
 AGGATATATT CGGGAACATC TTCTTCAGAA GAGCGGGAAT AACGTGACAT ATTGTATTCA 360
 GnTTTGGAAT GTTTnnTTAA CATTnCAAAA AAATGGGGCC 400

(2) INFORMATION FOR SEQ ID NO: 3953:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3953:

TGATTTTGAC GTTTTAGACA TAAAAAAG AGACCTGCG GTCTCAAATG CGGCTCATCG 60
 CATCCATTTT TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAATTGGCT ACCATCGACG 120
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTTCTT CGGCTCTCGC 180
 TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 240
 TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTTGCTTTT TATTTTGACG TTTTAGACAT 300
 AAAAAAAGA GACCTTGCGG TCTCAATGCG GGCTCATCGC ATCCATTTT TGCCTGGCAA 360
 CGTTCTACTC nAGCGGGAAG TGAAGnCGGA CTGACCAAGC 400

(2) INFORMATION FOR SEQ ID NO: 3954:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3954:

AAACTACATA ATGAAAATGC CGTTTAAATC GGTAAATTAA ATATGGATGA GTTTGCAATG 60
 5 GGTGGTTCAA CAGAAACATC TTATTCAAAA AAAACAGTTA ACCCATTGGA CCATAAAGCA 120
 GTGCCAGGTG GTTCATCAGG TGGATCTGCA GCAGCAGTTG CAGCTGGCTT AGTACCATTG 180
 AGCTTAGGTT CAGACACAGG TGGTTCAATT AGACAACCGG CTGCATATTG TGGCGTTGTC 240
 10 GGTATGAAAC CAACATACGG TCGTGTATCT CGATTGGAT TAGTGCTTTG CATCTTCATA 300
 GACCAAATTG GGCCATGACT CGAATGTAAA GTAATGCCAT CGTATTAGAA GCTATTCTGG 360
 TGCAGATGnT AATGACTCTA CCAGTGCACC AGTGATGAGG 400

(2) INFORMATION FOR SEQ ID NO: 3955:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3955:

TCGATTGGCA TTTCTCCGCT ACCCTCAGTT CATCCGCTCA CTTTCAACG TAATCGGTTG 60
 GGTCTCCAT TCAGTGTAC CTGAACITCA ACCTGACCAA GGGTAGATCA CCTGGTTTCG 120
 30 GGTCTACGAC AAATACTAAA CGCCCTATTC AGACTCGCTT TCGCTACGGC TCCACATTTA 180
 CTGCTTAACC TTGCATCAA TCGTAACTCG CCGGTTTCATT CTACAAAAGG CACGCCATCA 240
 CCCATTAAACG GGCTCTGACT ACTTGTAAGC ACACGGTTTC AGGTTCTATT TCACTCCCCT 300
 35 TCCGGGGGTG CTTTTCACTT TTCTTTCAA GGTATGGGTT CACTATCGGT nACTAGAGAG 360
 TAATTAGCTT AGGnGATGGT CCTCCCAGAT TCGGAAGGGA 400

40 (2) INFORMATION FOR SEQ ID NO: 3956:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3956:

GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG AACCGGTAGT 60

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5 ATAAAAATGG AGCAGAAGAC GGGATTGCGAA CCCGCGACCC CAACCTTGGC AAGGTTGTAT 180
 TCTACCGCTG AACTACTTCT GCATATGCGG GTGAAGGGAG TCGAACCCCC ACGCCGTAAG 240
 CTTAGGATCC TAAGTCTAGT GCGTCTGCCA ATTCCGCCAC ACCCGCAAAT GGTGAGCCAT 300
 AGAGGATTCG AACCTCTGGA CCCTCTGGAT TAAAAGTCAG ATGCTCTACC AACTGGAGCT 360
 10 AATGGCTCTT TCCATGGTGC CGGGCCAGAG GACTTTGAAa 400

(2) INFORMATION FOR SEQ ID NO: 3957:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3957:

CAGACATGTG TTATACGGGA AATTGGGCGA ACCGCAACTA TTATACATTG ATTTACACCT 60
 TATACATGAA GTTACTTCTC CTCAAGCATT TGAAGGACTT AGGCTTCAAAC ACAGAAAATT 120
 25 AAGACGCCCA GATTTAACAT TTGCAACACT CGATCACAAT GTTCCTACTA TTGATATATT 180
 CAATATTAAA GATGAAATTG CAAACAAACA AATCACAACA TTACAAAAAA ACGCCATAGA 240
 TTTTGGGGTG CATATTTTTG ATATGGGTTT TGATGAACAA GGTATTGTTC ACATGGTAGG 300
 30 ACCTGAGACA GGAATTACAC AGCCTGGChA GACCATCCGT nTGTGGGTGA CTCTCACACA 360
 GCCACACATG GnGCCTTTT 379

35 (2) INFORMATION FOR SEQ ID NO: 3958:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3958:

TGTTAAAATA CGGTACATCT AAATTAATGT TAACTGATT TCAAAAAGAG AATTAAATAA 60
 ATATATTCAA GGTCAGAnAC AACGCGTGAT ATTTGAAAAT GGCCATTTTG TCTAATTGAT 120
 50 AGTGAATATA ATTAGAGTAA GAGGCTGGGA CATAATCCC TAAAAACAG CAGTAAGATA 180
 ATTTTCAATT AGAAAATATC TTAGTGCTGT TCTCTATTTA TACAATACTT CGTATTGAAT 240
 GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT GCTCCCTCAG 300

55

AATAAGACAT TTGnCCAACT TGACACTACC ATTAAAAACT

400

(2) INFORMATION FOR SEQ ID NO: 3959:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3959:

15

GAGCCGCACT	GGAATGAGGC	CCAAGCGACT	GTTTATCAAA	AACACAGGTC	TCTGCTAAAC	60
CGTAAGGATG	TGTTATAGGG	GCTGACGGCT	GCCCGGTGCT	GGAAGGTTAA	GAGGAGTGGT	120
TAGCTTCTGC	GACGTACrGA	ATCGAAGCCC	CAGTAAACGG	CGGCCGTAAC	TATAACGGTC	180
CTAAGGTAGC	GAAATTCCTT	GTCGGGTAAG	TTCCGACCCG	CACGAAAGGC	GTAACGATTT	240
GGGCACTGTC	TCAACGAGAG	ACTCGGTGAA	AATCATAGTA	CCTGTGAAGA	TGCAGGTTAC	300
CCGCGTACAG	GACGGAAAGn	CCCCTGGAGC	TTTACTGTAG	CCTGATATTG	AAATnCGGCA	360
CAGTTTGTAC	AGGATAGGTT	AGGAGCCTTG	GAAACGTGTG			400

(2) INFORMATION FOR SEQ ID NO: 3960:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3960:

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TGGTCCCAAA	CCAAGTGCTC	TACCAAGCTG	AGCTACTTCC	CGTATAATTA	ACGCGCCCGA	60
TAGGAGTCGA	ACCCATAACC	TCTTGATCCG	TAGTCAAACG	CTCTATCCAA	TTGAGCTACG	120
GGCGCATATG	TTTTTATTGA	AAATGGTGCC	GAGGACCGGA	ATCGAACCGG	TAGTGAnTnC	180
ACTCACC GCA	GATTTTAAGT	CCTGTGCGTC	TGCCAGTTCC	GCCACCCCGG	CACTATAAAA	240
ATGGAGCAGA	AGACGGGATT	CGAACCCGCG	ACCCCAACCT	TGGCAAGTTG	TTATTCTTAC	300
CGCTGGA ACT	ACTTCTGGCA	TATGCGGGTT	GAAGGGGAGT	CGAACCCCCA	CGCCGTAGGC	360
TTAAGATTCC	TGAAGTCTAG	TGCGTCTGGC	CAATTTCCGG			400

(2) INFORMATION FOR SEQ ID NO: 3961:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3961:

	TTTTGATACA TAATCTAAAT TTCTCAAAGC GCCAATAACA GAGGACCATC TCCTAAGGCT	60
10	AAATACTCTC TAGTGACCGA TAGTGAACCA GTACCGTGAG GGAAAGGTGA AAAGCACCCC	120
	GGAAGGGAGT GAAATAGAAC CTGAAACCGT GTGCTTACAA GTAGTCAGAG CCCGTTAATG	180
	GGTGATGGCG TGCCTTTTGT AGAATGAACC GCGGAGTTAC GATTTGATGC AAGGTTAAGC	240
15	AGTAAATGTG GAGCCGTAGC GAAAGCGAAG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA	300
	GACCGGAAAC CAGGTGATCT ACCCTTGGTC AGGTTGAAGT TCAGGTAACA CTGAATGGAG	360
	GACCGAACCG ACTTACGTTG AAAAGTGAGC GGATGAACTG	400

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(2) INFORMATION FOR SEQ ID NO: 3962:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 361 base pairs
25	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3962:

	TAATAATTAC AGTATATCGG GAAGACAGGA TTCGAACCTn CGACCCCTTG GTCCCAAACC	60
	AAGTGCTCTA CCAAGCTGAG CTACTTCCCG TATAnTTAAC GCGCCCGATA GGAGTCGAAC	120
35	CCATAACCTC TTGATCCGTA GTCAAACGCT CTATCCAATT GAGCTACGGG CGCATATGTG	180
	TTTATTGAAA ATGGTGCCGA GGACCGGAAT CGAACCGTA CGTGATCACT CACCGCAGGA	240
40	TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAnAAAT GGATCAGAAG	300
	ACGGGATTCTG AACCCGCGAC CCCAACCTTG GCAAGGTTGT ATTCTACCGC TGAACACTT	360
	C	361

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(2) INFORMATION FOR SEQ ID NO: 3963:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 375 base pairs
	(B) TYPE: nucleic acid
50	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3963:

AAGTGTCTTA TTTTTTTAAA GTATTTCAAA GTAAAATTAC ATGTTAATAC GTAGATTAAT 120
 GGCGAGACTC CTGAGGGAGC AGTGCCAGTC GAAGCCGTAG GCTGAGACGG CACCCTAGGA 180
 5 AAGCGAACCA TTCAATACGA AGATnTnATn AAATAGAGAA CAGCAGTAAG ATATTTTCTA 240
 ATTGAAAATT ATCTTACTGC TGTTTTTTAG GGATTTATGT CCCAGCCTCT TACTCTAATT 300
 ATATTCAC TAATTAGAC AAAATGGCCA TTTTCAAATA TCACGCGTTG GTTTCTGACC 360
 10 TTGGAATATA TTTAT 375

(2) INFORMATION FOR SEQ ID NO: 3964:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3964:

AAAATGGCCT TGATAGACTT GCTCAATGCA GGGTTGCCAC AAACCAATGA TGCACTTACA 60
 25 ATTTTAAATA GATTTTAAAG ACCTTGTTGG TTTTGACAA TTAATGTGAC ATGACTAGGT 120
 CTTGCACGTT TATATGCATC TTCATTACTG AGTTTTTGT TGATTTCGTT ATGATTTAAT 180
 30 ACGCCTAATT CTFTCATTTG TTGAACCAAT TTTATGAAAA TGTAAGCTGT TGCTTCTGTA 240
 TCATAAATGG CACGGTGATG TTGCGTTAAT TCTACGCCAT ATTTTTTAGC CAAGAAATTC 300
 AAACCATGTT TACCATATTC AGTATTAATC GTACGAGGAT AATTCTAAAG TATCGATAAC 360
 35 ACCATTCGTT GGATGGTCCA AACCCAAGAC GTTCATATCC 400

(2) INFORMATION FOR SEQ ID NO: 3965:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3965:

ACTTTTAATT TTGTCATGAT GTGCCTCCTT ACCGTATGAT GTTATTCAAA GTAAATTGCT 60
 50 TTGCCTGATT TTGCAGACTG ATAAATCGCT TCAAGAATTT TTGTAAC TAC CATTGCTTGT 120
 TCCGGTTTCA CAACTGGTTC AGTATCATTT ACAACTGCAT CAATCCAAGC TTTTGCTTCT 180
 TCTTCAGCTT CATCCACTTC ATTACCTTCA TAAAGTCGA CGCCTTTGTT TTCCAATTCA 240
 55

TCAGCACCTG CTTTAGGTTT CTGATAATGA ACATTTTGGC CTCATCCACT TCTAAAnGAA 360
 TTAATCGCCC AAGnGGGATT CCAAAAAGGA n 391

5 (2) INFORMATION FOR SEQ ID NO: 3966:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 398 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3966:

CGCTATCAGG TATTGTTTCA ACAATTTTCAT TAACATATCG TGAAATATCA TTTTGAGGGA 60
 TTCTAACAGA AGTTTCTATT GGTAGTGTAG TTGGGGCATG TTATAATTTT TATACATAAG 120
 20 GCACCTCGTT AATTTAGTTT AGTGGTATTT ATTAAATTAT AAGAAGGGAC CCAACACAGA 180
 AAATTCATTT TATTGAATTT TACATTTATG TGCAAGTTGG GCAAAGTGTC TTATTTTTTA 240
 AAAGTATTTT AAAGTAAAAT TACATGTTAA TACGTATaTa ATGGcGAGAC TCCTGAGGGA 300
 25 GCAGTGCCAG TCGAAGcCAA GGCTGAGACG GCACCCtAGG AAAGCGAcnC ATTcAATACG 360
 AAGATTGTAT AAATAGAGAA CAGCAGTAAG ATATTTTC 398

30 (2) INFORMATION FOR SEQ ID NO: 3967:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3967:

40 GCTATAGAAA AAATAAAATC ACAAGTTACG ATTAGCGTAC TTGATGGGGA GTGAAAATAA 60
 TGAGAGTAAC AGAGTTATTA ACAAAGATA CAATAGCAAT GGATTTAATG GCAAATGACA 120
 45 AAAATGGTGT TATTGATGAG TTAGTAAATC AATTAGACAA AGCAGGTAAA TTAAGTGATG 180
 TCGCGTCATT TAAGGAAGCG ATTCACAATC GAGAATCACA AAGTACAAC TGTATCGGCG 240
 AGGTATTGCC ATTCCACATG CCAAAGTGGC CGCAGTTGAA GTCACCAGCT ATTGCGTTTG 300
 50 GTAAATCTAA AGCAGGCGTG GATTATCAAn TTTGGnTATG CAACCAGCAC ACTTnTTCTT 360
 TGTGGTTGGC AGCG 374

(2) INFORMATION FOR SEQ ID NO: 3968:

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- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3968:

10 ACCCCGGCAC TATAAAATG GAGCAGAAGA CGGGATTCTGA ACCCGCGACC CCAACCTTGG 60
 CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC 120
 CACGCCGTAA nCTGAGGATC CTAAGTCTAG TCGCTCTGCC AATTCCGCCA CACCCGCAAA 180
 15 TGGTGAGCCA TAGAGGATTC GAACCTCTGG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC 240
 AACTGAGCTG AATGGCTCTT CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTGACT 300
 GGATTACAAG TCAGTTGCTC TACCAATTGA GCTAAGGCCG GGCAATATGT AAGAATAAAT 360
 20 GGTGGAGAAT GACGGGTTTC GAAncGCCGA CCCTCTGCTT 400

(2) INFORMATION FOR SEQ ID NO: 3969:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3969:

GCGAGTTGGG GTGTGGGCCC CAACATAGAG AAATTGGATT CCCAATTTCT ACAGACAATG 60
 35 CAAGTTGGCG GGGCCCCAAC ACAGAAGCTG ACGAAAAGTC ATTAnCAATA ATGTGCAAGT 120
 TGGCGGGGCC CCAACACAGA AGCTGACGAA AAGTCATTAn CAATAATGTG CAAGTTGGCG 180
 GGGCCCCAAC ACAGAAGCTG GCGGAAAGTC AGCTTACAAT AATGTGCAAG TTGGGGTGGG 240
 40 ACAACGATAA AGTAATACTT TTTCTATAGA AATTAGTATT TCTTATGCAT GAGTTTTACT 300
 CATGTATTCC TATTTTAAAG TACACATTAG CTGTGGCTAA TGTTTAAGAC CCACTACATA 360
 45 ATAAATCATT AGTGGCTCTn TATCATTTCT GTCCCACTCC 400

(2) INFORMATION FOR SEQ ID NO: 3970:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 419 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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5 GATAAGATCA GCCGAAAATG GATGGTGTTA AGAGCGTTAC TTGGTTTGGC GGTATGCTTA 60
 TTTTAAATGG CATTGTGTAC GACACCATTa CAGTTTGTAC TTGTGAGGTT ATTGCAGGGA 120
 CTATTTGGTG GTGTGTTGA TGCATCAAGT GCGTTTGCga GTGCAGAGGC GCCACTGAKA 180
 GATCGTGGAA AGtATTAGGA gACTGCAAAT TCAGTCAGCG CAGGtCTCTT GTGGGGCCAT 240
 10 TAATTGGCGG TGTACAGCT TCGATATTAG GTTTTAGTGC GTTACTGATG AGTATTGCCG 300
 TTATTACTTT TATTGTCTGT ATTTTCGGTG CATTAAATg ATTGAAACGA CACATATGCC 360
 AAaATCACAA ACACCAAATA TTAATAAAGG TnTTCGCCGT TCCAnTtnCA ATGTCTAAT 419

15 (2) INFORMATION FOR SEQ ID NO: 3971:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3971:

25 AAACCTGGGA GACTTCAATA ACAGATTTAG GTTTATCTAA AAATCAGGCA TATAATTTCT 60
 TAATTACATC TAGTCAAAGA TGGGGCCTTA ATCAAGGGAT AAATGCAAAT GGCTGGATGA 120
 30 GAACTGACTT GAAAGGTTCA GAGTTTACTT TTACACCAGA AGCGCCAAAA ACAATAACAG 180
 AATTAGAAAA AAAAGTTGAA GAGATTCCAT TCAAGAAAGA ACGTAAATTT AATCCGGATT 240
 TAGCACCAGG GACAGAAAAA GTAACAAGAG AAGGACAAAA AGGTGAGAAG ACAATAACGA 300
 35 CACCAACACT AAAAAATCCA TTAAGTGGAG TAATTATTAG TAAAGGTGAA CCnnAAGGAG 360
 GGGTTTCCAn AGTCCGTTAT G 381

40 (2) INFORMATION FOR SEQ ID NO: 3972:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3972:

50 GGGTTCAGAA CGTCGTGAGA CAGTTCGGTC CCTATCCGTC GTGGGCGTAG GAAATTTGAG 60
 AGGAGCTGTC CTTAGTACGA GAGGACCGGG ATGGACATAC CTCTGGTGTA CCAGTTGTGC 120
 TGCCAACGGC ATAGCTGGGT AGCTATGTGT GGACGGGATA AGTGCTGAAA GCATCTAAGC 180

55

5 GAnGTTAATA GGTTCGAGGT GGAAGCATGG TGACATGTGG AGCTGACGAA TACTAATCGn 300
 TCGAnGACTT AATCAAAATA AATGTTTTGC GACCAAATCA CTTTACTTAC TATCTAGTTT 360
 GAATGATAAA TACATCATAT GCTGGnGCCA TACCAAGGGG 400

(2) INFORMATION FOR SEQ ID NO: 3973:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3973:

TCTTTTAATT ACGTAATGGC TTACCAGTTT TTAACATATG TGCAATTCTT TCATATGATT 60
 TTTTAGATTT TAGTAAGTCA ATAAAGCCAA TTTTCTCCAA CGATTGAATG TAACGTTGAT 120
 TGATAAATGT ATTCTTGGT AAATCACCAC CCGCTAAAAT TGTGGCGATA TTTAAGGCAA 180
 TATGATAATC ATGGTCGCTA ATAAAATGAC CCCGTCTTTG CGCATCTAAT TGTCCTTGGA 240
 TCAATGCTTT GAAGTCTTCA CCTAAAGCGA TATATTGATG TCTAGGATTC GGAATATAGT 300
 TTGTTTCTGC TTCATATTTT GCACGTGTGA GCGCAACTTC GACACGnTGG TGCCTGGATT 360
 nGAAAATAAA CCGGAnCCnG GGATCCACGG GAAATAACCC 400

(2) INFORMATION FOR SEQ ID NO: 3974:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3974:

TGCCATGTTC ACCTTGTTTA AAATCAAGGT TTGTAATGTT TCCTTGTGTC ACGATAATAG 60
 GCGTAATATC ACTCTTTGCA TGATTGCGGA TGTAGTCTAA ATCAAAGTTG ATTAATAAAT 120
 CACCTTGTTT AACTTCTTGA CCTTCTCAA CATGTAAAGT AAAGCCTTCT CCGTTTAATT 180
 TAACAGTGTC TAAACCGATG TGGATTAATA GTTCTAAACC ACTATCTGAA TACAAGACCA 240
 ATTGCATGTT TTGTTGGGAA AATCATTTGT TACTTTACCG TTGAAATGGT GCACGAACT 300
 TCACCTTGTG AnGTTTTTGG ATAGCGATAC CGTCACCCCA TCCATTTTTT TTCGCTGAAA 360
 CACTTGGATC AnGGCACTTC TGAATAAATG GTGGTTAACT 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 372 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3975:

CCTTTGCAGC GCCTCCGTTA CCTTTTAGGA GCGACCGCC CCAGTCAAAC TGCCCGCCTG 60
 AACTGTCTC CCACCACGAT AAGnGCGGgn GTTTAGAAAG CCAACACAGC TAGGGTAGTA 120
 TCCCACCAGC GCCTCCACGT AAGCTAGCGC TCACGTTTCA AAGGCTCCTA CCTATCCTGT 180
 ACAAGCTGTG CCGAATTTCA ATATCAGGCT ACAGTAAAGC TCCACGGGGT CTTTCCGTCC 240
 TGTCGCGGGT AACCTGCATC TTCACAGGTA CTATGATTTT ACCGAGTCTC TCGTTGAGAC 300
 AGTGCCCAA TCGTTAACGC CTTTCGTGCG GGTCGGAACT TACCCGACAA GGAnTTTCGC 360
 TAACTTAGGA CC 372

(2) INFORMATION FOR SEQ ID NO: 3976:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3976:

AGGGAATCGA ATTTTCTTTC TCTTCCTnCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT 60
 GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120
 CCCATTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180
 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AAATAACTTA 240
 ATCTATGTTT CCACCATTTT TATAAGTCAA ACGCTCACAT ACGGCTTCGT TTTCATTATT 300
 TTAAAGCTCA TTACATAAG TAACTCTGC TTTAAATGAT TTAACCTATT GTCTGCTAAA 360
 ACGGTTTnTT TTATGAAAAG GTTTGAAACG GGTTn 395

(2) INFORMATION FOR SEQ ID NO: 3977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3977:

5 TTGGTCCCAA ACCAAGTGCT CTACCAAGCT GAGCTACTTC CCGTATAATT AACGCGCCCG 60
 ATAGAGTCGA ACCCATAACC TCTTGATCCG TAGTCAAACG CTCTATCCAA TTGAGCTACG 120
 GGCGCATATG TTTTATTGA AAATGGTGCC GAGGACCGGA ATCGAACCGG TAGTnnTTCA 180
 10 CTCACGCAGA TTTTAAGTCC TGTGCGTCTG CCAGTTCCGC CACCCCGGCA CTATAAAAAT 240
 GGAGCAGAAG ACGGGATTTC AACCCGCGAC CCCAACCTTG GCAAGTTGTT ATTCTACCGC 300
 TGAACTACTT CTGCATATGC GGGTGAAGGG AGTCGAACCC CCACGCCGTA GGCTTAGATC 360
 15 CTTAAGTCTA AGTGCCTCTG GCCAATTTCC GCCAnACCCG 400

(2) INFORMATION FOR SEQ ID NO: 3978:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3978:

25 AAGTGGTTAA ATATTATAGA AAACATCAAA GGATGTTAAG AAATACAATT TATTACCCAG 60
 30 CATTTAATAA TGGTGCTATA GAAGGAATTA ATAATAAGAT AAAATTAATC AAGTGAATTT 120
 CTTTGGTTA CAGAAATTTT AACAACTTTA AAGCACGTAT AATGATGATT TTCAGCTTGT 180
 ACAAGGAGA AAAAAAGAAG ACAACCAAGC CCAATAATGG ACTGGCCGCC TAATAATAAA 240
 35 AGCTCTAAAA GTTGTATTTT AAAAATAGTT CTTTAAATTA TATACCCACC ACATTTGGTG 300
 GAGGAACCTA AAAAAAGCA CTCCCAAAA ATGGGAAAGT GCAGTnAGTG GAGCCATAGA 360
 GGATTCCGAA CCTCGGACCC TCnGAnT 387

(2) INFORMATION FOR SEQ ID NO: 3979:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3979:

50 TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCCAACCTT GGCAAGGTTG TATTCTACCG 60
 CTGAACTACT TCTGCATATG CGGGTGAAGG GAGTCGAACC CCCACGCCGT AAnTTAGCAT 120
 55

CGAACCTCTG GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTT 240
 CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTT CAGTTGCTCT 300
 5 ACCAATTGAG CTAGGCCGGn CAATATGTAA GAATAAATGG TGGAGAATGA CGGGTTTCGA 360
 ACCGCCGAAC CCTCTGCTTG TnAAGGGCAG ATGGCTCnTC 400

(2) INFORMATION FOR SEQ ID NO: 3980:

- 10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3980:

20 TTACCACGTA TTTAGGTTTC TTTGGTGGCT CTAGATTGTG CCCTATTGTC ACAGCATTTG 60
 CCGCAATCTT TTTAGGTGTA TTGATGTTTT TCATTTGGCC AAGCATACAA GCCGGCATTT 120
 ATCATGTTGG TGGATTGTGA ACGAAAACAG GTGCCATCGG TACTTTTGTT TATGGCTTCA 180
 25 TCTTAAGATT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTAATTACCG TTTTGGCAGA 240
 CGGCACTTGG TGGTACTTTA GAAGTCAAAG GGCACTTAGT TCAAGGTACG CAGAACATCT 300
 TCTTTGCTCA ACTTGGTGAT CCAGATGTGA CGAnTATTAT TCCAGGTGTG TCACGCTTTA 360
 30 nGTCAGCCGT TTTAATACGA GGATGTTCCG CTAnTGGTG 400

(2) INFORMATION FOR SEQ ID NO: 3981:

- 35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3981:

CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC 60
 45 GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG 120
 CTGGAATAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GATACAATTC 180
 50 AAGTTGTTGC AACGCAAGGG AAGCGGAGAG ACAGTGTAGT GGATGGAGCA ACGTATAGTT 240
 GGATTTCAACA GTTGTCGCAC CACAACCGAA CCAAGCGACT GACTGAAGAT TTGGCAAAAT 300
 GGnCATATTG ATATCACGCC TAATGAnTCC ATTCAGGACA TTTAATTAAT CCAACTCAAG 360

(2) INFORMATION FOR SEQ ID NO: 3982:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3982:

TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA 60
 TAATGTTTCAT ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAAGCAA 120
 GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTT 180
 AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG AAAATTATAG GTGTTGAACC 240
 TTCAGTGCAA GTAGTATGTA TGAATCTGTT GTGGTAAATA ATCAGGTAGT CACATTGCCT 300
 AATATCGATA AATTGTGGG ACGGTGCATC TGTAGCTAGA GTTGGCGATA TTACATTGGA 360
 AATTGCCAAA GAAAAGTAGA GGATTACGTT CCAGTAGAGn 400

(2) INFORMATION FOR SEQ ID NO: 3983:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 390 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3983:

CCACCATTAT TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT TTACCAAGCA 60
 AAACCGAGTG AATAAAGAGT TTAAATAAG CTTGAATTCA TAAGAAATAA TCGCTAGTGT 120
 TCGAAAGAcG CGACAAGATT AATAACGCGT TTAAATCTTT TTATAAAAGA AAACGTTTAG 180
 CAGACAATGA GTTAAATTAT TTAAAGCAG AGTTTACTTA TGTAATGAG CATTTAAAT 240
 AATGAAAACG AGGCCGTATG TGGAGCGTTT GACTTATnAA AAATGGTGGG AAACATAGAT 300
 TCAAGTTATT GAAGGGCGCA CGGTGGGATG CCTTGGGCAC TAGnAAGCCG nTGGAAGGAC 360
 GTTACTAACG ACGATATGCC TTGGGGGAGC 390

(2) INFORMATION FOR SEQ ID NO: 3984:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3984:

5
 GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTTGC CTTGTATCTG CAAATGTTTT 60
 GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC ACAAATTCAA ATGTATCAGG 120
 10 CGTTTCTTTT ATCCATTTCA ATATATTTCT TTCCGGTTGT ATCGCATAGT ATGTCGCATC 180
 TAATTCGACA ACCGGAAAAT GTCCAGCATA TGTTTTAAGT TTATCGGTTT GCGGTTCTAA 240
 ATCTTCATAT AATGAATAGT GATCACCCCA ACCTGTTAAT CCGATGTTTT ATCATATATA 300
 15 TCACCAATGT CATCATACCA TATAACTTTT ATCATnATCA TTTCAGCGAA CTTTAGGTTT 360
 GnAGGTTTTT TGGCCTGGAT TAAAnATCTT TCGGGCGGAT 400

(2) INFORMATION FOR SEQ ID NO: 3985:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3985:

30 GCATTTGCTT ATATCTTTAA AAAAGATTTT GAAGATATTG AAAGAAAAC TAAAGAAATT 60
 ATTTCTGATA TTGAAAGTAA AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT 120
 AAAAAAnCAGC AGTAAGATAA TTTTCAATTA GAAATATCT TACTGCTGTT CTCTATTTAT 180
 35 ACAATACTTC GTATTGAAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTTGGTCTTC 240
 GACTGGCACT GCTCCCTCAG GAGTCTCGCC ATTGAATACT ACGTATTAAAC ATGTnAATTT 300
 TACTTTGGAA ATACTTTTAA AAAATAAGAC ACTTTGCCCA ACTTGGCACA TAAATGTTAA 360
 40 AATnCAATGA AATGAATTTT CTGTGTTGGG TCCCCTnCTA 400

(2) INFORMATION FOR SEQ ID NO: 3986:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3986:

55 TTCGTTCAAA GTCATCTAGG TCACATTATT CTATTTGGGA TTCTTAGTGC TGTTCTTATT 60

ATGACAATAC AAAACGTAAA AAAGTCGCAG TGATCGGTAG TATTTTAGTA TTTATCATT 180
 GTATTCCAGC AACCTTATCT TTTGGTATCT TAAAAGATGT AAGATTCGGT GCGGGAACGA 240
 5 TTTTGTATAA TATGGATTTC ATCGTTTCGA ATGTATTGAT GCCATTAGGC GCATTAGGTA 300
 CTACGCTTGT CGTAGGnCAA TTATTAGnTA AAAAATTATT ACAnCAATAT TTTGGTAAAG 360
 AnCGATTTAG GATTATTCAG TGGTTGGTAT TACTTAATTA 400

(2) INFORMATION FOR SEQ ID NO: 3987:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3987:

GGATTCGAAC CCCCGCGAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA TCCCTTCAGC 60
 CGGACTTGGG TATTCTCCA AAATTATATG GACCTTGCAG GACTCGAACC TCGGACCGAA 120
 25 CGGTTATGAG CCGTTAGCTC TAACCAACTG AGCTAAAGGT CCTAAATATA ATTTTACAAC 180
 TAATAAATAG TGGCGGTGGA GGGGATCGAA CCCCCGACCT CACGGGTATG AACCGTACGC 240
 TCTAGCCAGC TGAGCTACAC CGCCTTATAT AGTTTGTAAT TAATATGGTG GGGACTAnCG 300
 GGATCGGAAC CGCTGGACCT CCTGCGTGGC AAAGCAGGCC GCTCTCCCAG CTGGAGCTAA 360
 GnCCCCCATA ATAATnACAG TATATCnGGG AAGACAGGAT 400

(2) INFORMATION FOR SEQ ID NO: 3988:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3988:

CAGCTGATAA ACAAGTTGAT CTGGTCCCGA TTTGTGGGT AAACGGTTGA TTAATGnAAA 60
 ATGTTCCGCG AAGGATTCAT AATCCGAGAG GTCTAATTCA ACGTATCATT AATCAAGATG 120
 50 CGCCTATTTA TCAATCTGAA ACAAATTATC ATTGAAAGA TCGCGGTAAG TCTAAAAATG 180
 GTATTCAAAT GGTGTATCAA CATTTAATGA ACGGTGTATC GTTTATGGnT CCTTTTATCG 240
 TAGTTGGTGG ACTCCTTATC GCCATCGCGC TGACTCCTAG GCGGTGAACG ACCATCCAAA 300

CCTTTAAATT AATGGTCCCA TACCAGnCGG GATAAACGCT

400

(2) INFORMATION FOR SEQ ID NO: 3989:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3989:

15	CCAGAGATTT CCGAATGGGG GAAACCCAGC CATGAGTTAT GTCATGTTAT CGATATGTGA	60
	ATACATAGCA TATCAGAAGG CACACCCGGA GAACTGAAAC ATCTTAGTAC CCGGAGAAGA	120
	GAAAGAAAAT TCGATTCCCT TAGTAGCGGC GAGCAAACGG GAAGAGCCCA AACCAACAAG	180
20	CTTGCTTnGn GGTnGTAGG ACACTCTATA CGGATTACAA AGGACGACAT TAGACGAATC	240
	ATCTGGAAAG ATGAATCAAA GAAGTAATA ATCCTGTAGT CGAAAATGTT GTCTCTCTTG	300
	AGTGGATCCT GAGTACGACG GAGCACGTGG AAATTCGTC GGAATCTGGG AGGACCATCT	360
25	CCT	363

(2) INFORMATION FOR SEQ ID NO: 3990:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3990:

40	TTTCCAAGAA CATGAGCCTG TACAGTTAAC ACCATGTnTG nTTCTTACTT CTTTATCGTG	60
	GCTCCAACGT TCTCTGTACA TTTTTCCTCA TTCTTACTT TTACTTTCTA GGATCGACCA	120
	ATTCCCATTA AATTTTCTG TTGGCTTAAA GAAATTCAT CCAAATTTTC CCATATTTAT	180
45	ATCCTCCTAC GTATAAAAT ACGATGTGTA GATGTCGTGT TTTTAAATAC TTTAAATGC	240
	CCAAGACTAT TGCTTTAATT AGATTGTACA TTTTTCACA AACATAAAAT ATTAGGGAAT	300
	CACCTAATTA CTTAAGGnAT TCCCTATCAA TAACGGGATT TCATTGAAAT AATACACAAT	360
50	CAGTAnGGTC AGCCTAATGC CAGGCTAAAT CGTTCAAATT	400

(2) INFORMATION FOR SEQ ID NO: 3991:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3991:

AAAGTGGTTA AATATTATAG AAAACATCAA AGGATGTAA GAAATACAAT TTATTACCCA	60
GCATTTAATA ATGGTGCTAT AGAAGGAATT AATAATAAGA TAAATTAAT CAAGTGAATT	120
TCTTTTGGTT ACAGAAATTT CAACAACCTT AAAGCAGTA TAATGATGAT TTTCAGCTTG	180
TACAAAGGAG AAAAAAGAA GACAACCAAG CCCAATAATG GACTGGCCGC CTAATAATnn	240
GAGCTCTAAA AGTTGTATTT TAAAAATAGT TCTTTAAATT ATATACCCAC CACATTTGGT	300
GGAGAACCTA AAAAAAGCA CTTCCCAAAA ATGGAAAGTG CAAGTAGTGA GCCATAGAGG	360
ATTCGAACCT CTGACCCTCT GATTAAAAGT CAGATGCTCT	400

20

(2) INFORMATION FOR SEQ ID NO: 3992:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3992:

AGTGTATGGT TATCAAAGAT TTGATACGAC GGTCATTATT ATTACCGTTA TTGTATTAGT	60
CATTATTGTC CAAGTGATTC AAACGCTAGG GAATGTTCTA GCTAGATTCA TACGTnGACA	120
TTAATGATAT ATAGTGAAGA TTTTGAAAGG AATTGATAGA ATGAAAAGAT TGATTGGGTT	180
AGTTATCGTA GCACTTGTAT TAATTAGCAG CGTGTGGTGG TAACAATGAT AAAAAAGTAA	240
CAATTGGTGT CGCATCAAAT GACACTAAGG CTTGGGGAGA AGGTAAAAG AATTAGCTAA	300
AAAAAGATGG ATnTTGATGT GGGAGATTAA GCACTTCCTC nGGATTACAA TTTACCGGAT	360
TAAAGCCTTn AAATGGATGG TGATATTGAT AATGAATGCC	400

45

(2) INFORMATION FOR SEQ ID NO: 3993:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3993:

55

TTATCAGAAG AACAAATTCGA CATTTTACTG AATCATCCAT TAATCGATGA AGAAGTAGCC 120
 AATAGTTTAA TTGAAAATGT CATCGCGCAA GgngCATTAC CCGTTGGATT ATTACCGAAT 180
 5 ATCATTGTGG ACGATAAGGC ATATGTTGTA CCTATGATGG TGGAAGAGCC TTCAGTTGTC 240
 GCTGCAGCTA GTTATGGTGC AAAGCTAGTG AATCAGACTG GCGGATTTAA AACGGTATCT 300
 10 TCTGAACGTA TTATGATAGG TCAAATCGTC TTTGATGGCG TTGACGATAC TGAAAAAnTnT 360
 CCGCCGGCAT TGAGAGCCTT AGA 383

(2) INFORMATION FOR SEQ ID NO: 3994:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3994:

GGTACTATGA TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGCCTTTCGT 60
 25 GCGGGTCGGA ACTTACCCGA CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC 120
 GCCTTTACTG GGGCTTCGAT TCGTAGCTTC GCAGnnAAAC CnACTCCTCT TAACCTTCCA 180
 30 GCACCGGGCA GGCGTCACCC TGATACATCA CCTTACGGTT TAGCAGAGAC CTGTGTTTTT 240
 GATAAACAGT CGCTTGGGCC TATTCAGTGC GGCTCTTCTG GCGGTTAACC CTGAAAGAGC 300
 ACCCCTTCTC CCGAATTACG GGGTCATTTG CCGATTCCTT AACGAGATTC GCTCGCTCAC 360
 35 CTTAGA 386

(2) INFORMATION FOR SEQ ID NO: 3995:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3995:

AGATATTTTA CATGTGAATC AAGTAGGTAT TCATGATAAT TTCTTTGAAT TAGGTGGCCA 60
 50 TTCATTAAAA GCAACGTTAT GnTGAATCGG ATAGAGGCAT CTACTGGGAA ACGATTACAA 120
 ATTGGTGATT TATTACAAAA GCCAACTGTA TTTGAACTAG CACAAGCGAT TGCTAAGGTT 180
 CAAGAACAAA ACTATGAAGT GATTCCAGAA ACTATAGTTA AAGATGATTA TGTGCTGAGC 240

55

GTACCTTTTT TATGGCGGTT ATnCATCAGA ACTTAATGTA GTCAnTGCG ACAAGCATG 359

(2) INFORMATION FOR SEQ ID NO: 3996:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3996:

15 CAATTATTGG TATTCAACTT AAAGATCATG ATGATTTAAT ACAACTCAAA CAACGTTnAA 60
 ATCATTTTCA TCCTTCCAAT ATTTATATTA ATGAAAATAA GATGTTATAT TCATTGTAA 120
 TTTAACACAT AGTAAGAAAA ACAGTCATAA ATTGATTCTT AATTGAAATC ATCTTATGAC 180
 20 TGCTTTTTTAT TATACTTTAC ATTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA 240
 AGCCATCITT CTTTGTGTTT GCTTTTATTT TGACGTTTAA GACATAAAAA AAGAGACCTT 300
 GCGGTCTCAA ATGCGGCTCA TCGCATCCAC TTTTTCCTG GGCAACGTTT TACTCTAGGC 360
 25 GGAAngTAAG TGGGACTTAC CATCGACGGn TAAGGGGCTT 400

(2) INFORMATION FOR SEQ ID NO: 3997:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3997:

GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC TTATCGTGGT GGGAGACAGT 60
 40 GTCAnGCGGG CAGTTTGACT GGGGCGGTCG CTCCTAAAAG GTAACGGAGG CGCTCAAAGG 120
 TTCCCTCAGA TGTTTGAAA TCATTCATAG AGTGTAAGG CATAAGGGAG CTTGACTGCG 180
 AGACCTACAA GTCGAGCAGG GTCGAAAnCG GACTTAGTGA TCCGGTGGTT CCGCATTGAA 240
 45 GGGCCATCGC TCAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG 300
 TTCACACGAC GGGGAGGTTT GGCACCTCGA TGTCGnCTCA TCGCATCCTG GGGCTGTA 358

(2) INFORMATION FOR SEQ ID NO: 3998:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3998:

5 TAGGAGGAAT TTATATGACA TTTGAAAAAG AAACGGTCTT AAAACATTA TTTCCTGAAG 60
 ATGTACTTAG TATTGCTAAA GGTTTAACAG ACGGTGAAGT CGAATTTTTA CAACAAGTAG 120
 ATTCATTGCT AGAAAGTAAG TACCGTGAAA ATATTAATCA ACATTGGATA GACGCTACTG 180
 10 TACCCGAGGA CTATTTTAAA GATCTGGGAG ArTTAAATTA TTTTAACArT CCATTACTTT 240
 ACAAGGATCG TCCAAACGCC AAAATGCCTA GTCAnCTATT TCAGTTTTC ATGTCTTACC 300
 TACTCGCGCG ATTTGATATT TCCTTAGCTA CCCTACTCGG TGTTCAACAA GGTTAGGGCA 360
 15 TAACACTTTC TATTTTCGGAG GTAGCAAAGA CAAATTGCGA 400

(2) INFORMATION FOR SEQ ID NO: 3999:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 398 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3999:

CGCCCCCTTAG TGCTGCACtA ACGCATTAAg CACTCCGsCT GGGGAGTACG ACCGCAAGTg 60
 30 AAACtCAAAG GAATTGACGG GGACCCGCAC AAGnGTGGAG CATGTGGTTT AATTCGAGGC 120
 AACGGtAGAA CCTTACCAAA TCTTGACATC CTTTGACAAC TCTAGAGATA GAGCTTTCCC 180
 CTTCGGGGAC CAAAGTGACA GGTGGTGCAT GGTGTGCGTC AGCTCGTGTC GTGAGATGTT 240
 35 GGGTTAAGTC CCGCAACGAG CGCAACCCtT AAGCTTAGTT GCCATCATTa AGTTGGGCAC 300
 TCTAAGTTGA CTGCCGGTGA CAAACCCAGG AAGGTGGGG ATGACGTCAA ATCATCATGC 360
 40 CCCTTATGGn TTTGGGTTAC ACAAGTGGTT ACAATGGG 398

(2) INFORMATION FOR SEQ ID NO: 4000:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4000:

TGTTCTTGCA ACGCTATTa GTATCAGGTT TAACAACAGG TGCGACAAA GGTTAGTTTG 60

55

GACGTTATGA TGACGATTAA AGTTGGAATC ATTGGGTGTG GTGGTATTGC GAATGGCAAG 180
 CACATGCCAA GTTTACAAAA AGTTGAAAAT GTTGAAATGA TCGCATTTTG TGACGTAGAC 240
 5 ATTCGAAAG CAGCGaGTGC GGCAGAAGCA TACGGAACTG ACAATGsCAA aGtTTATGAT 300
 GATTACmAAAG CaTTGTtAAA AGATGACACG ATTGATGTTA TCCATGTTTT GTACCCCCAA 360
 TGGACCCCGC ATTGTGG 377

10

(2) INFORMATION FOR SEQ ID NO: 4001:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4001:

TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACATGTAG GCCGTGTGCA 60
 CTTAACTTCT TGTTTTTCCG ATGACAGCTT CTATTTAGAG AATGTCATGA TTATTTTATA 120
 25 TTCACTTCAA TGTTATCAAT ATTAGTGCCA TCTATGACAT CTGCCATGCG ATTTTCTTGT 180
 AATTTTTTGT GCAATTCAAA CGTGACTTTT CCACCGTTTT TCATTTTAAT AACAAATTTA 240
 CCTGAACCAA CGTTACCGTA CAGATTATTT TTTTCAATAA GTGTTTCTC AATTAAAAAT 300
 30 CAAGTTCTTT CAAGGAAATC TGTTCCTTAG TAATCTTGAA TTCTGAAACA TCATGGGnGA 360
 TTGTACCGTA TnATCTTnCC TAGTAAT 387

35

(2) INFORMATION FOR SEQ ID NO: 4002:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4002:

CTATTACGAT TGCTGCGAAA GAAGGTATTA AAAATATACA AATAGGCATG GCTCACCGTG 60
 GACGTTTAAA CGTTTTAACG CATGTCTTAG AAAAACCGTA CGAAATGATG ATTTCAGAAT 120
 TTATGCATAC AGATCCAATG AAATTCTTAC CTGAAGATGG TAGCTTGCAG TTAAGTCTG 180
 50 GATGGACTGG TGATGTGAAA TATCACTTGG TGGGCATTAA AACTACTGAT TCATACGGTA 240
 CAATGCAGCG TATTGCACTG GCTAACAATC CAAGTCACTT GGAAATTGTT GCACCTGTTG 300

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TCCATCATAA AnGCAATGnC CATTGTTGAT ACATGGCGAT

400

(2) INFORMATION FOR SEQ ID NO: 4003:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4003:

15 AGAAATATAT GCATTTCCGA TATCATGGTA AAGAGAATGG ATTAAGCGGT AAATCACGTG 60
 ATGAAGTGCG AGCGAAATGA AACAAAATTT AGATGTCATG CGAGACGATA ATCAAAGGGA 120
 CGACAGGTGA TGGGGTTGAA AGTGTAAACGn GCTACACTGG TCATGATGCT GCTAAACTAC 180
 20 GTGATTATAA TGAAACACAT CATGCTTTGT CTGGATATGA AATGATTGAC GCAGCAAAGG 240
 TGCCATTGCA ACAAATGAAG TCAATGCTGC GATGGGTATT ATTTGTGCAC GCCAACAGCT 300
 GGTTCCTCGG GTACCATTCC CGGTGCACTT TTAAATTAG GAAAAACAC ATGATTTAAC 360
 25 AGAAGAGCAA ATGATTTGAT TTCTTATTCA CTTCAGCATT 400

(2) INFORMATION FOR SEQ ID NO: 4004:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4004:

40 TGAAATAGAA CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCCTTAAT GGGTGATGGC 60
 GTGCCTTTTG TAGAATGAAC CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT 120
 GGAGCCGTAG CGAAAGCGAG TCTGAATAGG GCGTTTAGTA TTTGGTCGTA GACCGAAACC 180
 AGGTGATCTA CCCTTGGTCA GGTGAAGTT CAGGTAACAC TGAATGGAGG ACCGAACCGA 240
 45 CTTACGTTGA AAAAGTGAGC GGATGAACTG AGGGTAGCGG AGAAATTCCA ATCGACCTGG 300
 AGGATAnTGG TTCTCTCCGA ATAGTTTAGG GCTAGCCTCA AGTGTGATTA TTGAGGTAGA 360
 nACTGTTTGA CGAGGGGCCC TCTCGGTAC CGAATTCAGG 400

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(2) INFORMATION FOR SEQ ID NO: 4005:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 415 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4005:

	ATACTAAGGC GTTATTAGAC GaTTAGACAA TGGTGTGATT AAAGGTGCAG CACTTGATAC	60
10	GTATGAATTT GAACGCAAAC TTTTCCCAAG TGATCAAAGG GGCAAAACAC TGAACGATCC	120
	ATTGTTAGAA TCGTTGATTG ACAGGGAAGA TGTCATATTA ACACCACATA TTGCGTTTTA	180
15	TACTGAAGCT GCAGTTAAAA ATCTAATTGT CGATGCATTA GATGCAACAT TAGATGTATT	240
	GGCAGACTGG AGATACTAGG TTACGAGTAA ATTAAAAATC GAACTGATGA GATAATTTGG	300
	ATTGTTGGGG ATTCTGCATC CAGTTCGATT TTTTAAATTT GGTGTTGGAT GACGTTGnAA	360
20	TGTTGCCTAA TTAAACGAC ATCGTAAACC nTGGATCCTC CAATGGCGTC CTTnC	415

(2) INFORMATION FOR SEQ ID NO: 4006:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 444 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4006:

	CTAACAGAAG CTAGTATAGG AAATCGGTAC TCGTTAAGGC TGATCTGTGA TGGGGAGAAG	60
35	ACATTGTGTC TTCGAGTCGT TGATTTCAACA CTGCCGAGAA AAGCCTCTAG ATAGAAAATA	120
	GGTGCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG	180
	AACTCTCGTT AAGGAACTCG GCAAAATGAC CCCGTAACTT CGGGAGAAGG GGtGCTCTTT	240
40	AGGGTTAACG CCCAGAAGAG CCGCAGTGAA TAGGCCCAAG CGACTGTTTA TCAAAAACAC	300
	AGGTCTCTGC TAAACCCGTA AGTGATGTAT AGGGGCTGAC GCTGCCCGGT GCTGGAAAGT	360
	TAAngAGAGT GGGTTACTTC TTGCGACTTA nCGAAATCGA GnCCCCAGTA AACGGCGGGC	420
45	CGTAACTATA AChnGCCTAA GGTA	444

(2) INFORMATION FOR SEQ ID NO: 4007:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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TTTGAACTCT ATCAAAGCAT CAGCAATCAA AACATACGTA TCTTTACAAC AGTAATCATG 60
 CATTCTATGA TGCTTCTAAC TGAATTAAAG CATCGAACAA TCGGAAGCAT ATTTCTAAAT 120
 5 TATTTATTCA TTATAGTCTT AAACATAACA TGACCTAATA TATTACTAAC CTATTAAAAAT 180
 AAACCACGCA CATCTAAGTG ATATACGACA ATCACAGCAA TAATAATTGC TTTAGAAAGT 240
 CGTGCCGAAC TGGAACCTAC AAGTCTAGTT CGAACACACA CTGATGTGAG TGGTTTTCTT 300
 10 TATTTTAAAC ATGAACAATC AGATAAGTTA CTAGCATTAG CAAATATTAT TAAATCAAGG 360
 GCTTCGnTTC ATAAATTAA AACATGTTAA ATTAGACGTG 400

15 (2) INFORMATION FOR SEQ ID NO: 4008:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - 20 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4008:

TATACTTGTT TTTACAAACC ACAAAAAGCT CTAAACATTA GTTTAAACCA ATGCTTAGAG 60
 CTTTCTAATT ATTTTATGCT TTAAAAGATA CTGTGTTATC TACGATGACC TTACCGTCTT 120
 30 TAATAACTTT TTCTGCGTGA TTGATACCAA AATGATATGG AATATATTCA TGATTGGTG 180
 CATCCCAAAT TACTAAATTA GCCTTATCAC CTGTGTTAAT TGTACCCGCG TTAATGTCTA 240
 TTGCTTTAGA GCCATTGACC GTAACAGCAT TCCAACTTC ATTAGGTGAT AGCTTTAATT 300
 35 TCAAGGCTGC AATCGCCATA ACAAGTTGTA AGTTGTTTGT GGACACTACT ACCAGGGTTA 360
 TAATCAGTTG GCTAATGCCA TCGGCACCGG TTAATGGTCC 400

40 (2) INFORMATION FOR SEQ ID NO: 4009:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 400 base pairs
 - (B) TYPE: nucleic acid
 - 45 (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4009:

50 ACAACATTG AAATTAGAGG TATATAAAAA ATGCTTCTGC AATAGATGCA ATAAACATGC 60
 AATACAATAT GGAGGCGAAG TAAATGAAAA GTATTACGTT TGAAGAACAT TATGTCATTG 120
 55 AAGATATTCA AAAAGAAACG ATGAATGCGA TATCAGCAGA TCCTAAAGGT GTACCGATGA 180

ATCATGATGA ACGTATCCAA TTTATGAATA ATCAAGACGT TCAAATTCAA GTCTTATCTT 300
 ATGGAAATGG TTCTGCTTCA AATTGGTTG GTCAGAAAGC CATTGAATTA TGTCAAAAG 360
 5 GCAAATGATC CATTGGGCAA ACTATATTGC ACCATATCCC 400

(2) INFORMATION FOR SEQ ID NO: 4010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4010:

ACTAGAGAAG GTATGTTACG TGACAATGAA TTAATAATG GTATTTATTC ATCGAGTTAC 60
 20 ATCTATAGTT TATTAAATC AGAATACGAC CAAAATGAC AAATTAGACT TACAAAAGAG 120
 TGATGACATT TAAATGGCA GCGCTCTTTT ATTTAATTTT TGAAAATAAA AGGTGTGTTGA 180
 CAGTATTATT TTATAACAAT ATAATGATTT TGATAATTAT TATCAACTAG ATGATGTTTA 240
 25 TGGGAGGATG CTTTAAACA GCCGTTTAA GTGTAATGTA TTATTTTAGC GTGTAGGGAT 300
 GCGAAAATAT ATTTATAGGA CACATCTTGG GGATAATnGA TTTCTATAAT GAGGTGTCAA 360
 30 ATGGAAAAGT TACCACGCTA TTATTAGCCn CCACGTTATT 400

(2) INFORMATION FOR SEQ ID NO: 4011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4011:

TnTCAATTAG AAAATATCTT ACCGCTGnCT CTATTTATAC AATCCTCGTA TTGAATGGnT 60
 CGCTTTCCTA GGGTGCCGTC TCAGCATCGG CTTGACTGG CACTGCTCCC TCAGGAGTCT 120
 45 CGCCATTAAT ACTACGTATT AACATGTAAT TTTACTTTGA AATACTTTAA AAAAATAAGA 180
 CACTTTGCCC AACTTACACT ACCAATAAAA ACTTCTGTGA GAATTCCTCA AAATGATATT 240
 50 TCGCGACATG TTAATGAAAT TGTTGAAACG ATACCTGATA GCAAATTCGA TGAATTCAGA 300
 CATCATCGTG GCGCAACATC CTATCATCCA AAGATGATGT TAAAAATCAT CTTATATGCA 360
 TATACTCAAT CTGTATTTTC TGGTCGTAGA ATAGAGAAAT TACTTCATGA CAGTATTCGA 420

GAATCCnAAT ACTG

494

(2) INFORMATION FOR SEQ ID NO: 4012:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4012:

15 TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGACATA 60
 AAAAAAGAGA CCTCACGGTC CAACITGCCT GGCAACGTTT TACTCTAGCG GAAGTAATTG 120
 GCTACCATCG TCGCTAAAGA CCTTTCTTGA CTTGTGACAA TCGCTTGCTT CTTTCCTCTC 180
 20 CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGGCTCTTT TCTCGTTTCG 240
 TCAGATTCAA ACGTTTTCAC TTCGCCAAGC CATTTTTCCT TGTGTTTACT TTTTATTTTG 300
 ACGTTTTAGG CATAAAAAAA AGAGACCTTG CGGTCCCAAT GCGGGCTCAT CGCATCCATT 360
 25 TTTTGGCCTG GGCAACGTTT TnATnCCAGC GGAAnTnAAT 400

(2) INFORMATION FOR SEQ ID NO: 4013:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4013:

CGAACTGCCG AACCCGAAGA GCGGATTTAC AGTCCGCCGC GTTTACCACT TCGCTACCCC 60
 40 TCCAGCTTAT TCATATAATT TAATAATCAA AATGGTGGAG AATGACGGGT TCGAACCGCC 120
 GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGACT 180
 CCTACGGGAC TCGAACCCGT GTTACCGCCG TGAAAGGGCG GTGTCTTAAC CGCTTGACCA 240
 45 AGGAGCCATG GCTCCACAGG TAGGACTCGA ACCTACGACC GATCGGTTAA CAGCCGATAG 300
 CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTTA CTCTnAGCGG 360
 50 AACGTGAATT CGACTTACCA TCGACGnTAA GGAGCTTnAC 400

(2) INFORMATION FOR SEQ ID NO: 4014:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4014:

	ATTAGGACCT CAAGACGATA TTACTAAATT TGAATACTTA AAAAAATCTT CTCAAAATAC	60
10	AGGTACTTCA TTATTGGTAT TCAACTTAAA GATCATGATG ATTTAATACA ACTCAAACAA	120
	CGTGTGAAAT CATTCGATC CTTCCAATAT TTATATTAAT GAAAATAAGA TGTTATATTC	180
	ATTGTTAATT TAACACATAG TAAGAnAAAC AGTCATAAAT TGATTTCTAA TTGAAATCAT	240
15	CTTATGACTG CTTTACATT ATACTTTACA TTTCTCGTTT CGTCAGATTC AAACGTTTTTC	300
	ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTATTTT GACGTTTTAG ACATAAAAAA	360
	nGnGACCTGC GGTCTCAATG CGGCTTCATC GCATCCACTT	400

20

(2) INFORMATION FOR SEQ ID NO: 4015:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4015:

	GAATGAAAAG CTCTAAAAGT TGTATTTTAA AAATAGTTCT TTAAATTATA TACCCACCAC	60
	ATTTGGGGAG GAACCTAAAA AAAAGCACTT CCCAAAAATG GAAAGTGCAA GTAGTGAGCC	120
35	ATAGAGGATT CGAACCTCTG ACCCTCTGGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT	180
	AATGGCTCTG AATGGCTGGG CTAGCTGGAT TCGAACCAAC GAGTGACGGA GnAAAGGTCC	240
	GTTGCCTTAC CGCTTGGCTA TAGCCCAATA TATAGATGGT GGAGGGGGGC AGATTCTGAAC	300
40	TGCCGAACCC GAGGAGGCGG ATTTACAGTC CGCCGCGTTT AGCCCACTTC GnTACCCCTG	360
	CCAGnTTATT CATATGA	377

45

(2) INFORMATION FOR SEQ ID NO: 4016:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4016:

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ATGACGCACC TGACATCCTC TCGGTTTCATA TTCAGGCATA TCCGGACCAC AACTTGGATA 120
 GTCAGTTTGT TGATTTTCCC AGGTAATCAC ACCATTTTTC ACAAATACTT TCCAAGAACA 180
 5 TGAGCCTGTA CAGTTAACAC CATGTGTTGT TTCTTACTTC TTTATCGTGG CTCCAACGTT 240
 CTCTGTACAT TTTTTCCTAT TCTCTACTTT TACTTTCTAG GATCGACCAA TTCCCATGA 300
 10 AATTTTCTG TTGGCTTAAA GAAATCAATC CAAATTTCCC ATATTTATAT CTCCTACGG 360
 GTGAAAAATA CGGTGTGTAG AnGTCGTGGT TTTTnAAATA 400

(2) INFORMATION FOR SEQ ID NO: 4017:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4017:

25 CTTTGAGCGC CTCCGTTACC TTTTAGGAGG CGACCGTCCC AGTCAAAGTG CCCGnCTGAC 60
 ACTGnCTCCC ACCACGATAA GGGCGTGGGT TAGAAAGCCA ACACAGCTAG GGTAGTATCC 120
 CACCAGCGnC TCCACGTAAG CTAGCGCTCA CGTTTCAAAG GCTCCTACCT ATCCTGTACA 180
 30 AGCTGTGCCG AATTTCAATA TCAGGCTACA GTAAAGCTCC ACGGGGTCTT TCGTCCTGT 240
 CGCGGGTAAC CTGCATCTTC ACAGGTACTA TGATTTCAAC GAGTCTCTCG TTGAGACAGT 300
 GCCCAAATCG TTACGTCTTT CGTTGCGGGT CGGAACTTAC CCGACAAGGA ATTTCGTTAC 360
 35 CTTAGGACCT TATAGTTACG GCCGnCTTTA ATTGGGGTTT 400

(2) INFORMATION FOR SEQ ID NO: 4018:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4018:

45 TGTCGATTTA AGAGGCATGC TACGAGGAAT GATTGGTCAT CCGAAAAAG ATCGAGCGGC 60
 50 ATATGAGGCA CGCCAAGCGA TTCCAAACAT TAATGAAAAC AGTCCGCCAA TATTAATTGT 120
 ACATGGAGGG AAAGACCAGC AAGTTGGTAT TCATCATGCG TATTATTTAG CGGACCAACT 180
 AGAGTTAAAA GGTGCCACGC ATGnAAACAT TTTATCAAAT GGCAGAAGGA CATGTGCCAA 240
 55

CGCATAGCTT ACTTATGGAA ACGTGGTGTG CGCATGGGGA ACTATTCAAG CTTTGGAGGA 360
 TGTGGTACTT ACATGCGTTG GAATTAGGGG TCCGTTACT 400

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(2) INFORMATION FOR SEQ ID NO: 4019:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4019:

15

GGAGGTTTGG CACCTCGATG TCGGCTCATC GCATCCTGGG GCTGTAGTCG GTCCCAAGGG 60
 TTGGGCTGTT CGCCCATTAAG ACGCGGTACCA AGCTGGGTTT AGAACGTCGT GAGACAGTTC 120
 GGTCCCTATC CGTCGTGGGC GTAGGAAATT TGAGAGGAGC TGTCTTAGT ACGAGAGGAC 180
 CGGGATGGAC ATACCTCTGG TGTACCAGTT GTCGTGCCAA CGGCATTAGC TGGGTAGCTA 240
 TGTGTGGACG GGATAAGTGC TTGAAACATC TTAAGCATGA AGCCCCCTC CAAGATGGAG 300
 ATTTCCCAAC TTCGGTTTnT AAGATCCCTC CAAAGnTGAT GGAGGTTTAA TAGGTTTCGA 360
 GGTGGGAAGC AnGGTGGACA GTTGGGAGCT GGACGAnTAC 400

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(2) INFORMATION FOR SEQ ID NO: 4020:

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4020:

40

GAAGATGTTT GTCATTCTTC AAATAAACCA GAGCTAGTTG CAATTGCTGA ACCAGCATCT 60
 AATAGACCGA AAAAGAGAAG TAGACGTGCG GCACCGGCAG ATCCTAATGC AACTCCAGCA 120
 GATCCAGCGG CTGCAGCGGT AGGAAACGGT GGTGCACCAG TTGCAATTAC AGCGCCATAT 180
 ACGCCAACAA CTGATCCTAA TGCCAATAAT GCAGGACAAA ATGCACCTAA CCGAnTnTTG 240
 TCATTTTGAT GACAATGGTA TTAGACCAAG TACCAACCGT TCTGTGCCAA CAGTTAAACG 300
 TTTGTTAATA ACTTGCCGGG CTTCACTA ATCAATGGTG GGCAAAGTAn GGGTGTTTAG 360
 TCATGCAATG GGTAAGAACG AGCATGTTTG GATTTACGGG 400

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(2) INFORMATION FOR SEQ ID NO: 4021:

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(A) LENGTH: 396 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4021:

10 CTAAGTCATG AATGGGAAGT GGCTCGCGTT GAAGAAGGAC TGACTACTGC TGCCACACAG 60
 CTTGCTAAAC AATTATCAGA ATTAGATTTA GCGTCACATC CTTTGTGAT GTCAGAGCAG 120
 TTTGCAAGTh TAAAAGATCG TCCATTTTCAT CCATTAGCTA AAGAAAAAAG AGGATTAAGA 180
 15 GAAGCGGATT ATCAAGTGTA TCAAGCTGAA TTAAATCAAT CATTTCCTTT AATGGTTGCA 240
 GCAGTTAAAA AGACACATAT GATTCATGGC GATACTGCAA ATATCGATGA ATTAGAAAAT 300
 TTGACAGTAC CTATAAAAGA ACAAGCGACA GACATGTTAA AATGATCCAA GGTATCAnT 360
 20 AGATGACTAT GTACCATTCC GGTACnTCCT GGCCAT 396

(2) INFORMATION FOR SEQ ID NO: 4022:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 376 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4022:

GATTGGTCTG nAAGAAGAAT TAATGGAAAA GCTACGTGAA AAATTAGAAG CGGCATTTGA 60
 35 TACGATTTAC GAATTGTCTC AAAACCGAAA AATAGATATG AGACTTGCAG CATATATCAT 120
 AGGTATTAAA CGTACAGCAG AAGCAGCTAG ATATCGTGGT TGGGCATAAT TAATTATCAT 180
 ATGTGATTTA ACGAGCTTGG GACAGAAAAC AAAGCCCTAA GTCGTTAAT TTTATTTTAG 240
 40 CAGTAGTTGA CTGTAAAACA ATGCCCGTGT AAACGCTCTT TTCAAAAATA GTCGGGGCCC 300
 CAACACAGAG GCTGGTGGGA AAGTCAGCCT ACAATAGnGT GCAAGTTGGC nGGGGCCCCA 360
 45 ACACAGAGGC TGGCGG 376

(2) INFORMATION FOR SEQ ID NO: 4023:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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CAAATGGTGG AGCCATAGGA GGATTGGAAC CTCTGACCCT CTGATTAAAA GTCAGATGCT 60
 CTACCAACTG AGCTAATGGC TCTTCCATGG nGcngGCCAG AGGACTTGAA CCCCCAACCT 120
 5 ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC GGCAATATGT AAGAATAAAT 180
 GGTGGAGAGT GACGGGTTTC AACC GCCGAC CCTCTGCTTG TAAGGCAGAT GCTCTCCCAG 240
 CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTT TACTCTAGCG GAAnTAATTC 300
 10 GGACTACCAT CGACGCTAAA GGAGCTTAAC TTCTGTGTTT CGGCATGGGA ACAGGTGTGA 360
 CTCCTTGCTA TATCACCAGA C 381

15 (2) INFORMATION FOR SEQ ID NO: 4024:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4024:

25 GCCCCTTATG ATTGGGGCTA CACACGTGCT ACAATGGACA ATACAAAGGG CAGCGAAACC 60
 GCGAGTCGAA GCAAATCCCA TAAAGTTGTT CTCAGTTCGG ATTGTAGTCT GCAACTCGAC 120
 TACATGAAGC TGGAATCGCT AGTAATCGTA GATCAGCATG CTACGGTGGA ATACGTTCCC 180
 30 GGGTCTTGTA CACACCGCCC GTCACACCAC GAGAGTTTGT AACACCCGAA GCCGGTGGGA 240
 GTAACCTTTT AAGGAGCTAG CCGTCGAAGG TGGGGACAAA TGGATTGGGG TGAAGTCGTG 300
 AACAAAGGTAG CCGTGATCGG AAGGTGCGGC TGGGATCACC TCCTTTGCTG AAGGATGATG 360
 35 ATTTCCGnAA CATCnTTCTT CCAGAAGATG CCGGTAATAA 400

(2) INFORMATION FOR SEQ ID NO: 4025:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4025:

CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGGG TGAGAATCCC GTCCACCGAT 60
 50 TGCTAAGGTT TCCAGAGGAA GGCTCGTCCG CTCTGGGTTA GTCGGGTCCT AAGCTGAGGC 120
 CGACAnGTAn GGCGATGGAT AACAGGTTGA TATTCCTGTA CCACCTATAA TCGTTTTAAT 180

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GCTGAGTATT AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT 300
 GTGTCTTCGA GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AA 352

5 (2) INFORMATION FOR SEQ ID NO: 4026:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4026:

TGGGGCTCTT CCCGTTTCGC TCGCCGCTAC TAAGGGAATC GAATTTTCTT TCTCTTCCTC 60
 CGGGTACTAA GATGTTTCAG TTCTCCGGGT GTGCCTTCTG ATATGCTATG TATTCACATA 120
 TCGATAACAT GACATAACTC ATGCTGGGTT TCCCCATTCTG GAAATCTCTG GATCAAAGCT 180
 TACTTACAGC TCCCCAAAGC ATATCGTCGT TAGTAACGTC CTTCATCGGC TTCTAGTGCC 240
 AAGGCATCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA 300
 AnGTTAACAT GAAGTTAGGT TCTTTTATAA AAGGATTAAA nGGGTTATTA ATCTTGtGnG 360
 TGTTCCTTCG 370

(2) INFORMATION FOR SEQ ID NO: 4027:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4027:

TCATGTTTCG CTTGGTTTAA TGCTGTAAAT GCGTTATCGA CACGATGTTT TTCATCTGAA 60
 AATTGTTGTG CAGTTGCATC GCCATTGTCA ATAACACGTT GAGCTGCAGT TATTTAGTT 120
 TCTGCTTCG CTTCTTCGCA TTATAGTTAT CAATACTTTG TTGCGTCATA CCAGCAGTTG 180
 ATGGTACTTG GTTCACAGAA CTTTGTAAGT TATTTTAGA CGTACTAAT TGGCTATTAT 240
 CTTCTTTATT TTGAAGTAAT GCTTTACTTG GATCAATCTT AGTTTGtGCG CACGAACTTT 300
 AGTTAGTGCG TGCAGAACT TGTTGTGGTG TTGCACGCTC ATThATGAAG CACTGTTGGT 360
 GCCTCCGTTT TCGCATAnTG GATTGTTGTT GCGCATGAGG 400

(2) INFORMATION FOR SEQ ID NO: 4028:

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- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4028:

10 CTCATCGCAT CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC 60
 CATCGTCGCT AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG 120
 GCTCTCGCTT ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTGTCGACA 180
 15 TTCAAACGTT TTCACTTCGC CAAGCCATTT TTCTTTGTGT TTACTTTTTA TTTGACGTT 240
 TTAGACATAA AAAAAAGAGA CCTTGCGGTC TCAATGCGGC TCATCGCATC CATTTTTTGC 300
 CTGGGCAACG TTCTACTCTA GCGGGAACGn AAGTTGGGCT TACCATCGAC GCTAAGAACC 360
 20 TTTCTTGGAC TTGGTGGACA AACGGnGTGG CTGCTTTTCC 400

(2) INFORMATION FOR SEQ ID NO: 4029:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4029:

AGGACTTGAA CCCCCAACCT ACTGATTACA AGTCAGTTGC TCTACCAATT GAGCTAGGCC 60
 35 GGCAATATGT AAGAATAAAT GGTGGAGAAT GACGGGTTTCG AACCGCCGAC CCTCTGCTTG 120
 TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTTT 180
 TACTCTAGCG GAAnTAATTC GGACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTTCG 240
 40 GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGAATG TAATTTGATA 300
 CATTCAAAAC TAGATAGTnA ACTGAAAAGT GATTTTGGnT TCGCAAAACC ATTTGATTTT 360
 GATTGAAGTC CTTGATCGA TTGAGTGATT CGTGCAGCTn 400

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(2) INFORMATION FOR SEQ ID NO: 4030:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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GATGATAAAT CATGTTTTTC ATACCAAGTC GCTGCCGGCA AAACAATGTC AGAATATAAC 60
 GGTGTTGCCG TCATTCTGAA GTCTAAAGAG ACCACTAAAT CTAACCTACC TGTTGTTTCT 120
 5 TCACGCCACG TAATTTCTTC TGGCTTTTCA TCTTCATTG GTGTAGCTAA TAACCCTGAT 180
 TTTGTGCCAA GTAAATGCTT CATAAAGTAT TCTTGACCTT TTGCAGAACT TGAAATTAAG 240
 TTTGAACGCC ATATAAATAA TGATTTTGA TGATTCTTTT CAAATCAGGA TCTTCTATTG 300
 10 CAAATTGTGG TTTGTnTTGG ATTTCAChTC ATCAATTGCA CGTTGCAAAA TCGCTTCATG 360
 TGAATCTATA CCCTGCATCT TGTAGChTCC 390

15 (2) INFORMATION FOR SEQ ID NO: 4031:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4031:

TGGTTCGAAT CCAGCTAGCC CAGTTATTGG CGGCATAGCA AGTGGTAAGG CAGAGGTCTG 60
 CAAAACCTTT ATCACCGGTT CAAATCCGGT TGCCGCCTCC AGGTTTATGC GGGAGTAGTT 120
 30 CAACTTTTAG AACACGTTCC TTCCCGGAAn GAGGTATAGG TGCAAATCCT ATCTTCCGCT 180
 CCATAATTTA ATAATAATGC GGGAGTATTT CAACTCTTAG AATACATTCC TTCCTGGAAT 240
 GAGGTATAGG TGTAATCCT ATCTTCCGCT CCATAATTTA ATATTGCGG GGAGTAGTTC 300
 35 CAACTTTTAG AACACGTTCC TTCCCGGGAA GGAGGTATAn GTGTATCCTA TCTTCCGChC 360
 CATAATGCCT TCCAAAGGGG AATTTTTTGG TTTnACCATT 400

40 (2) INFORMATION FOR SEQ ID NO: 4032:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4032:

GTATCGATGA GTTTCTTCGG TCGTCTTCG ACAGCCATTT TGACTTCGAC AAAATGCATC 60
 ACATCGGGAT GACCATTAAT TGCATTAAAC GTGTCTTGTA AATCTTTTGA TGATCAACG 120
 TCATGAATTT CAACATTTTT ACCACCAAAT ACAGCTGGTA AAGCTTTATA ATCCACATG 180

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TTATTAATCA CCAATAATAC CGGGTTAATA TGCTGTCTAA TCATAGTTGG AAATAGCTTG 300
 AACAGTTAGT TGGCCATGAG CCATCACCCA TTTAATAATA AGTTACGACG GATCTTTGGT 360
 5 CTGCCAATTG GGGGAnCnCA ATGTTGCAGG GnAATGGTAT 400

(2) INFORMATION FOR SEQ ID NO: 4033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4033:

CACGACGTTT TGAACCCAGC TCGCGTACCG CTTTAATGGG CGAACAGCCC AACCCTTgGG 60
 20 ACCGACTACA GCCCCAGGA TCGATGAGC CGACATCGAG GTGCCAAAct CCCCCTCGAT 120
 GTGAACTCTT GGGGGAGATA AGCCTGTTAT CCCCGGGGTA GCTTTTATCC GTTGAGCGAT 180
 GGCCCTTCCA TGCGGAACCA CCGGATCACT AAGTCCGTCT TCGACCCCTG CTCGACTTGT 240
 25 AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACACTCTAT GAATGATTCC AACCATTCTG 300
 AGGGAACCTT GAAGCGCTCC GTACCTTTTA AGAnGGCGAC CGGCCAGTC AAACTGGCCG 360
 30 CTGACACTGT CTTCCAACAC GATAAGTGGT GCGGGTTAGA 400

(2) INFORMATION FOR SEQ ID NO: 4034:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4034:

AATTCCATGT GTACGGTTGA AATGCGCAGA GATATGGAGG AACACCAGTG nCGAAGCGAC 60
 TTTCTGGTCT GTAAGTGACG CTGATGTGCG AAACGTGGGG ATCAAACAGG ATTAGATACC 120
 45 CTGGTAGTCC ACGCCGTAAA CGATGAGTGC TAAGTGTTAG GGGGTTTCCG CCCCTTAGTG 180
 CTGCAGCTAA CGCATTAAGC ACTCCGCCTG GGGAGTACGA CCGCAAGTTG GAAACTCAA 240
 50 GGAATTGACG GGGACCCGCA CAAGCGTGGn AGCATGTGGT TTAnTTCGAA CAACGCAGAG 300
 AACCTTACCA AATCTTGACA TCCTTTGACA ACTCTAGAGA TAAAGCCTCC CCTTCGGGGA 360
 CAAATGACAG TGGTGCanGT TGTCTCACT CGTGTCTGTA 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4035:

10 TTCGCTTTGC CCGTCTGTCA CATTACTGTA AAATTCTATA AATAGAATTT TTGATGACGG 60
 GTCCCTTCCT AGGGTGCCGT CTCAGCCACC CCAACCGGCA CATTGTTGTA AGCTGACTAT 120
 15 ATGTCACTTC TGTGTTGGGG CCCCTGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC 180
 CATTAATACT ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACATTAAAGC CCAAATTAAT 240
 CAAAAGCTTT CTGAACCAGA AACGAAAAAA ATCTATAGTC ATAGAAAAAT TTATGTAGAG 300
 20 CCTGTTTTTG GATTATGAA GGCTATTTGG GGTTCACG AATGTCAGTT CGAGGAATAA 360
 TnAAGTnAAC GAGAGCCAGG TTTGTAATTA TGGCACTnAT 400

(2) INFORMATION FOR SEQ ID NO: 4036:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4036:

35 TAAATGTTGA AAAAGCACGA TTAGATAGAA TTTTGAATAA CAATGAAATT CGTCAAATGA 60
 TCACAGCATT TGGTACAGGA ATCGGTGGCG ACTTTGATCT AGCGAAAGCA AGATATCACA 120
 AAATCGTCAT TATGACTGAT GCCGATGTGG ATGGAGCGCA TATTAGAACA TTGTTATTAA 180
 40 CATTCTTCTA TCGATTTATG AGACCGTTAA TTGAAGCAGG CTATGTGTAT ATTGCACAGC 240
 CACCGTTGTA TAAACTGACA CAAGGTAAAC AAAAGTATTA TGTATACAAT GATAGGGGAC 300
 TTGATAAACT TAAATCTGAA TTGAATCCAA CACCAAAATG GCTATTGCAC GTACAAAGGC 360
 45 TTGGAGAATG AATGCAGTCC ATTTGGGAAC ACATGACCTG 400

(2) INFORMATION FOR SEQ ID NO: 4037:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4037:

TCGTCGCTAA AGACCTTTCT TGACTTGTGA CAATCGCTTG CTTCTTTCCT CTCCTTCGGC 60
 5 TCTCGCTTAC TCATTTAGCT CTAATAACT CGTTGCGCTC TTTTCTCGTT TCGTCAGATT 120
 CAAACGTTTT CACTTCGCCA AGCCATTTTT CTTTGTGTTT ACTTTTTATT TTGACGTTTT 180
 AGACATAAAA AAAAGAGACC TTGCGGTCTC AATGCGGCTC ATCGCATCCA TTTTTCGCTT 240
 10 GGCAACGTTT TACTCTAGCG GAAATAAATT GGGCTACCAT CGACGCTAAG AACCTTTCTT 300
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TTCTTCGGCT CTCGCTTACn CATTTAGCTC 360
 15 TACnAAACTC GTTTCGCTCT T 381

(2) INFORMATION FOR SEQ ID NO: 4038:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4038:

CTGTTTGTCA TACTTCATAA ATCCTTTAAA TTCACCCATC GTATCTCCCC CTTTCCTTAA 60
 TACACAACGG CTGTTTTATG TTAGCATCG ATTGTTTTAC TGTCATCGTA AAATGCAGCT 120
 30 AACATCGCTT CATCTTCATT GTCATGTAAT GATTTGTGCA AATGAATTTT TTGCATCATT 180
 AATTGATAAT CTTTAGGAAT AACTTTAACG ACGACATCTT CAATGCGATC AAAATGTTTT 240
 35 AACACATGAA TCGCTCTCGT ACTATTCGTG TGTGACACAT GTnCTTCCAG CATTTGCTTA 300
 ATGAATGCTT TnCTTCTTG GTGTTTAATC TTTGTAAACG AAAGCGTATC TAGTGATAnG 360

(2) INFORMATION FOR SEQ ID NO: 4039:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4039:

AGTGCGAACC CATAACCTCT TGATCCGTAG TCAAACGCTC TATCCAATTG AGCTACGGGC 60
 GCATATGTTT TTATTGAAAA TGGTGCCGAG GACCGGAATC GAACCGGTAG TGAnTGCACT 120
 CACCGCAGAT TTTAAGTCCT GTGCGTCTGC CAGTTCCGCC ACCCCGGCAC TATAAAAATG 180

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GAACTACTTC TGCATATGCG GGTGAAGGGA GTCGAACCCC CACGCCGTAA GCTnAGGATC 300
 CTAAGTCTAG TCGCTCTGCC AATTCCGCCA CACCCGCAAA TGGTGAGCCA TAGAGGATTC 360
 5 GAACCTCTGG ACCCTCTGGA TTAAAAAGTC AGATGCTCTA 400

(2) INFORMATION FOR SEQ ID NO: 4040:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4040:

CTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCCTCTCC TTCGGCTCTC GCTTACTCAT 60
 20 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 120
 TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAG 180
 AGACCTCAG GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA 240
 25 CCATCGTCGC TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCTTCTTT CCTCTCCTTC 300
 GGCTCTCGCh TACTCATTTA GCTChACTAA ACTCGTTGCG CTCTTGTTCT CGTTTCGGGC 360
 AGATTCAAAC GnTTGTCA 378

(2) INFORMATION FOR SEQ ID NO: 4041:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4041:

GTACCTTAAC AATATCTCGA AATGGACGAA CTAAATTATG AACCGCATGA AAGGATACTT 60
 GCGAATCATT TGAGCATGCT TGAATCATAA TATCACCATC GCTGTAATCG TCTATTAACT 120
 45 GATCATTTCG AAAATGCGGT AAATCTTTAA AGGCATCGGG AATTTTACTA GATAACCCAA 180
 TTTTCTTCAT CAAAGACTTA CTAATCCCAA AGGTAATCGT TAACTTGCTT GCACCTAATC 240
 50 CTATCGATTG ACCGGTATCT ACTGGTGGGC ATTAAAGGAT TGTTACTCGG GCTTGGCCAA 300
 CTGTATCACC ATCCATCATA CGATTGAGCC ATAACGGTCC ACTTTTTTAA ACATTGGCTT 360
 TATTGGCACC ChAACCTTTG GACTTChAAT CTAACGGCCA 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4042:

10 GACTTGCAAA CGTTGTGATG ACGGTCAAGA AAAGTGGTAA CACACCAGAC GGACGTAAAG 60
 CTGGCGAACC ATTTGCTCCA GGTGCAAACC CAATGCATGG CCGTGACCAA AAAGGTGCAT 120
 15 TATCTTCATT AAGTTCTGTA GCTAAGATCC CTTACGATTG CTGTAAAGAT GGTATTTCAA 180
 ATACATTCAG TATCGTACCA AAATCATTAG GTAAAGAACC AGAAGATCAA AACCGTAACT 240
 TAACTAGTAT GTTAGATGGT TACGCAATGC AATGTGGTCA CCACTTAAAT ATTAACGTAT 300
 20 TTAACCGTGA AACATTAATA GATGCAATGG AACATCCAGA AGGAATATCC ACAGTTAACA 360
 ATCCGTGTAT CTGGTTACGC TGTTAACTTC ATTAAATTAA 400

(2) INFORMATION FOR SEQ ID NO: 4043:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4043:

35 CTATTTTATC TAAAGTTAAA CTGACCCAC CTAGAATTGA CGAAACTCT GTGACATATA 60
 AAGCAGGTCT TACAAACCAA GAAATTAAAG TTAATAACGT ATTAAATAAC TCGTCAGTAA 120
 AATTATTTAA AGCAGATAAT ACACCATTAAT ATGTCACAAA TATTACTCAT GGTAGCGGTT 180
 40 TTAGTTCGGT TGTGACAGTA AGTGACCGGT TACCAAATGG CGGAATTAAA GCAAAATCTT 240
 CAATTTCAAT GAACAATGTG ACGTATACGA CGCAAGACGA ACATGGTCAA GTTGTTACAG 300
 TAACAAGAAA TGAATCTGTT GATTCAAATG ACAGTGCACA GTGAACAGTG GACACCACAA 360
 45 TTGACAAGCC AACTACTGAA GGCGCnGTGn TTATTAAAAG 400

(2) INFORMATION FOR SEQ ID NO: 4044:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4044:

5 AAAATGGCTT GATTTGAAAA ACGACCAGCA TCGCCTACTG G_nATAATAGC GAGGCTACCA 60
 TGTGTGTTTCA TCGTAG_nCGC ATGTTAGTTA ATCCAGGGAT ACAAGCATCA TGATCAATAT 120
 TAAAGCCATA TTCAAACAAT TGACCATAAG GTTCAATGTA AGCAGCGCCG GTGCACTTGC 180
 10 ATTCCAGCTG AATTAGAGCG ACGTGCAGCA TAAGCCAAGT CTTCTTTTGT AATATAGCCT 240
 TCTTTTGTG ATGTGTTTAC GGTCCATTGG GTGGATAATA CAAAGCGATT CGAAATTTTG 300
 ATGCCATTAG GTAAGTGGAT TGATTGTAAA AGTGGTTTGT ATCGGTACAT ACTATGATTC 360
 15 C_nTTTCCATT GCAAT 375

(2) INFORMATION FOR SEQ ID NO: 4045:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4045:

GTTCCAATGA AGATAGCTAG AAATGATATC CAAAACACAT GATGCATCAC TGGTGATGCT 60
 30 CGACTAATTG TATTCCATGA TGCATTAATA ATAATGACCA ATACACATAA AATAAGCAGC 120
 CATTATCGT TTATTTTAAA AATATAATGC AGCAAAAATC CAAAATGAT TAATTGCACA 180
 ACTGCTCGTA ATGTCGCAAC AATTAAATCT TTAATAATAT GTAAACCTTC TTTATATGAA 240
 35 ATGATAATCG GAATGACTAA AAGCAATGCC GTCAATCCAA GTGCCGTATT ACTCATGT_nG 300
 ATTCAACTCC TCTGTATTAG AAATTTGACC ATCAACAATT GTTATACGCT TTTTG_nAAGT 360
 GGTCGCATAC TTTGGGGCAT CGCTGTGGGG TAGGGGG_nC_n 400

(2) INFORMATION FOR SEQ ID NO: 4046:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 375 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4046:

50 CGAGTCTGAG TCGCTGTCTG AATCTGAATC GCTGTCTGAG TCCGAATCGC TATCTGAATC 60
 TGAGTCGCTG TCTGAGTCTG AATCGCTATC TGAATCTGAG TCGCTATCTG AGTCTGAGTC 120

TGAGTCTGAG TCGCTATCTG AGTCTGAGTC GCTGTCTGAA TCTGGAGTCG CTGTCTGAAT 240
 CTGGAATCGC TGTCTGGAGT CTGAATCGCT ATCTGAGTCT GGAATCGCTA TCTGAGTCTG 300
 AATCACTGGT CTGGAGTCCG AGTCACTGTC TGAATCTGAC TGCACThACn GGATTCTGAG 360
 TCGCTAACnG GAATC 375

(2) INFORMATION FOR SEQ ID NO: 4047:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4047:

ATGGGTAAAA AGGCATTAGA GTCAATCATT GATAACGCTG ATGAAACAAC TCAAGAGCGT 60
 TTACGTTTACG GATATGAAGA TGCTGTAGAT TATAACCGTT ATGTCGGTAA TATTTATACT 120
 GGATCATTAT ATTTAAGCCT AATATCATT CTTGAAAATC GAGATTTACA AGCTGGTGAA 180
 ACAATCGGTT TATTCAGTTA TGGCTCAGGT TCAGTTGGTG AATTTTATAG TGCGACATTA 240
 GTTGAAGGCT ACAAAGATCA TTTAGATCAA GCTGCACATA AAGCATTATT AAATAACCGT 300
 ACTGAnGTAT CTGTTGGATG GCATATGGAA ACATTCTTCC AAACGTTTTG GATGACGGTG 360
 GAATTTGACG GnGGACCAAG ATGCnTGTT CAGGAGGTCC 400

(2) INFORMATION FOR SEQ ID NO: 4048:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4048:

CAAACCATCT GACATAATAT ACACTTGGAT GTTAGATAAG GGTTTGCCAA TTGGAATCGT 60
 CTCAGGTATC AATCACCACA ATGATGTGAC CAATACGATG TGATGACTGT TGACTCAGAT 120
 GGTCCATAGG CATTGAAATA CGTGCCACAA TGCTTCTCAA TATATTTAAC AAAGGATGCC 180
 GTA CTAGTTG CCCCGCCTGT AATCAACTTT TCAATATAAA AGTCTTCCAT AACACTACAC 240
 ATCTGTAACG GAATCGACGC AACCGTCACA CGATGCTTAT TAATGAGTTG TTGTAAGTGT 300
 TCTGGATTAA CACGnTCCTC TCTATCTGGA nTCACAAGCG TATGACCATT AACAAACAAC 360

(2) INFORMATION FOR SEQ ID NO: 4049:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4049:

TCTGCATGTT CTCGAGATCC ACCAAATGTT AAATGGGTAT GTGCATCTAC TAATGCTGGG 60
 GACACTACCT TCCCACTAGC ATCAATCGTC TCAGTCGCAT CGTAGTCATC TGTATGTGTT 120
 CCAGCATATA CAATTTTGGC CATCTTTAAT GACAACTGTA CCATTTTTC CAACATTGTA 180
 ATTCATCTAA TTCCTTACCC TTCAAAGGTT TATCTGTTGA TCTCGGTAAA ATTAATTGCT 240
 GCTATATGAT TAAATATTAAA TCATTCATTA CTATCACCTG CTTATCAATC ATGGAATAGA 300
 ATACCTTTTC nTTAGCGTTT GAATAGCGAG TCATAGCCAG CATCAACATG TCGGGCAACA 360
 CCCATACCGG GGTTCATCGTC CAATACACGT TCCAACTnC 400

(2) INFORMATION FOR SEQ ID NO: 4050:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4050:

ATCACCCATG TTCTGACTCC CAAGTTAAAT TAATTGGCAT TCGGAGTTTG TCTGAATTCTG 60
 GTAACCCGAG AGGGGCCCCCT CGTCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG 120
 GCTAGCCCTA AAGCTATTTC GGAGAGAACC AGCTATTTCC AGGTTCGATT GGAATTTCTC 180
 CGCTACCCTC AGTTCATCCG CTCACCTTTT AACGTAAGTC GGTTCGGTCC TCCATTCACT 240
 GTTACCTGAA CTTCAACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACAAATA 300
 CTAAACGCCT ATTCAGCTCG nTTTCGTACGG CTCCACATTT ACTGCTAAAnC TTGCATCAAT 360
 CGTACTCGCG GTCAATCTAC AAAAGnACGC ATCACCAnTA 400

(2) INFORMATION FOR SEQ ID NO: 4051:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4051:

5 AGTGAAAATG ACTTTATCGG GCTGTTTCAGC GATATGGATT TGAGTTCAAC GCGACTAGGT 60
 AACAAATGTCA AAGAACGTAC TGCTTTAATC TCTAAAGTCA TGGTTAATCT TGACGACTTA 120
 10 CCATTTCGTTT ACAGTGACAT GGAAATTGAT ATGTTAGGTG ATGCATATGA ATTCCTAATC 180
 GGGCGCTTTG CGGCGACAGC GGGTAAAAAA GCAGGCGAGT TCTATACACC ACAACAAGTA 240
 TCTAAGATAC TGGCGAAGTT GTCACAGACG GTAAAGATn ATTACGTCAC GTGTAACGAC 300
 15 CCAACATGTG GGTCCGGTT CATGTGGTA ACGTGTGGT AAAGAACGCA AGTGTATCGT 360
 TAATTCGGAC nAAGAACGTA ACAATACTAC nTACGACTTA 400

(2) INFORMATION FOR SEQ ID NO: 4052:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 390 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4052:

30 TCCTACAACC CCAACAAGCA AGCTTGTGGT GTTGGGCTCT TCCCGTTTCG CTCGCCGCTA 60
 CTAAGGGAAT CGAATTTTCT TTCTCTTCCT CCGGGTACTA AGATGTTTCA GTTCTCCGGG 120
 TGTGCCTTCT GATATGCTAT GTATTCACAT ATCGATAACA TGACATAACT CATGCTGGGT 180
 35 TTCCCATTTC GGAAATCTCT GGATCAAAGC TTAATTACAG CTCCCCAAAG CATATCGTCG 240
 TTAGTAACGT CCTTCATCGG CTCTAGTGC CAAGGCATCC ACCGTGCGGC CCTTAATAAC 300
 TTAATChATG TTTTCCACCA TTTTTTATAA GTnCAAAGGC TTCACATACG GCTTCGGTTT 360
 40 TTCATTAATT TTAAATGGCh CAATTTAACA 390

(2) INFORMATION FOR SEQ ID NO: 4053:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4053:

55 AACATACCGA TGTATATAAT CTATACACAA AGGATAATTA CTTATGCAAA GGCGGAGGAA 60

5 GTCGATTGCG AATGATTTAA GAGGGAACAT GGATGCGAGT GAATTCCGTA ATTACATTTT 180
 AGGCTTGATT TTCTATCGCT TCTTATCTGA AAAAGCCGAA CAAGAATATG CAGATGCCTT 240
 GTCAGGTGAA GACATCACGT ATCAAGAAGC ATGGGCAGAT GAAGAATATC GTGAAGACTT 300
 AAAAGCAGAA TTAATTGATC AAAGTCGGTT ACTTCATTGA GCCACAAGAT TTATTCAGTG 360
 10 CGATGATCGT GAAATTGAA CGCAATGTTT CCGATATAGA 400

(2) INFORMATION FOR SEQ ID NO: 4054:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4054:

GTAAGACCAT CGTACTTGAG TCTTCAAGTG TTCTTGATAA AACGGAACGA GAGACTTGGT 60
 ATTTTTCGAA CAAATCTTTC ATTAACACAC CGACCATAAT AATTACAATC GAAGCAACAC 120
 25 CTGCAGCGAA TACAAGCGCA ATACAACAAA TAACAGTAAT ACATATTAAA CTCCTACAG 180
 AATGGATGCC TTTAGAAATA GTAGTTAATA AGACTTCTAA ACATCCTGCT TTTTCTACAA 240
 TACCTGCAAA TGCATATCCG CAAAATATCG TTAATAATAT TTGGGnCATA CTCATCATAC 300
 30 CACCCTGTTC TAACAAGCTT TCACACTGGA TGAATATGAG nTGATGTATC ATTGATCGTT 360
 AAACCCTAAT GTGCTTTGAA CCATCGTCAT TTGAATGTGA 400

35 (2) INFORMATION FOR SEQ ID NO: 4055:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4055:

CGTCTACAAG TTCAAAATTC AAGTCTTCCA TAATTGGTTT AACAACTACT TCTACTTGTT 60
 CTGTAATTTT ACTCATACAG GCCTCCCTTT TTGGCAAATA GAAAAGAGCG GGAATCTCCC 120
 50 ACTCTTCTGC CTGAGTTCAC TAATTTTTAA GCAACTTAAT TATAGCATAA GTTTATGCTT 180
 GAAACAAATG ACTTCACTAT TAATCAGAGA TTCTTGTAAG AGTTTGTTCC TTTATTCAC 240
 CATTACATTT GAATAGACTC GTAAGACATT GAAAAGAAAT ACGGGCATAA TTTTGTGTCC 300

55

TCATTTTACA TATCAAATAT CGGAAGTTGA GCTTTATCTG

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(2) INFORMATION FOR SEQ ID NO: 4056:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 481 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4056:

15	ATTTTGGTTT ACTTCATGTT GAGTTTTAGA CATTTTAACC ATCTCCAATA TAAAAATAAA	60
	TTAAATTAAA TTCTCAGGGA CTTCATGAC GCCACCTGTA TTGCGCTAG TTAGTAGGGC	120
	AGTATAACGA GCTAGATAAC CTGTTTTTAC TTTCGCTTTA AATGGTGTTA AAGATTCTCG	180
20	GCGACGCGCT AGAACATCTT CAGGCTGGTT TACGTTTAAT GTACGATTTG TTAAATCAAT	240
	AGTAATCTCA TCACCATCTT CAATTAAGGc AATTGGTCCA CCAGATGCAG CTTCAGGGGA	300
	AATATGaCCA ACTGcAATAC CTCTTGTGGc ACCGGtAAAA ACGCCCATCA GTKaATTAAT	360
25	GCaACATCTT TACCTAAGCC GCGaCCAACA ATAGAGGAAG TAGGTGCTAA CATTTTCAGG	420
	nCATACCTGG GTCCACCTTT TAGGTGCCTT TCAnTATCTn ATGGACAACG ACGTGGGCCT	480
30	G	481

(2) INFORMATION FOR SEQ ID NO: 4057:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 379 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4057:

	TTTTTGCTG GCAACGTTCT ACTCTAGCGG AACGTAAGTT GGCTACCATC GTCGCTAAAG	60
45	ACCTTTCTTG ACTTGTGACA ATCGCTTGCT TCTTTCTCTT CCTTCGGCTC TCGCTTACTC	120
	ATTTAGCTCT ACTAACTCG TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA	180
	CTTCGCCAAG CCATTTTTCT TTGTGTTTAC TTTTATTTT GGACGTTTTA GACATAAAAA	240
50	AAAGAGACCT TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT	300
	ACTCTAGCGG AAGTAAATTG GGCTACCAnc GACGCTAAGA ACCTTTCTTG GACTGTGACA	360
55	ATCGGCTGCh TCTGTnCCT	379

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4058:

CTGCATCACT GCCATAAAAA CTACCGTCAG CAGCGATAGn CGGCCAATCA TACCAGGAAC 60
 AAGACCGGGC TTGTCAGCGA TACTAACAGC GATATATCCA GCTAGTATTG GAACCATAAA 120
 TTTAAAGGCT AAATAACCAA TGTTTTCAAT GGATTTCCAA AATGAATCAT CTGGGATGAC 180
 TAATCCTTTT GATGTCGTTT CACCGCCTAG AGTCAGCGCG ATGGCGATAA GGAGTCCACC 240
 AACTACGATA AAAGGAACCA TAAACGATAC ACCGTTTATT AAATGTTGAT ACACCATTG 300
 AATACCATTT TAGACTnACC GCGATCTTTC GAATGATAAT TTGTTTCAGA TGGTTAAATA 360
 GGCGCATTG ATTTAATGAT ACGTGGATTT GGACCTTCGG 400

(2) INFORMATION FOR SEQ ID NO: 4059:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4059:

TTAAAAAACT GCCTGGCAAC GTTCTACTCT AGCGGAACTA AGTnGAnCTA CCATCGACGC 60
 TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC 120
 CAGACATATG AATGTAATTT ATACATTCAA AACTAGATAG TAAGTAAAAG TGATTTTGCT 180
 TCGCAAAACA TTTATTTTGG ATTAAGTCTT CGATCGATTA GTATTCTGTA GCTCCACATG 240
 TCACCATGCT TCCACCTCGG AACCTATTAA CCTCATCATC TTTGGAGGGA TCTTATAAAC 300
 CGAAATTGGG GAAATCTCAT CTTGAGGGGG GCTTnCATGC TTAGATGCTT TCCAGCACTT 360
 ATCCCGT 367

(2) INFORMATION FOR SEQ ID NO: 4060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4060:

5 TTCCGnACTC ACATAGCGAC TCAGGATTCA GACAGCGCAT TCAGATTCAG ACACCGCATT 60
 CAGATTCAGC ATAGCGATTG AGCATTCCGC ACAGTGACTC AGnATTCCGA CAGTGACTCG 120
 GATTCAGATA GCGATTCAGA TTCCGACAGT GACTCAGATT CCGACAGTGA CTCAGACTCA 180
 10 GACAGTGATT CGGATTCAGC GAGTGATTCT GATTCAGATA GTGATTCCGA CTCCGACAGT 240
 GACTCGGATT CAGATAGCGA CTCAGACTCG GATAGCGACT CGGATTCAGA TAGCGATTCTG 300
 GACTCAGATA GCGATTCAGA ATCAGACAGC GATTCAGATT CAGACAGCGA CTCAGACAGT 360
 15 GACTCAGATT CAGA 374

(2) INFORMATION FOR SEQ ID NO: 4061:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 432 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4061:

25 AAAATCATAA TATTTGGCAA TTTTTTCAAC TTGACTCTGG TCCTTCTGCA TAACTGCCGT 60
 30 AAATAATTCA CCTTCATCAC ACGCTGTACC TACCAATAAT CCCTCACGAT ATTCATCTAA 120
 CAATGAACGT GGAATTCGAG GTGTACGGTA GAAATACTTC ACCAATGATG CACTTACAAT 180
 TTTAAATAGA TTTTAAAGAC CTTGTTGGTT TTGTACAATT AATGTGACAT GACTAGGTCT 240
 35 TGCACGTTTA TATGCATCTT CATTACTGAG TTTTtKGTtG ATTTCGTTAT GATTTAATAC 300
 GCCTAAWTCy TTCAATTGTT GAACCATTTT TATGAAAATG TAAGCTGTTG CTTCTGTATC 360
 ATAAATGGCA CGGTGATGTT GCGTTAATTC TACGCCATAT TTTTtagCCA AGAAATTCAA 420
 40 ACCATGTTTA CC 432

(2) INFORMATION FOR SEQ ID NO: 4062:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4062:

55 TATCTTCGTT CTCAATAGAA TGATTTAAAC CTTGATTTC TTTATCTAAA TGACTIONCAA 60

TTTTTCTTC AACTAAGTCA CGATATAATG TTTTGAATT TTCGTTCAAT TTCGATTCGT 180
 GATTTTGAAT ACTTTTCTTC CACACAAATG TATACCTATT GGCATTAGCT TCTACTTTTG 240
 5 TACCATCAAT AAGATTTTGC TTAAACATT GACTATGAAA CTGGGATAAA TAAAGAnTCA 300
 ATTAACGCAT CAGTATTAGG GAnTCACTCT AATACGATTA ATAGTTTnTA TAAGAAGGTG 360
 nTTGGATTTG GAGCTAACCA CATCCA 386

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(2) INFORMATION FOR SEQ ID NO: 4063:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 386 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4063:

TAGGAGAGCG TTCTAAGGGC GTAGCATGAT CGTAAGGACA TGTGGAGCGC TTAGGAGAAT 60
 GCCGGTGTGA GTAGCGAAAG ACGGGTGAGA ATCCCGTCCA CCGATTGACT AAGGTTTCCA 120
 25 GAGGAAGGCT CGTCCGCTCT GGGTTAGTCG GGTCTTAAGC TGAGGCCGAC ACGTAGGGCG 180
 ATGGATAACA GGTTGATATT CCTGTACCAC CTATGAATCG TTTTAATCGA TGGGGGGACG 240
 CATAGGTATA GGCGAGGTGA CGATTGGGAT TGCACGTCTT AAGCAGTAAG GCTGAGTATT 300
 30 AGGCAAATCC GGTACTCGTT nAAGGCTTGA GCTGTGGATG GGGAGAAGAC ATnGAGTCTT 360
 CGAGTTCGTT GGnTTTCACA ATGGCC 386

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(2) INFORMATION FOR SEQ ID NO: 4064:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 386 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4064:

TAAGGCAGAT GCTCTCCCAG CTGAGCTAAT TCTCCGATTT AAAACTGCCT GGCAACGTT 60
 TACTCTAGCG GAACGTAAGT TGGAGCTACC ATCGACGCTA AGGAGCTTAA CTTCTGTGTT 120
 50 CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA TGTAATTTAT 180
 ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACATTT ATTTTGATTA 240
 AGTCTTCGAT CGAnTAGTAT TCGTCAGCTC CACATGTCAC CATGCTTCCA CCTCGAACCT 300

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AGGGGGGGCT TCATGCCTTT AGAATG

386

(2) INFORMATION FOR SEQ ID NO: 4065:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4065:

15 AATTCTTTTCG CTACTTGAAT GACAACACTT TGTTTTACGC CTGAAATGGC TTCTTGCCAA 60
 GCAGGTGTAT ATTTTGATTG TGCATCGTCG TATCCTTTTG ATTCTAATTT ATGATCAAAA 120
 CGACGCACGC CATATTGACT TGCCATTAAAG TCAAAAATTG TAGCAATACG GACTTTGTCA 180
 20 CCATTTGCTA AAGTGACTTG TCGAGTTGGA ATTGGACGAT TGAATATCCC ATCTCCATCA 240
 CTATCAAAGT ATGGGAATTG AATTGTTTCT AATTCGTATC CACCTTCTGT CATTGATAAT 300
 GTAGGGTTAA TTTAGAACC ATCTTCTGTT TCTAGTTTAA AGTTCCACTT CTTACCTTCT 360
 25 TCCCAACGTG GACCCATGGT GCCATTAnGn ACTACTAAAC 400

(2) INFORMATION FOR SEQ ID NO: 4066:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4066:

ATTTTGAAAT TGAGAAAACA ACTTATTGAA AAACATAATC TTTACGGTAA CATGGGTTC A 60
 40 GGAACAATCG TTATTAATAA GAAAAACGGT GGGAAATATA CGTTTGAATT ACACAAAAAA 120
 CTGCAGAGCA TCGTATGGCA GACGTCATAG ATGGCACTAA TATTGATAAC ATTGAAGTGA 180
 45 ATATAAAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA TCGGAAAAAC AAGAAGTTAA 240
 GTGACAACGG TTTACATGTT GCTTAGCTTC TTTTATTATG CGTAATGATG TAAAAAGACG 300
 nATATTCAAT TGTGTGTAAG AGTGGCATTG TATGTCTTAA AGTGACGnAA CTTCCAATGT 360
 50 GCCCAGTGTT TGATTCACAT CAAATCCATT TTTATTAAAC 400

(2) INFORMATION FOR SEQ ID NO: 4067:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4067:

	CCTCATTCCA GGAAGGAATG TATTCTAAGA GTTGAAATAC TCCCGCATT A TTATTAAATT	60
10	ATGGAGCGGA AGATAGGATT TGCACCTATA CCTCGTTCCG GGAAGGAACG TGTCTAAAA	120
	GTGAACTAC TCCCGCATAA ACCTGGAGGC GGCAACCGGA TTTGAACCGG TGATAAAGGT	180
	TTTGCAGACC TCTGCCTTAC CACTTGGCTA TGCCGCCAAT AACTGGGCTA GCTGGATTCTG	240
15	AACCAACGAG TGACGGAGTC AAAGTCCGTT GCCTTACCGC TTGGCTATAG CCCATTAATA	300
	ATAAGGGCGG CTGAAGGGGA TCGAACCCTC GAATGTCGGA ACCACAATCC GATGTGTAA	360
	CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC	400

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(2) INFORMATION FOR SEQ ID NO: 4068:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4068:

	TATCTAATAG TTTTACTTTA AGTCCAGCAT TCACAAAAG TGCTGCCAGT TGAGCGCCCA	60
	TTGTGCCTGC GCCAAGAACG GTTACTTTAT TAATTGTCAT AGTGATTCCT CCAATTTAGT	120
35	TGAGGATAAG ATAACCATT AAGATAATTGG AATAACGTTG CTATTTTATA AAATTAATTA	180
	AGTATCTTTG ACAGTCATCT TAGCCTCTTA TTTAAGGAAA AAGCTTTATG CTTAAAATAA	240
	GTCTTTTTTA GTGAAATTAA TGCATCTCAT ATAATTATTT GCTATTTATA CGAAAGCAGA	300
40	ATCTCCAGTC AAAGCGCGTC CANTACTAAG GCATTAATTT CATGTGTACC TCGTACGTGT	360
	AAATCGnTTC TGCATCAGnG AGGAAACGTG CAATATCATA	400

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(2) INFORMATION FOR SEQ ID NO: 4069:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4069:

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AAAAAGAAGA ATTGAAACGC CATATAAGT AACGTTAAAT AATAACGAAA AAAGGGCACT 120
 ATTCAAACAA TTAGCGTATG TTGAAGGGTT TGAAAAATAT CTTCATAAAA ACTTCGTTGG 180
 5 TGCAAAGCGT TTTTCAATTC nCGGGGTAGA CGCACTTGTA CCGATGTTAC AACGTACTAT 240
 TACGATTGCT GCGAAAGAAG GTATTAAAAA TATACAAATA GGCATGGCTC ACCGTGGGAC 300
 10 GTTTAAACGT TTTTAACGCA TGTnCTTAGA AAAAACCGTA CGAAATGATG ATTTCh 356

(2) INFORMATION FOR SEQ ID NO: 4070:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4070:

AAACGTTTAG GGAAAATTAT CACACAGATA CAACAATACA CAGATATTGA TTACCCGATA 60
 GCGATTGTCT TTCAAGCATC GTGTTTTAAC GAGTTTGTG TTAAGGGGCG TTAAAGTAAT 120
 25 ATTATTTCAA AATTGCAACA CTATTCAATT GAGGCGAAAC CAGGTATATG TATTATAGGG 180
 GAAGTTGTTG ATTATACTGA AAACACTCCT AAATCATATG ATCCTATGAA GCAATTTTAT 240
 GTAGTAAGTG GTTCTAAACA TGACGCCCTT ATGCTCTGTG AACATTATAT GACGAAGGTT 300
 30 ATGGCTGTTG CTAAACCCCA ATGATACATC GAATGGGCAC CATTATCCAn TCGTCGCAAT 360
 AATGGATTAC CCAAGGATGC CATTTAnTTA AGCCnGCCAn 400

35 (2) INFORMATION FOR SEQ ID NO: 4071:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4071:

CCTCTGGAAG CCTTAGTCAA TCGGTGGACG GGATTCTCAC CCGTCTTTTCG CTACTCACAC 60
 CGGCATTCTC ACTTCTAAGC GCTCCACATG TCCTTACGAT CATGCTTCAA CGCCCTTAGA 120
 50 ACGCTCTCCT ACCATTGTCC AAAGGnATn CCACAGCTTC GGTAATATGT TTAGCCCCGG 180
 TACATTTTCG GCGCATGTGC ACTCGACTAG TGAGCTATTA CGCACTCTTT AAATGGATGG 240
 CTGCTTCTAA GCCAACATCC TAGTTGTCTG GGnAACGCCA CATCCTTTTC CACTTAACAT 300

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361

(2) INFORMATION FOR SEQ ID NO: 4072:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4072:

ATGGTGACAA AAACATCGCA TTATTACTAG GTGTCGGCAC AGGCGTTTGT GGTGCTGCTG 60
 CTATTGCCGC AGTCGCTCCA ATATTCAAAT CACGTGAAAA GGATACAGCT ATTAGTATCG 120
 GTATCATCGC ATTGATTGGT ACGATATTTT CACTTATATA TACAGCTATC TACGCTATCT 180
 TTTCAATGAC GACAAATGTT TATGGCGCTT GGTCTGGTGT TAGTCTTCAT GAAATTGnCA 240
 CACGTTGTCT TAGCTGGTGG CTTTGGTGGT AGTGATGCAC TTAAAATTGC ACTTCTTGGT 300
 AAAC TTGGTA GGAGTATTCT TACTGGATTG CCATTAACCA TCGTACTTAA TTTTAAATAT 360
 GCGGTTnCCG TnCATCAGG AnTCATCTAG GCAAGGGGTC 400

(2) INFORMATION FOR SEQ ID NO: 4073:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4073:

GCGACGATCA TTTTAGAATC CGCTTGGGCG ATTAATTCTT TAGAAGTGGA TGAGGCAAAA 60
 TGTTCAATTAT CAGGAACTAA AGCAGGTGCT GATATGAAAG ATGGTCTACG TATTCATGGT 120
 GAAGACATGG GTACACTTTA TACCAAACAC GTTGAATTGG AAAACAAAGG CGTCGACTTT 180
 TATGAAGGTA ATGAAGTGGA TGAAGCTGAA GAAGAAGCAA AAGCTTGGAT TGATGCAGTT 240
 GTAAATGATA CTGAACCACT TGTGAACCGG AACAAGCAAT GGTAGTTACC AnAATTCTTG 300
 AAGCGATTTA TCCGTCTGCC AAATCCAGGC CAAAGCCATT TACTTTGGAA TAACATCnTA 360
 CCGGTAAGGG GGcncATCCT GGACCAAATT TAAAAGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 4074:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4074:

TCTTCCTAAT	ACCTTTCCAC	GATCTTCAGC	TGGCGCCTCT	GCACTCGCAA	ACGCACTTGA	60
TGCATCAACA	ACACCACCAA	ATAGTCCCTG	CAATAACCTC	ACAAGTACAA	ACTGTAATGG	120
TGTCGTACAC	AATGCCATTA	AAAATAAGCA	TACCGCCAAA	CCAAGTAACG	CTCTTAACAC	180
CATCCATTTT	CGGCTGATCT	TATCACCTAG	CTTCCCCCAT	ATCGGCGGAG	TTATGCATCG	240
TCGTTACAGC	TGGAGCAGCA	ATCGCTATAC	CACTCCACAn	CTGTATTTCT	ACGGACTGAT	300
AGGATTTTGT	AGTGATGnCC	ATGATGAAAT	GGGCAATAAT	GGGCACAAGT	ACTGTTCAGT	360
CCAGCCAATC	GTTATGAAAC	TGGACTGGGG	CCATnAAATG			400

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(2) INFORMATION FOR SEQ ID NO: 4075:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4075:

GGTTCAGAAC	GTCGTATGnA	GTTCGnTCCC	TATCCGTCGT	GGGCGTAGGA	AATTTGAGAG	60
GAGCTGTCCT	TAGTACGAGA	GGACCGGGAT	GGACATACCT	CTGGTGTTACC	AGTTGTCGTG	120
CCAACGCATA	GCTGGGTAGC	TATGTGTGGA	CGGGATAAGT	GCTGAAACTC	TAAGCATGAA	180
GCCCCCTCA	AGATGAGATT	TCCCAACTTC	GGTTATAAGA	TCCCTCAAAG	ATGATGAGGT	240
TAATAGGTTT	CGAGGTGGAA	GCATGGTGAC	ATnTGGAGCT	GACGAATACT	AATCGATCGA	300
AGACTTAATC	AAAATAAATG	TTTTGCGACA	AATCCACTTT	TACTTACTAT	CTAGTTTGAA	360
TGATAAATTA	CATCCATATG					380

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(2) INFORMATION FOR SEQ ID NO: 4076:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4076:

TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC 120
 CTA CTGCGTC CCCCCATCGA TTA AACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA 180
 5 TCCATCGCCT ACGCCTGTCT GCCTCAGCTT AGGACCCGAC TAACCCAGAG CGGACGAGCC 240
 TTCCTCTGGA AACCTTAGTC AATCGGTGGA CGGGATTCTC AnCCGTCTTT CGCTACTCAC 300
 AnCGGCATTTC TCACTTCTAA GCGGTCCACA TGTCTTACGA TCATGCTTnA AGGCCTTAGG 360
 10 AAGGTTCTTA CCATGGTCAA 380

(2) INFORMATION FOR SEQ ID NO: 4077:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4077:

GCAGGTCTGA CTCTAGAGGA TnCCCACGCG CGCAAGATT AAATCGAAGA AACCAGCAAC 60
 25 AGATTCTCTCA AAATAGCGCG GCGAACAACG AAACATCAAA TAGTGCACCT GCAGCTGGTA 120
 ATGGTGTAGC ATCAACGCCA CCAAGTGCAC CAAGTGGCGA TACTGCACCA AATAATAATG 180
 TTACGCAAAA TACCGCACCA AATAGTAATA ATGCGCCTGT ATCGACTACA CCACAAAGTA 240
 30 CAAGGCGGGA AnAAAGATGG TCAAAGTTTT GTAGATATAA CAACAACACA AGTCAGCACA 300
 GCTAACGAGA ACACACAAAA CATTACAGAT AAAGATGTTA AATCAATGGA AGCGGCATTA 360
 35 ACGGGCTCTT 370

(2) INFORMATION FOR SEQ ID NO: 4078:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4078:

AAACATTTTA TCAAATGGCA GAAGGACATG TGCCAAGACC ACCAGCGATG GTTGAAACAT 60
 50 TGACTTATAT TAAAGAGTTT ATGAACCAAG TTGAGTCGCA TAGCTAGTAT GAAACGTGGT 120
 GTGCGCATGG GAACTATCAA GCTTTGAAGA TGTGGTACTA CATGCGTTGG AATTAGGGAT 180
 CGGTACTTTA TATGAAGACG TGCTGCTTCC ATTAAATGAG TGATGCGATT TTGGCATGAA 240

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TAAGAGGGGC CAACCATTTGT TAGAnATAAC AACGGTTGGC TCTTTAAntG T

351

(2) INFORMATION FOR SEQ ID NO: 4079:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4079:

15	TTGAAGTAAC TAAATTAATA TTATGTTGTT CAATTAAAAG CTTCATACAA ACCTAATCTA	60
	TTTGCACTCC ACCGCTAACA CCGAACACTT GTCCGGTTGT ATAACITGAT TCTTCTGACG	120
	CTAATAGCAC ATAAGTTCCA CATAACTCAA CAGGTTGACC TGCACGACCT AAAGGTGTTT	180
20	TTTGACCAAA TGTGGGATT TTACTTTGAG GTTGTCACC AGAAATTTGT AATGGTGACC	240
	AGAATGGACC AGGCGCTACA CAGTTCCTC TAATTCCTTT TGGTCCTAAT TCTTCTGAAA	300
	AACCTTTTAGT TAATGAAATA ATTGCTGCCT TTTGAAGGGG CATAATCCAT GAAGAATAnG	360
25	GCCAGGGAnT AAAACCCTGG ACnAAAGAAG CCGTGGAAT	400

(2) INFORMATION FOR SEQ ID NO: 4080:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4080:

	TCGTTGGACA CAATCTGAAA AATAAATAGA TATAAATTCG CGAGATATAT TCGTATTTAT	60
40	AGTAAAATTA AATAAGAGA TTATATAACA CGAGGAGTAG TAAGTATGAA ATTTGAGAAA	120
	TATATAGATC AACTTTTATT GAAGCCTGAG TCAACACGTA CGCAAATCGA TCAAATCATC	180
	GATGAAGCGA AACATTACAA TTTTAAATCT GTATGTGTGA ATCCAACACA TGTAAATAT	240
45	GCAGCAGAGC GACTAGCTGA TTCAGAGGTG CTCGTTTGTA CGGTAATAGG ATTCCCATT	300
	GGTGCGTCGA CAACTGGCAA CGAAAGCATT TGAAACAGAA GATGCAATTC AAAATGGTGC	360
50	AGATGAATTG GACATGGTCA TCCACATCGG CGCATTAAAA	400

(2) INFORMATION FOR SEQ ID NO: 4081:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4081:

	CGACTAGTGA GCTATTACGC ACTCTTTAAA TGATGGCTGC TTCTAAGCCA ACATCCTAGT	60
10	TGTCTGGGCA ACGCACATCC TTTTCCACTT AACATATATT TTGGGACCTT AGCTGGTGGT	120
	CTGGGCTGTT TCCCTnChCG AACACGGACC TTATCACCCA TGTTCGACT CCCAAGTTAA	180
	ATTAATTGGC ATTCCGAGTT TGTCTGAATT CGGTAACCCG AGAGGGACCC CTCGTACCAA	240
15	ACAGTGCTCT ACCTCCAATA ATCATCACTT GGAGGCTAGC CCTAAAGCTA TTTACGGAGA	300
	GAACCAGCTA TCTCCAGGTT CGATTGGAAT TTCTCCGChA CCCTCAGTTC ATCCGCTCA	359

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(2) INFORMATION FOR SEQ ID NO: 4082:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 379 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4082:

30	TTTGACATTT AGTGTAAAGCG TnTTACAAAT AAAGCGTGT TTTTTGAAT TAAATGCATT	60
	TCACATTAGT ATTCATATTA TTTTtaggag GAATTTATAT GACATTTGAA AAAGAAACGG	120
	TCTTAAAAAC ATTATTTCTT GAAGATGTAC TTAGTATTGC TAAAGGTTTA ACAGACGGTG	180
35	AAGTCGAATT TTTACAACAA GTAGATTCAT TGGCTAGAAA GTAAGTACCG TGGAAAATAT	240
	TAATCAACAT TGGATAGACG CTACTGTACC CGAGGACTAT TTAAAGATC TGGGGAGAAT	300
	TAAATTATTT TAACAATCCA TTACTTTACA AGGGATCGTC CAAACGCCAA AnGGCCTAGT	360
40	CCAACATTTT nCAGTTTTTT	379

40

(2) INFORMATION FOR SEQ ID NO: 4083:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4083:

55	TTGAAACAGC CAGAGGTGTT TTATACCCAG GTGTTTCAGA TATGTATGAT GCGAAACAAT	60
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TTGGAACATA TGGTCCTAAC AAAGATGTTG TAGGCATATC TACTCGTCTT ATTAGAGTGA 180
 CATATGATAA TAGACAAACA GAAGATTTAA CTATTTTATC TAAAGTTAAA CCTGACCCAC 240
 5 CTAGAATTGA CGCAAACCTCT GTGACATATA AAGCAGGTCT TACAAACCAA GAAATTAAAG 300
 TTAATAACGT ATTAATTAAC TCGTCCGTGA AATTATTTAA GCCGATAATA CACCATTAAA 360
 TGTnCAAT ATTACCCnGG GTAGCGGGTT TTAGTTCGG 400

10

(2) INFORMATION FOR SEQ ID NO: 4084:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4084:

AGCATATCGT CGTTAGTAAC GTCCTTCATC GGCTTCTAGT GCCnAGGCAT CCACCGTGCG 60
 CCCTTAATAA CTTAATCTAT GTTCCATCC TACAGGAAAC GCGTTAGTAA TCTTGTGAGT 120
 25 GTTCTTTTCGA ACATAGCGAT TATTCTTAT GAATTCAAGC TTATTTAAAA CTCTTTATTC 180
 ACTCGGTTTT GCTTGGTAAA ATCTATATTT TACTTACTTA TCTAGTTTTC AATGTACAAT 240
 TTCTTTTTAG TCAAGCGCTC GCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT 300
 30 TAAATAAACA TTCAAACTG AATACAATAT GTCACATTAT TCCGCCATCT nCTGAAGAAG 360
 ATGTTnCCGA ATATnATCCT TAGAAAGGAG GTGGATCCCA 400

35

(2) INFORMATION FOR SEQ ID NO: 4085:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4085:

TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60
 CCTCCTGCGT GCAAAGCAGG CGCTCTCCA GCTGAGCTAA GCCCCCAAAT AGGTATTAAA 120
 TTAATGGTGG GCCTAAGTGG ACTCGAACCA CCGACCTCAC GCTTATCAGG CGTGCGCTCT 180
 50 GAACCAGCTG GAGCTATAGG CCCATTAATT TGGAATGAAC AAACATTCAA AACTGGAATA 240
 CAATATGTCA CGTTATTCCG CATCTTCTGG AAGAAGATGT TTCCGAATAn ATCCTTAnGA 300

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AAGCATTGTG TCCCACCTTC GACGGCTGAG CTCCTAAAAG

400

(2) INFORMATION FOR SEQ ID NO: 4086:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4086:

15 GTCATTGGAA ACTGGAGnAC TTGAGTGCAG AAGAGGAAAG TGGAAATCCA TGTGTAGCGG 60
 TGAAATGCGC AGAGATATGG AGGAACACCA GTGGCGAAGC GACTTTCTGG TCTGTAACTG 120
 ACGCTGATGT GCGAAACGTG GGGATCAAAC AGGATTAGAT ACCCTGGTAG TCCACGCCGT 180
 20 AAACGATGAG TGCTAAGTGT TAGGGGGTTT CCGCCCCTTA GTGCTGCAGC TAACGCATTA 240
 AGCACTCCGC CTGGGGAGTA CGACCGCAAG TTGnAACTC CAAAGGAATT GACGGGCGCA 300
 CAAGCGTGGG AGCATGTGGT TTAATTCGAA CCAACGnATA GAACCTTACC AAATCTTGGA 360
 25 C 361

(2) INFORMATION FOR SEQ ID NO: 4087:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4087:

GACCTTGCAG GACTCGAACC TGCGACCGAA CGGTTATGAG CCGTTAGCTC TAACCAACTG 60
 40 AGCTAAAGGT CCTAAATATA ATTTTACAAC TAATAAATAG TGGCGGTGGA GGGGATCGAA 120
 CCCCCGACCT CACGGGTATG AACCGTACGC TCTAGCCAGC TGAGCTACAC CGCCTTATAT 180
 AGTTTGTAAG TAATATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TGCCTGCAAA 240
 45 GCAGnCGCTC TCCCAGCTGA GCTAAAGCCC CCATAAATAA TTACAGTATA TCGGGAAGAC 300
 AGGATTCGAA CCTGCGACCC CTTTCCCAA CCAAGTGCTT TTACCAAGTT GGTACTTCCn 360
 GTATAATTTA ACGGGCCCGA TAGGAGTTCG GAACCCTTAA 400

50

(2) INFORMATION FOR SEQ ID NO: 4088:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4088:

AGCTATTATT TTTGACAGAT TCCATATCGT TCAACATTTA AATAGAGAAC TTAATAAGTA 60
TCGTGTACAA GTTATGAATG AATACCGTAA TAAAAAAGGA CCTGATTATA CAATTTTAA 120
GAATAACTGG AAAGTCCTAT TGATGGATAC TAGTAAAACC ATATTTAGTA AATACAGATG 180
GAATAAATCT TTAAAGGCTT ATAAACGCTC ATCTGACATT GTAGGAATTC ATGCTTTCAA 240
AAGACGATAT ACTACGACAC TCCTACGAAC TTGTCCCAAG GGATTACGGA AAAGGCCCTA 300
AGGGTTATGT TAATTGGCCC TAAATTTATT AAATGCGTTT GAAATTCAGT TAGTTAAAAA 360
GTCTGTGAGT GAnGGGTGTA TGGGAAAGTG GTTAAATAT 400

20

(2) INFORMATION FOR SEQ ID NO: 4089:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 374 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4089:

30

ATCGTTTTAG ATAAGACGGG TACATTACAA ATGGTCGTCC AGTCGTGACA GATTATCATG 60
GTGACAATCA AACGCTACAA CTACTTGCTA CTGCTGAAA AGATTCTGAA CACCCATTGG 120
CAGAAGCCAT TGTCAATTAT GCAAAAGAAA AGCAATTAAT ATTAAGTGA ACAACAACAT 180
TTAAAGCAGT ACCTGGGCCA TGGTATTGAA GCAACGATTG GATCATCACC ATATATTGGT 240
TGGTAACCGT GAAATTAATG GCTGACAATG GATATTAGCT TGCCTAAGCA TATTTnnGGA 300
TGGATTTAAC ACATTATGAA CGAGATGGTA AACTGCTAG CTCATTGCTG TTGAATTATT 360
nCATAACGGT ATCA 374

40

(2) INFORMATION FOR SEQ ID NO: 4090:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 367 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4090:

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TTAATAACGT ATTAAATAAC TCGTCAGTAA AATTATTTAA AGCAGATAAT ACACCATTAA 120
 ATGTCACAAA TATTACTCAT GGTAGCTGTT TTTGTTCCGT TGTGACAGTA AGTGACGCGT 180
 5 TACCAAATGG CGGAGTTAAA GCAAAATCTT CAATTTCAT GAACAATGTG ACGTATACGA 240
 CGCAAGACGA ACATGGTCAA GTTGTTCACAG TAACAAGAAA TGAATCTGTT GATTCAAATG 300
 ACACTGCACC AGTAACAGTG ACACCACAnT TACAAGCAAC TACTGAAGGC GCTGTATTTA 360
 10 TTAAGTT 367

(2) INFORMATION FOR SEQ ID NO: 4091:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4091:

TAATATTATA TTGCTAGTAG TTGACTGAAT GAAATGCGC TTGCAACAAG CTTTTTTCAA 60
 25 CTCTAGTCAG GGGCCCCAAC ACAGAGAATT TCGAAAAGAA ATTCTACAGG CAATGCGAGT 120
 TGGGGTGTGG GCCCAACAC AGAGAATTTT GAAAAGAAAT TCTACAGGCA ATGCGAGTTG 180
 GGGTGTGGGC CCAACACAG AGAATTTTGA AAAGAAATTC TACAGGGCAA TGCGAGTTGG 240
 30 GGTGTGGGCC CCAACATGAG AGAAATTGGA TTCCCAATTT CTGACAGACA ATGCAAGTTG 300
 GCGGGGGCCC CAACACAGAA GCTGGACGAA AATCCTTGAA CGAATGAATG TGGCAATTGG 360
 35 CGGGGGCCCA ACACAGAAGn TGACGAAAAT nCTnGAACCA 400

(2) INFORMATION FOR SEQ ID NO: 4092:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4092:

GCATTTCTCA TAACACAAGG AATTTCAACA AGTCCGGCTA CTGGATCACA AACTAAACCT 60
 AATAAATTAC TTATCGCTAA TGCCATAGCG TGCCCGGATG CTTCTGGTGA TCCTCCGAAT 120
 50 ATAGCTACTG CTGCAGCTGC GGCCATTGCA GATGCTGAAC CAACTTCAGC TTGGCAGCCA 180
 CCTGTTGCAC CAGCTACACT TGCATTGTTT GCTACGACAC GCCCAAACAA TGCTGAAGTG 240

55

CCGGGAATGG TAnCCGAGGG AAnCAGCTGT GGGCGTTGCA CAAATAATAC CCCATCGCAG 360
 CATTTGACCT TCATTGTTT GCAATGGGAA CCTTTGACTG 400

(2) INFORMATION FOR SEQ ID NO: 4093:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4093:

TGACTTACGT ACTGTTCAAC CAATCGATGT TGACACAATT GTAGCTTCAG TTGAAAAAAC 60
 TGGTCGTGCA GTTGTAGTTC AAGAAGCACA ACGTCAAGCT GGTGTTGGTG CAGCAGTTGT 120
 AGCTGAATTA AGTGAACGTG CAATCCTTTC ATTAGAAGCA CCTATTGGAA GAGTTGCAGC 180
 AGCAGATACA ATTTATCCAT TCACTCAAGC TGAAAATGTT TGGTTACCAA ACAAAAATGA 240
 CATCATCGAA AAAGCAAAAG AAACTTTAGA ATTTTAATAC ATTTTAAAAG TTAACGAATT 300
 AGCGTATTTT AGTCTCATTG ATTAAAnTGA AATGnGnTAA TTTACGGAAT CCTA 354

(2) INFORMATION FOR SEQ ID NO: 4094:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4094:

CGTTAACATG AAGTTACGTT CTTTTATAAA AAGATTTAAA CGCGTTATTA ATCTTGTGAG 60
 TGTTCTTTTCG AACACTAGCG ATTATTTCTT ATGAATTCAA GCTTATTTAA AACTCTTTAT 120
 TCACTCGGTT TTGCTTGGTA AAATCTATAT nTTACTTACT TATCnAGTTT TCAATGTACA 180
 AATAATGGTG GAGACTAGCG GGATCGAACC GCTGACCTCC TCGGTGCAAA GCAGGCGCTC 240
 TCCCAGCTGA GCTAAGCCCC CAAATAGGnA TTAAATTAAT GGTGGGCCTA AGTGGACTCG 300
 AACCACCGAC CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT A 351

(2) INFORMATION FOR SEQ ID NO: 4095:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4095:

5 ATGTTGCGA CTGGCACACC CGAAGATATT GCTCAGACAA AGTCATCATA TACAGGAAAG 60
 TATTTAAAAG AAGTACTTGA ACGAGATAAA CAAAATACTG AAGATAAATA AGATTAAAAG 120
 AAGTGAAGGA TGTTATAATT TATCCTTCGC TTCTTTTAT TAATTTAGTA ATGAATAGTA 180
 10 GAAAGAAAAG ATGCGTAAAA AGAATTATGT TAAGATAGGG TCAATCTAGA GTAGTTAAAC 240
 ATAAATCGAA CTnGGAGTGG GACAGAAATG ATAAAGAATC ACTAATGATT TATTATGTAG 300
 TGGTTCTTTG TCATTAGCCA CAGCTATTTG TGTACTTAAA AnTAGGTATG CCAGTGTGCA 360
 15 CTCCTTGAGA GGAAATACTn ATTT 384

(2) INFORMATION FOR SEQ ID NO: 4096:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 387 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4096:

CTGCATCTTC ACAGGTACTA TGATTTACACC GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60
 30 TTACGCCTTT CGTGCGGGTC GGAACCTACC CGACAAGGAA TTTCGCTACC TTAGGACCGT 120
 TATAGTTACG GCCGCCGTTT ACTGGGGCTT CGATTCTAG CTTCGCAGAA AGAGCCGACT 180
 CCTCTTGAAC CTTCAGCAC CGGGCAGGCG TCACCCTGAT GACATCACCT TACGGTTTAG 240
 35 CAGAGACCTG TGTTTTTGAT AAACAGTCGC TTGGGCCTAT TCACTGCGGC TCTTCTGGGC 300
 GTTAACCCTn AAAGAGCACC CCTTCTCCCG AAATnACGG GGTCATTTTG GCCGAGTTCC 360
 TTAACGAGnA TTCGCTCGGT GCAACTT 387

(2) INFORMATION FOR SEQ ID NO: 4097:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4097:

50 CCACTCACAT TCACACATCG ATTCACACAC CGCACTCAGC ACTCAGnATA CCGCATTACG 60

TCAGATAGCG ACTCAGATTC GGATAGCGAC TCAGACTCAG ATAGCGATTC AGATTCAGAT 180
 AGCGATTCGG ACTCAGACAG TGATTCAGAT TCAGACTCAG ATAGCGACTC AGATTCAGAT 240
 5 AGCGATTCAG ACTCAGACAG CGACTCAGAC TCAGACAGTG ATTCAGATTC AGACAGCGAC 300
 TCAGATTCAG ATnGCGACTC AGACTCAGAT AGCGACTCAG ATTCAGATAG CGATTCGGAC 360
 TCAGACAACG ACTCAGATTC AGATAGCGAT TCAGATTCAG 400

10

(2) INFORMATION FOR SEQ ID NO: 4098:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4098:

TCGTACCTGA ACTACTTTGT ATTAAAATAG TTACAACGAT ACCTGCAATA ACACCTAATA 60
 CTGGATTTGA TGTAATTTG TTAAAATAT CTCGTAGCCT GTCTCCTGCT GATGCTTGAA 120
 25 GCCCGTCTCC CATGATTTTT AAGCCGTAAA GGAAAATACC TAAACCACCT AAAAAGGAGA 180
 AAATGACTTC TGTAACCGAC ATTTCCATTA TTTCACCTCA AATAAGCTTT ATATTTAGAT 240
 TATCGCTTAT AATTGTAAAT TTAATGTAA GATTAGGTAA AATTATTTAA CAATATATGT 300
 30 TATTTGTATA TGACTTGTA AATATCGTCA CTTATTATGT AAATTTTCAG TGGTGGAAT 360
 GGCCAGTTTG CCAAGCACTG GTTTGACCA n ATGGnGGCA n 400

35

(2) INFORMATION FOR SEQ ID NO: 4099:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4099:

ATCCTTTTCC ACTTAACATA TATTTTGGA CCTTACCTGG TGGTCTGGGC TGTTTCCGGA 60
 CCGAACACGG nACCTTATCA CCCATGTTCT GACTCCCAAG TTAAATTAAT TGGCATTCCG 120
 AGTTTGTCTG AATTCGGTAA CCCGAGAGGG CCCCTCGTCC AACAGGGCT CTACCTCCAA 180
 50 TAATCATCAC TTGAGGCTAG CCCTAAAGCT ATTCGGAGA GAACCAGCTA TCTCCAGGTT 240
 CGATTGGAAT TTCTCCGCTA CCCTCAGTTC ATCCGCTCAC TTTCAACGTA ATCGGTTCCG 300

55

(2) INFORMATION FOR SEQ ID NO: 4100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4100:

TAGAACTTGT TGCCAAACAG CATGCTTAAT TTCAATATCT TCTTTGACTG CTTCGATATA	60
TAAATCAGCA TCATCATTTA CCAAGTCATC ATCAAAATTA CCATATGTTA AATGACTCGC	120
TAGATTTAAG TCGAATAGTA GCGGCCGTTT CTTATCTGTA ATTTTATCGT AAGATTTTTT	180
CGCAATGAGA TTTGGATCGT TTTTGTCCAC TACAATATCT AATAGTTTTA CTTTAAGTCC	240
AGCATTCACA AAAAGTGCTG CCAGTTGGAG CGCCCATGT GCCTGCGCCA AGAACGGnTA	300
CTTTATTAAT TGGTCATAGT GAnTCCnCCC ATTTAGTTGA GGGATAAGAT AACCATT	357

(2) INFORMATION FOR SEQ ID NO: 4101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4101:

TAACTCAGGC TGGGGACATA AATCAATATT CTATGCTCTA CGAATTATAT TGGCAGTAGT	60
TGACTGGnCG AAAATGCGCT TGTAACAAGC TTTTTTCAAT TCTAGTCAGG GGCCCCAACA	120
CAGAGAATTT CGAAAAGAAA TTCTACAGGC AATGCGAGTT GGGGTGAGGG CCCCAACACA	180
GAAGCTGACG AAAAGTCAGC TTACAATAAT GTGCAAGTTG GGGATGGGCC CCAACAAAGA	240
GAAATTGGAT TCCCAATTTT TACAGACAAT GCAAGTnGGG GTGGGACGAC GnGATAAATT	300
TTGCGAAAAT ATCATTTCTG TCCCACTCCC ATCAAAAGAA TGACAT	346

(2) INFORMATION FOR SEQ ID NO: 4102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATGATGAAA ATCAATTAGA CAAAGCAGGT AAATTAAGTG ATGTCGCGTC ATTTAAGGAA 60
 GCGATTCACA ATCGAGAATC ACAAAGTACA ACTGGTATCG GCGAAGGTAT TGCCATTCCA 120
 5 CATGCCAAAG TGGCCGCGAGT TAAGTCACCA GCTATTGCGT TTGGTAAATC TAAAGCAGGC 180
 GTAGATTATC AAAGTTTGGG ATATGCAACC AGCACACTTA TTCTTTATGA TTGCAGCGCC 240
 AGAAGGTGGC CCCAAACACA TTCTAGATGC TTTACTAAAG TTGnCTGGTA TTTTAATGGG 300
 10 ATGAAAATGT ACGTGAGGAA ATThTTACAT GGCTTCATCA nCTGAAGAAG TACTAGCGAT 360
 CAT 363

15 (2) INFORMATION FOR SEQ ID NO: 4103:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4103:

25 GAGTGCAGCG GATAACATTA AACCGACGAC AnCTTTTTTA TGITCAGGTT TAGCTGTGTG 60
 ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC GGCCTGACAT 120
 AAAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGa TCACCAAGTT GAGCAAAGAA 180
 30 GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC CAAGTGCCGT 240
 CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA ATCTTAAGAT 300
 35 GAAGCCATAA rCAAAAGTAC CsGTTGGcAC CTGTTtTCGT TACAAATCCA CCAACATGtK 360
 AaTGCCGGTT TGTATGGTTG GCCCAAnTGA nAACATCATA 400

(2) INFORMATION FOR SEQ ID NO: 4104:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4104:

50 AATTGAGAAT TTGTCGCTAT TTGTAAATTG TATCCTGGCT TAAGTTGGCC AAAGTGTCTT 60
 ATTTTTTTAA AGTATTTTAA AGTAAAATTA CATGTTAATA CGTATATTAA TTGGCGAGAC 120
 TCCTGAGGGA GCAGTGCCAG TCGAAGCAGG GGCCCCAACA CAGAAGCTGA CATATAGTCA 180

55

CAAAAATTCT ATTTATAGAA TTTTACAGTA ATGTGCCAGA TGGGCATAGC GACCCATTCA 300
 ATACGAnTAT nTGAnTAAAT AGAGAACAGC AGTAAGATAT TTTCTAATTG AAAATTAT 358

5 (2) INFORMATION FOR SEQ ID NO: 4105:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4105:

GACGCGTTAC CAAATGGCGG AATTAAAGCA AAATCTTCAA TTTCAATGAA CAATGTGACG 60
 TATACGACGC AAGACGAACA TGGTCAAGTT GTTACAGTAA CAAGAAATGA ATCTGTTGAT 120
 20 TCAAATGACA GTGCAACAGT AACAGTGACA CCACAATTAC AAGCAACTAC TGAAGGCGCT 180
 GTATTTATTA AAGGTGGCGA CGGTTTTGAT TTCGGACACG TGGAAAGATT TATTCAAAC 240
 CCGCCACATG GGGCAACGGT TGCATGGCAT GATAGTCCAG ATACATGGAA GGAnTACAGT 300
 25 CGGTAACACT TCATAAACT GCGGTTTGTh ACCATTACCT AATnGTCAAG GGTACGGCGT 360
 TAATGTTTGA AGGTTCCCGT TCCAAGGTTT TTTCCCGTTT 400

(2) INFORMATION FOR SEQ ID NO: 4106:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4106:

40 GAAGTTAAGC TCCTTAGCGT CGATGGTAGT CGAACTTACG ThCCGCTAGA GTAGAACGTh 60
 TGCCAGGCAG TTTTTTAATC AAATTTTGGT TAAAAAATAA AATGGACAAG ATAAAAAAG 120
 TTATTGACTT AAATGTTAAT AAAATGTATA ATTAATTCTT GTCGGTAAGA AAAATGAACA 180
 45 TTGAAAAC TG AATGACAATA TGTCAACGTT AATTCCAAAA AACGTAAC TAAGTTACAA 240
 ACATTATTTA GTATTTATGA GCTAATCAAA CATCATAATT TTTTCATGGGA GAGTTTGAT 300
 CCTGGGCTCA GGATGGAACG CTGGGCGGCG TGCCCTAATA CATGGCAAGT CnGAGCGAAC 360
 50 GGGACGAGAA GGCTTTGCTT CTCCTGGATG TTAACCGGCh 400

(2) INFORMATION FOR SEQ ID NO: 4107:

55

(A) LENGTH: 343 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4107:

10 GATTGTGCCA CGCTTTTAAC CGAAATACAA CATCATCATT GACAATTTGT TGATTTGAAA 60
 AATCTTTCTC TTCAATAAAT ACATACGTTT GCATCGTATG TGCTTTCATG TAACTCAATA 120
 TTGGTTTAA ATGCATTCA GGAATTAAAT AATGTTTACT AGAACCTGCT GTCGCTACAA 180
 15 GTCCTATTAC CTTGTACGA AACGCATTGA CTGGAAGTAG ATCAAACACA TTTnnCAAAG 240
 CACCAGGGAT GGAAAGCTTG AAAAATTGGA AAACCAATAA AAATCACATC AGCCTGCATT 300
 AACGACGTCG TTAATTATA TACATCTCCT GTAGTATCTA Gnt 343

20

(2) INFORMATION FOR SEQ ID NO: 4108:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4108:

30 ATACAAAACA CCAGGTCGTG AAGATAAACA ATCACAAGCG GCTACTGCTT CAGCAACTGA 60
 ATTACCATAT GCAGTATTAG AAGCTATGGG TGGCAAAGCA AACATTAAAC ATTTAGACGC 120
 35 TTGTATCACA CGTCTACGGT TGAAGTTAAC GACAAATCTA AAGTTGATGT TCCTGGTTTG 180
 AnAGATTTAG GCGCATCTGG TGTATTAGAA GTCGGCAATA ATATGCAAGC AATTTTGGT 240
 CCTAAATCTG ACCAAATCAA ACATGAAATG CAACAGATTA TGAnTGGTCA AGTAGTAGAA 300
 40 AATCCTACTA CTATGGAAGA CGATnAAGAC GAAACTGTTG TGGGTTGGCA G 351

40

(2) INFORMATION FOR SEQ ID NO: 4109:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4109:

CCTTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60

55

CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGnAT CACACCTTCT 180
 GCGGCCACCAC GGAATAATAC ACCATGTGGG AGTACGACTG CnATGGTACC TTCATCGTCT 240
 5 AAGGTAATGT ACCCTGTGGT TGAATAAAGG CAAAATCTGC TTTGGGATTT TGGCGCAACT 300
 TTGCCCGTAA CCACTGAATC GTTCATCATT TTCAAATTTT TGAATCnGCT GGTCCATTCTG 360
 CACTGTA 367

10

(2) INFORMATION FOR SEQ ID NO: 4110:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 15 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4110:

GTCTGCCGAT TGAAGGATGG AGTACTGTCTG CATTTGCGAA AGACTGGCAA GGACCACCAC 60
 GTTTGCAAAA CGGAACAAGT TGGTTCTATT TTGCAACAGA CCAATGGAAA TATGAAGAGT 120
 25 CAAATGTAGA TCGTTTAAAA TCTCCATTAG CTAAACAGA GGAGTTAAAG CATCAACATC 180
 CAGCTGATTA TAATGTTTTA GCAGCTAGAC TTGGTTGGTT ACCATCATAT CCACAATTTA 240
 ATAAAAATAG TTTGTTGTTT GCAGAAGAAG CTAAAGATGA AGGTATAGAT TCAAATGAAG 300
 30 CGATTTTGCC ACGTGCAATT GATGAAGTGA ATCAAAACCA AACACCATTT GCCATAnGAA 360
 AATCCTGATT TGGAAAAGGA TCCTnCCAAA ATCCAnnATT 400

35

(2) INFORMATION FOR SEQ ID NO: 4111:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4111:

TCAGATGAAG CTAAAAGTAA AGGTATTACA TGTGCAAGTG CAGGTAATCA TGCTCAAGGT 60
 GTTGCCCTATA CAGCTAAAAA ACTTAATTTA AACGCTGTTA TCTTTATGCC AGTCACTACA 120
 CCTTTACAAA AGGTAAATCA AGTAAAGTTC TTTGGAAATA GTAACGTTGA AGTTGTACTC 180
 50 ACTGGTGATA CATTTGATCA CTGTTTAGCT GAAGCTTTAA CTTATACAAG TGAACATCAA 240
 ATGAACTTTA TAGATCCATT CAATAATGTT CATACAATTT CTGGACAAGG TACGCTTGCT 300

55

AATTGGTGGT GGCGGTTTAA TTTCCAGTAT TAGTACTAAC

400

(2) INFORMATION FOR SEQ ID NO: 4112:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4112:

GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATATA GTCAAACGCT CACATACGGC 60
 TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120
 ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATT AAACGCGTTA TTAATCTTGT 180
 GAGTGTTCCT TCGAACACTA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACTCTT 240
 TATTCACCTCG GnTTTGCTTG GGAAATCTA TATTTTACnT ACTTATCTAG TnTTCAATGT 300
 ACAAATAATG GTGGGCCCAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGGCGTGC 360
 GG 362

(2) INFORMATION FOR SEQ ID NO: 4113:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4113:

CAGGTGGTTT TCGGAAAAGT GAAGTATGGC GTCAAATGAT GTCAGATATA TTTGACACAG 60
 AGTTAGTGGT TCCTGAAAGT TATGAAAGTT CATGCTTAGG TGCCTGCGTG CTCGGACTTA 120
 AAGCTGTAGG TGACATTGAA GATTTTTTCAA TCGTTTCATC GATGGTCGGT GCCACAAACA 180
 ATCATACGCC GATTGAAGAA AATGTCACTG TTTACCAAGA GATCGTATCC ATTTTATCA 240
 ATTTAAGTCG TTCTTTAACA GAGAATTATG ACAAATTGCA GATTCAACG CCACATATCG 300
 CTGAAATAAA ACnCCATAAA TACGnCACTC AAGCATCTTA GATAAAGTTG TnGGCCATGC 360
 TAC 363

(2) INFORMATION FOR SEQ ID NO: 4114:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 394 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4114:

	GGTCTGGGCT TGGTCCGGT TCTGGGCTG GACTTGGTTC TGGATCTGGC GTTGGTTCTG	60
10	GTTCTGGGTC TGGACTTGGT TCTGGGTCAA CCGGCGGCC TGGAGTTGGG TCTTTCGGAT	120
	TTACTGCTGA ATCACCATCA GCACTTCCAC CACCATAACG TACAACATTC TCATTATTCC	180
	AACCGAAAAT ACTGTAGTCT CTATTTGTGA CAGGATCAAC ATTTTCTTGA ATAACCTGAG	240
15	TTTTTAAGTT CTTACCTGTA TTGTCGTAAT GCCCTTCTAC TAATACTACA TATGTTTTAG	300
	TAATATCACC AAATTAATAC TAGCTACATT GGATGCnCAT AATAGATCTA TTTTAAATGG	360
	nCTGTACTCC TTAAGGTAGA GCATTGGACT GCAn	394

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(2) INFORMATION FOR SEQ ID NO: 4115:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4115:

	GGCGATTATA TTAAAAAGCC AATTACAGAA TGtagTGGTA ATGAAATATG CCAAGAATGG	60
	CTGTATCACT TAGGTGTATC AACTGACAAA ATTGAAGACT TAGCAAAACA TGCATCTAAT	120
35	ACGATTCTCTG TTTATATGCC ATATATCACA TCTTATTTCa TGACGCGTGC TATCGGCGAC	180
	AGACCTTTAG TCGTCCCGCA TCAATCTCAG AACTTAGCAT TTATTGGTAA CTTTGCCAGA	240
	AACAGAGCGA GACTGTAT TTACAACAGA ATATTCCGTT CGTACTGCCA GGAAGCTGT	300
40	TTATCAATTA CTAAATATAG ATCGTGGTAT TCCAGAAGTC ATCAATAAGT CCATTGGATC	360
	TTnCGCGTnC TTAATGGGAT GGCCATATAC GAACTGGATG	400

45

(2) INFORMATION FOR SEQ ID NO: 4116:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4116:

55

TTAAAGGGCG AAATAGAAGT GCCGGGCGAT AAGTCAATGA CACACCGTGC AATCATGTTG 120
 GCGTCGCTAG CTGAAGGTGT ATCTACTATA TATAAGCCAC TACTTGGCGA ATGTCGTCGT 180
 5 ACGATGGACA TTTTCCGACT GTTAGGTGTA GAAATCAAAG AAGATGATGA AAAATTAGTT 240
 GTGACTTCCC CAGGATATCA ATCCTTTAAC ACGCCACATC AAGTATTGTA TACAGGnAAA 300
 TTCnGGGTAC GACAACACGA TTATAGGTTG TTAAGTGGGT TAGGTATTGA AAGTGTTTG 360
 10 GTCnGGGCGA ATGTTTTCCA ATTGGGTAAA AGGCCCATGG 400

(2) INFORMATION FOR SEQ ID NO: 4117:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4117:

AATAAAAAGG AACAAAACGA TGGCTATTGA TATGGACACA AATCATAAAT AGCTGCTTTG 60
 25 TTCCTTTTTT AATTTATATA TTTAnAATAC ACATATTCAA GAGCCTCGAG ATATAAGTCA 120
 ATGTACTAGG CCACACAATT TAATATTGAC AGTAATTACC CGAACGAAAA TCGCCCCCGG 180
 30 GGCCCCAACA TGGGGAATTT CGAAAAGAAA TTCTACAGAC AATGCAAGTT GGCGGGGCCC 240
 CAACATAGAA GCTGGCCAAT AGTTAGCTTT CAATAATGTG CCAGTTGGGG TAAGGGCCCC 300
 AACACAGAAG CTGGCCAATA GTCAGCTTTC AATAATGTGC CAAGTTGGGG TAAGGGCCCC 360
 35 CCACCACAGG GAATTTGAA AGAAATnCT 389

(2) INFORMATION FOR SEQ ID NO: 4118:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4118:

AGGTAGGACT CGAACCTACG ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC 60
 50 TGTGGATTAA TATTATGCCT GGCAACGTTT TACTCTAGCG GAAnTAAGTT GACTACCATC 120
 GACGCTAAGG AGCTTAACTT CTGTGTTCCG CATGGGAACA GGTGTGACCT CCTTGCTATA 180
 GTCACCAGAC ATATGAATGT AATTTATACA TTCAAACTA GATAGTAAGT AAAAGTGATT 240

55

ACATGTCACC ATGCTTCCCA CTCGAACCT ATTAAACCTC AnCATCTTTG AAGGGGATCT 360
TATnAACCGA A 371

5 (2) INFORMATION FOR SEQ ID NO: 4119:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 341 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4119:

GCACTATTAG CCCAGTTAGA GAAAGATTGA CCTAATCTAT CCAACCAATC AGCCGACCAT 60
TGAAACAGTG GTGCTAATTG CGGTGAATAC ATTGACTAAT CCGTCACCAA AACCACCTGC 120
20 AGCACTTAAT AGCTTGTTAA ATACCGAAAC ACCCGTTGTA TTCATCATAT TAAAGAATCT 180
TGAAGCTACA CTGCTATTTT CAGCCCATTn AAGCACGCTT TGAGACGCTT CTTCCATTCC 240
TCTTGAAATA CCACTAAAAA ACGGnTGTA GCTCTGCATT GCAGTTTTAA CAGTATTTAA 300
25 ACCATTTGCA AGAGTTGTGA AGnTAGCGGA TTGATTTTGC T 341

(2) INFORMATION FOR SEQ ID NO: 4120:

- (i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4120:

GGTTGAGAAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCCTCCAC GTAAGCTAGC 60
40 GCTCACGTTT CAAAGGCTCC TACCTATCCT GTACAAGCTG TGCCGAATTT CAATATCAGG 120
CTACAGTAAA GCTCCACGGG GTCTTTCCGT CCTGTCGCGG GTAACCTGCA TCTTCACAGG 180
TACTATGATT TCACCGAGTC TCTCGTTGAG ACAGTGCCCA AATCGTTACG CCTTTCGTGC 240
45 GGGTCGGAAC TTACCCGACA AGGAATTTTCG CTACCTTAGG ACCGTTATAG TTACGGCCGC 300
CGTTTACTGG GGCTTCGATT CGTAGCTTCG CAGAnAAACG CACTTCCTGT TAAACCTTTC 360
50 CAGCACCGGn CAGGCGTTCA CCCTnATTAC ATCAACTTTA 400

(2) INFORMATION FOR SEQ ID NO: 4121:

- (i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4121:

	AATAAATCTT GCTTTATTCT TTTTACCAAGT AATATCTAAA TGAGTTGGAT ATTTAACTTT	60
10	CGCATTAAATT TCAATATTAA ATTGCGTTAC CGCGACAAGC GCAAACACAA CATACATAAT	120
	AAGATTGGCT AAAAAGATAT AGTTAAAGCT AAATTCTGCG ACAAAGCCGC CCATTGCAGC	180
	ACCGACAGCC ACACCAATAT TTTGCGCTAA GTATATCGCA TTAAACGTTT GTCTTCCGCC	240
15	ATTTGGCCAC ACTGCTCCAG CCATAGCGTA TATCGCAGGA ATAATCATTC CGCCACCAAA	300
	CCCTAACATT ACCAGGCCAT ACCAGCATAC CCAGGGCCAC CCGnGGAAGG AAATTAAGTA	360
	GCGGTGGTAC TACCAAnGAC CAGTGAAGG TnCCAATTAA	400

20

(2) INFORMATION FOR SEQ ID NO: 4122:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4122:

	GATAACTAAT AAAGTTTAGT TAAGTATTTT AATAACAAGT AGTATGTCAT TCTAGTAGCT	60
	AGAACAGATA TACTACTTGT TTGTTTTTGT GGAAAATTGA GTATATTCAA AAGGATAAGn	120
35	ACGAGAATTT CGTTATTAAA CTACGAATTC TCGATTTTTT TATATTTTAA GATAGGTTTA	180
	TTTCTGAAAA CTTAATAGAA AGGGGTTTGA CAAAGCTAAA GTGAAGTTTG ACGgTATAAA	240
	CGCAAATTAA ATATACTTTT ATAGAAAATT AACTCAGGCT GGGACATAAA TCAATATTCT	300
40	ATGCTCTACG GAGGTATATT GGCAGTAGTT GACTGAACGA AAnGCGCTTG TnACCAGCTT	360
	TT	362

45

(2) INFORMATION FOR SEQ ID NO: 4123:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4123:

55

CGCGAGGTGG TTTACAAGGA TTGTTGACAT TTCAAGACTT ACCAGTAACA AGTTATACAA 120
 TCTGGGGTGG TGTCTCAGAT ATTGATTTAA TGTATGAAGA ACGTGTCTGAT TTAAGAGGCA 180
 5 TGCTACGAAG AATGATTGGT CATCCGAAAA AAGATCGAGC GGGCATATGA GGCACGCCAA 240
 GCGATTCCAA ACATTAATGA nAACAGTCCG CCAATATTAA TTGTACATnG GAGGGGAAAG 300
 10 ACCCAGCAAG TTGGGTATTn CATCATGCGT ATTATTTTAA GCGGACCAAC TA 352

(2) INFORMATION FOR SEQ ID NO: 4124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4124:

AACCAGGTGA TCTACCCTTG GTCAGGTTGA AGTTCAGGTA AACTGAATG GAGGACCGAA 60
 CCGACTTACG TTGAAAAGTG GAGCGGATGA ACTGAGGGTA GCGGAGGAAA TTCCAATCGA 120
 25 ACCTGGAGAT AGCTGGTTCT CTCCGAAATA GCTTTAGGGC TAGCCTCAAG TGGATGATTA 180
 TTGGGAGGTA GAGCACTGTT TGGACGAGGG GCCCCCTCTC GGGTTTACCA ATTTGAGACA 240
 AACTTCCGAA TGCCAATTAA TTTGAACTTn GGAGTTCAGA ACATGGGTGA TAAGGTCCnT 300
 30 GTTTCGnAAn GGGAAACAGC CCAGACCACC AGTTAAGGTC CCCAAATGTA TGTTTAAGTG 360
 GAAAAGGGTT TTGGCGTTGC CCCGACAACT AGGATGTTGG 400

(2) INFORMATION FOR SEQ ID NO: 4125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4125:

GGCTTATTAA TCAAAAAATT TATAAGAAT ATGTAGAAAA CTTTTATTTA CATCGAGGCT 60
 ACACGCTACA ACAGAAAATT AAAATTTTAA TTAGCTTATA CATTGTAATA GGTTTTTTCAA 120
 50 TTTATATGGT GGATGTTCTT GCAGTCCGTG TAGGATTAAT CATAATGGTT ATCATACAAA 180
 CCGCTGTACT CTTTACATTT GTAAAAACAT TACCCAAATC AAATCATAAA ATAGAGGAGT 240
 GATTGCCCCAT GTTTATGGCA GAAAATAGAT TACAATTACA AAAAGGCAGT GCGGAAGAAA 300

TTGTCACTAA AACATTAAAT ACCGGGATAC AGCCGAGTAA

400

(2) INFORMATION FOR SEQ ID NO: 4126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4126:

15	AATCTATATT TIACTTACTT ATCTAGTTT CAATGTACAA TTTCTTTTTA GTCAAGCGCT	60
	CGCATAAGCA ATATCACTTT AACCAAAAAA TATTTGAATG TTAAATAAAC ATTCAAAACT	120
	GAATACAATA TGTACATTA TTCCGCATCT TCTGAAGAAG ATGTTCCGAA TATATCCTTA	180
20	GAAAGGAGGT GATCCAGCCG CACCTTCCGA TACGGCTACC TTGTTACGAC TTCACCCAA	240
	TCATTTGTCC CACCTTCGAC GGCTAGCTCC TAAAAGGGTT ACTCCACCGG CTCGGGTGT	300
	TACAACTCT CGTGGGTGTG GACGGGGCGG TGTGGTACAA nGACCCGGGG AACGtnATTC	360
25	AnCGGTAGCA TGGCTGGATC TAACGATTTA CTAnGCGGAT	400

(2) INFORMATION FOR SEQ ID NO: 4127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4127:

	CGAAATTTGT AGTAAAAGAT GTGCAACCAG CGAAACCAAC TGTGACTGAA ACAGCGGCAG	60
40	GAGCGATTAC AATTGCACCT GGAGCAAACC AAACAGTGAA TACACATGCC GGTAACGTAA	120
	CGACATACGC TGATAAATTA GTTATTAAAC GTAATGGTAA CGTTGTGACG ACATTTACAC	180
	GTCGCAATAA TACGAGTCCA TGGGTGAAAG AAGCATCTGC AGCAACTGTA GCAGGTATTG	240
45	CTGGAACTAA TAATGGTATT ACTGTTGCAG CAGGTACTTT CAACCCTGCT GGATACAATT	300
	CCAAGTTGGT TGCAACGCCA AGGAAGCGGA GAGACCACTG AAGTGATTGA GCCACCGTAA	360
50	TGGTTGGnTT CCCAGTTTG TCGGCAnCCA CAACCGGAAC	400

(2) INFORMATION FOR SEQ ID NO: 4128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4128:

GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT GGAGATTATC TGTCGTCTTC	60
AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC CATGTCAAAG TACCATTTCG	120
AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GCCTACGCGT TACATGAAAA ACGGAGAACA	180
AGCAGAACAA TTATTACGTC AGCTTATAGA AAAAGATGAA GCACTAGCTA AGTATGTCAT	240
GGGTTGTGAT GAAACAGCTT GGTGGTCATA TATGGGTCCA GATAATGATA TTTTCCAAGA	300
TCCATTAnGG CCATCTAACT GTTCCAGCTA AGGAAAGTAT CCCCGAAGTG GCTAAGCCCA	360
AAAATGATTA CGCCAACCAG CTAGTGGTCC ATnGGCCAGC	400

20

(2) INFORMATION FOR SEQ ID NO: 4129:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4129:

30

AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCCAATATA TAGATGGnGG AGGGGGGCAG	60
ATTCGAACTG CCGAACCCGA AGAGCGGATT TACAGTCCGC CGCGTTTACC ACTTCGCTAC	120
CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG GGTTCGAACC	180
GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGG AGCTAATTCT CCAAATAAT	240
GACTCCTGAC GGGACTCGAA CCCGTGTTAC CGCCGTGAAA GGGCGTGTTT TTGAACCGCT	300
TGGACCAAGG GAGCCATGGC TCCAACAGGT GAGGGACTCG AACCTnACGG ACCGATTCGG	360
TnAACAGCC GGAT	374

40

(2) INFORMATION FOR SEQ ID NO: 4130:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 431 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4130:

55

ATTAAATTTTC AGTTGTTGCA ATTTCTTCAT CTGTAGGTAC ATCATCGTTA AGGCCAACAA 120
 GTGCTTCAGA AACATTTTCGT GAATGATAAC CGATACGTTT AAGAACrCsA ATCATATCGA 180
 5 TATATAGTAA TCCGCCTTTT GTTGACATT CACCACGATT AAGGCGTTTA ATATGACCTT 240
 TGGCTAGTTT ATGTTCAATA TTAAATGATT CTCTACTACG TTCTACAATT TCATCTTTTT 300
 TCGTTTTGTC ATAAACATCT AACATGTCGA TGGCTTTATC AAATGACTCA GCAACATGGT 360
 10 TGAATAAAnT TATCCATACC GCGTTGTGCA TCTnCTGGTA ATGCGAATAT CTTCATCATG 420
 TTGGCGGTTT T 431

15 (2) INFORMATION FOR SEQ ID NO: 4131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4131:

25 TTTAGTTGAA GGCGGTGTTG TCGCATTGTC TGTTTGTTGC GGTGCTTCTA CTTTAGTTGA 60
 GGGCGGTGTT GTCGCGTTTG GTTTTGATTG CGGTGCTTCT ATTTTAGTTG AGGGCGGTGT 120
 TGATGTGGTG CTTCCACTTT AGGnAAAnTGA GTGTTGTCGC GTTTGCTGCT TCGGTTGTCG 180
 30 TTGTGATTAC ACCTGTTGTT AAAAGGCCTA GTGCTAAACT TGTMTTAGCA ATCGTTGTTA 240
 TTTTCATAGT TGTATGCTCC ATTCGTAATT ATTAGATTTG TTCGATACAT TCATTGAATC 300
 35 ATACAGCTTT ATTATAGAGG CGTATTGCTC CATTACATT AAACCTGTnT AACCAGATTG 360
 GAAGCAGCGT TGAATnAAAT GAAGAAAGCC AGAAGTTCGT 400

(2) INFORMATION FOR SEQ ID NO: 4132:

40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4132:

CCATTCACTG TATGTCTTTG GCCACCACCT TGACGTTGTT GTTGCTGTTG TTGATTTTGA 60
 50 TTAGCTTGTT GTTGATTTTG ATTATTTTGT GCTTGATTGT TCGCTTGATT AGCGTTGTTT 120
 TGATCATTAT CAGATTCATC TTTAGTCGCT TTGTCTTGAT CCTCTTTTGA TTTATCACTG 180

55

TCAGCATTAT TTTTATTTGT ATTGCGGATT TTATTTTCTT TTGTACCATT ATTATGATTG 300
 TTTAATGCCA TGCCTCCAAA TATCGCTAAA TGCACCGATA AATnAGTACA GCTGCAATGA 360
 5 ATGGTAACAA TACTTTGGGC CAGnCACCGT TTTTACGGTn 400

(2) INFORMATION FOR SEQ ID NO: 4133:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 417 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4133:

TTGAATACTT TTCTTCCACA CAAATGTATA TCTATTGGCA TTAGCTTCTA CTTTTGTACC 60
 20 ATCAATAAAA ATTGAATTAT TATCAATAAG ATTTTGCTTT AACATTGAC TATGGAAGTG 120
 AATAAATAAA GATTCAATTA ACGCATCAGT ATTAGGATTC ACTCTAAAC GATTAATAGT 180
 TTTATAAGAA GGTGTTTGAT TTTGAGCTAA CCACATCATT CGAATACTGT CATGAAGTAA 240
 25 TTTCTCTATT CTTCGACCAG AAAATACAGA TTGAGTATAT GCATATAAGA TGATTTTTAA 300
 CATCATTTTT GGGATGATAG GATGTTGCGC CACGATGATG TCTGAATTCA TCGAATTCGC 360
 TAnCGGGTAC CGTTCCACCA ATTCCATTAA CATATCGCGG AATATCAATT TGAGGAA 417

(2) INFORMATION FOR SEQ ID NO: 4134:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4134:

GGTTTAATAT GGACCTTTGC CGTnTTTATG TTCAATATTA AATGGATTCT CTAACGTT 60
 CTACAATTC ATCTTTTTTC GTTTTGTCAT AACATCTAA CATGTCGATG GCTTTATCAA 120
 45 ATGACTCAGC AACATGGTTG nAATAATTTA TCCATACCGC GTTGTGCATC TTCTGTAATG 180
 CGnAATATCT TCATCATGTT GGTCGTTTTA ATTGAGCGAC ATACTCTTCT GTTAGCTCTG 240
 CTACTTTTAA AATAGAGCGA TTGACATCAA ACATAACTGC TAAACGCTCA ACGTCTGCCT 300
 50 TCGTAATGGC TTTTGTAGAA ATTCTAACTA AATAATTTTCG AATGCTATCA TTGT 354

(2) INFORMATION FOR SEQ ID NO: 4135:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4135:

10	CTGGGATCGC CACCTTTAAG TCTAACAACC TTGTTATATC GACGCGCTGC TTCCACGATA	60
	CAGTCATTTA TTTTCTCTG CTGAATATGT TTTGCATACG GCTTTTACC AACATCGATA	120
	ATTTCACTAG TCAAATTCGC ATATTGTAAA ATTAACGGAT TCACTAATCG ATCATATAGA	180
15	ATGACATCCG CTTACGTAT TAAACGCTCA GCCTTTTCG TCAAATAATT CGGATTACCT	240
	GGACCCGCAC CTATCAAGTA AACCTTGCCA TATTCCTCTA CAGACATATA TATACGGTCC	300
	CGTCTGTAAC TTCTACCTCA TAAACATCTA CACAACCTTC ATCAGGTCTG GACAATACCT	360
20	GnATTAAACA ATTTTGTATC GTGGGGGGGC AAATACATAT	400

(2) INFORMATION FOR SEQ ID NO: 4136:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4136:

	ACCACTGAAT CGTTCATCAT TTTCAAATTT TGAATCTGCT GTCCATTTTCG CACTGTATGG	60
35	TGGGTTTCGCA ATAACCGCAT CAAATGTATT GCCTAAAAAG GCTGGATTTT CCAATGTGTC	120
	ATCATTACGG ATCTCGAAGT TCTCATAACG CACATCATGT AATAACATAT TCATGCGTGC	180
40	TAAGTTGTAT GTAGTATTGn TACGTTCTTG TCCGAAATAA CGATACACTT GCGTTTCTTT	240
	ACCAACACGT AACAACAATG GAACCGGAnC CACATGTTGG GTCGTACACG TGGACGTAAT	300
	TTATCnTTAC CGTGCTGTGA CAATCTTCGC CAGTATCTTA GATACTTG	348

(2) INFORMATION FOR SEQ ID NO: 4137:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4137:

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TGGACAATAC AAAGGGCAGC GAAACCGCGA GTCAAAGCAA ATCCCATAAA GTTGTTCTCA 120
 GTTCGGATTG TAGTCTGCAA CTCGACTACA TGnAAGCTGG nAATCGCTAG TAATCGTAGA 180
 5 TCAGCATGCT ACGGTGAAAT ACGTTCCCGG GTCTTGTA CAACCGCCCGT CACACCACGA 240
 GAGTTTGTAA CACCCGAAGC CGGTGGAGTA ACCTTTTAAG GAGCTAGCCG TCGAAAGTGG 300
 GGACAAATGA TTGGGGTGAA TCGTAACAAG GTAAGCCGTG ATCGGnAAGG TCGGCTGGG 360
 10 AT 362

(2) INFORMATION FOR SEQ ID NO: 4138:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 384 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4138:

ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCCGAAAT CTCTGGATCA 60
 25 AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA 120
 GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAC CATTTTTATA 180
 30 AGTCAAACGC TCACATACGG CTTCGTTTTT ATTATTTTAA ATGCTCATTT ACATAAGTAA 240
 ACTCTGCTTT AAAATAATTT AACTGCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT 300
 TTAAACGCGT TATTAATCTT GTGAGTGTTT TTTCGAACAC CAGCGATTAn TTChTGAGGA 360
 35 ATTCAAGCCT AntTAAACC CTTA 384

(2) INFORMATION FOR SEQ ID NO: 4139:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4139:

CTCATTATGG GACGTGCACA AGATGGTTTT CTTGATCAAG ACAAATATGA CATTATTTTC 60
 50 AAAACAGCTG AAAATTTAGA CGTACCGATT TATCTACATC CCGCGCCAGT TAACAGTGAC 120
 ATTTATCAAT CATACTATAA AGGAAATTAT CCTGAAGTAA CTGCGGCAAC ATTTGCTTGT 180
 TTTGGTTATG GTTGCCACAT TGATGTCGGC ATTCATACAA TACATCTnGT nTnATCTGGT 240

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TCCTTAGAAC GAATGGATGA AGCTTATCCG TGAACATTG AACCACCCCG GAAGCAATAC 360
 TTAATAATAA ATTTAATATC ACACCGGGTG GCATGGTACC 400

(2) INFORMATION FOR SEQ ID NO: 4140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4140:

CAACCACATT CGCTCGGCTC ACCTTAGAAT TCTCATCTTG AACTACCTGT GTCGGTTTGC 60
 GGTACGGrCA CCTATTTTCT ATCTAGAGGC TTTTCTCGGc AGTGTGAAAT CAACGaCTCG 120
 AAGACTCAAT GTCTTCTCCC CATCACAGCT CAGCCTTAAC GAGTACCGGA TTTGCCTAAT 180
 ACTCAGCCTT ACTGCTTAGA CGTGCAATCC AATCGCACGC TTCGCCTATC CTACTGCGTC 240
 CCCCCATCGA TTAACACGAT TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT 300
 AAGCCTGTCG GGCTCAGCTT AAGGACCCGA CTAACCCAG AACCgGAAGA GCCTTCCTCT 360
 GGAAAACCTT AGTCAATCCG TTGGACCGGG ATCTCAACCG 400

(2) INFORMATION FOR SEQ ID NO: 4141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4141:

CATATCGATA ACATGACATA ACTCATGCTG GGTTCCTCCA TTCGGAAATC TCTGGATCAA 60
 AGCTTACTTA CAGCTCCCCA AAGCATATCG TCGTTAGTAA CGTCCTTCAT CGGCTTCTAG 120
 TGCCAAGGCA TCCACCGTGC GCCCTTAATA ACTTAATCTA TGTTTCCACC ATTTTATATA 180
 GTCAAACGCT CACATACGGC TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA 240
 CTCTGCTTTA AAATAATTTA ACTCATGTGC TGCTAAACGT TTTCTTTTAT AAAAAGATTT 300
 AAACGCGTTA TTAATCTTGT GAGTGTTCTT TCGAACATAG GCGGAGTATT TCTTAAGGAA 360
 TnCAAGCnTA TTTAAACTC TTAATCAnC GGTTTTGcNT 400

(2) INFORMATION FOR SEQ ID NO: 4142:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4142:

10 GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA GCCATTTTTC 60
 TTTGTGTTTA CTTTTTATTT TGACGTTTTA GACATAAAAA AAGAGACCTC ACGGTCTCAA 120
 CTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 180
 15 CTTTCTTGAC TTGTGACAAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 240
 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGGTTCGT CAGATTCAAA CGTTTCACTC 300
 GCCAAGCCAT TTTCTTGGG TTACTTTTAA TTTGACGTTT AAGGCATAAA AAAAAGAGAC 360
 20 TTGCGGGCTC AAATGCGGnT CATCGCATCC ATTTTTGnCh 400

(2) INFORMATION FOR SEQ ID NO: 4143:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 369 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4143:

TTTAAATG ACATTATTAC TGACCAAACA AGTGCACATG ATCCGCTAAA TGGATATGTG 60
 35 CCACAAGGAA GCGAAAGTAT TCGTGAAAA AGATCCGAAA AAATATGTTG AACTGTCACA 120
 AGCTTCAATG GCAAAGCATG TTGAATTAAT GCTTGAATT CCAAAAACGT GGCGCTGTAG 180
 40 CATTTGATTA TGGTAACAAT ATTCGTCAAG TAGCCTTCAA TAACGGAnGn ATAAATGCTT 240
 TTGGACTTCC CAGGTTTTGT ACCAGCTTAC ATTAGACCAT TnATTCTGTG TAGGTTAAAG 300
 GGCCATTCCG CTTTGCTGCG TTGGAGTGGT GGATCCAAAA GATATCGAGC GTGCCGGATG 360
 45 GAGGAAATG 369

(2) INFORMATION FOR SEQ ID NO: 4144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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GGAAAGATAA ATAGCTTCAT CAATGTCATG CGTCACTAAA ATAATAGTTG ATTGCGTTTT 60
 ATGTTTTAGT TGCCTAGTT GATCCTGAAG TTTATAACGT GTAAATGCAT CTAATGCACC 120
 5 TAATGGCTCA TCCATCAATA TAACGTTAGG CTTATGCACA TCGCTCGAC ATAGTGCCAC 180
 ACGTTGTTTC ATACCCCGG ACAGTTGCTC GGGAAAATGC TTTCCCTGT CTTCTAAATC 240
 AACTAATTTA AGCTGTGCT TAATCTCTTC ATCACTAATT TTCTGTTGTA ATCCAATCCT 300
 10 AATGTTGTCA TTAATCGTTT TCCAGGCAGC AAATTATGGT GTTGAAATAG CATAACAAn 360
 CGGGAGnGGC 370

15 (2) INFORMATION FOR SEQ ID NO: 4145:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4145:
 25 CGAGGTAGCA AAGAACAAAT TCGAAATAT GTACCTAAAT TACAGTCACA TGAAGTGCCT 60
 ACATGCTTTG CTTAACTGA ACCAGAACAC GGTTCGGACG TTGCnGGAGG TCTTGAAACA 120
 GTCGCTGAAC GCCAAGGCGA TACTTGGGTT ATCAATGGTG AAAAGAAATG GATTGGTGGT 180
 30 GCACATGTAT CTGATGTCAT TCCAGTATTC GCAGTAAATA AAGAACTGG GCAAACCCCA 240
 TTGCTTTGTA GTCAGACCAG AACAGATGG GCGTCGATAT TGAAGTCATT GGATAATAAA 300
 35 ATCGCACTTC GGCATTGTTT CTAACGCCCT AATTTnAATT AAnTAATGTT CAAAGTAGGA 360
 TTGAAGCGGG 370

(2) INFORMATION FOR SEQ ID NO: 4146:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4146:
 50 TGGGGTGTTC TTACCAATAA AGCGTTGCAA GGTGGCGGTA GTTTAATCGA TTATGGTTGC 60
 CACTTGTTAG CTACTAGGTA AAGATATGGT GCCGCATGAA GTCTAGGAAA AACATATAAT 120
 CAATTGAGCA AACAAACGAA TCAAATTAAT GATTGGGGAA CATTGATCA TACTAAATTT 180

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GAATGTTTCGT GGTCTGCAAA TATCAAAGAA GATAAGGTTT ACGTThTTTT ATCAGGAGGA 300
 GGATGGCGGT ATCCAATTTA TTTCCATTG GAAATATATG GnCCCCCGTT TTGGGAACnC 360
 5 ATTTTTTGA AAGCCAAGCT 380

(2) INFORMATION FOR SEQ ID NO: 4147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4147:

TACTTATCTA GTTTTCAATG TACAATTCT TTTTAGTCAA GCGCTCGCAT AAGCAATATC 60
 20 ACTTTAACCA AAAAATATTT GAATGTTAAA TAAACATTCA AACTGAATA CAATATGTCA 120
 CATTATTCCG CATCTTCTGA AGAAGATGTT CCGAATATAT CCTTAGAAAG GAGGTGATCC 180
 AGCCGCACCT TCCGATACGG CTACCTTGTT ACGACTTCAC CCCAATCATT TGTCCCACCT 240
 25 TCGACGGCTA GCTCCTAAAA GGTTACTCCA CCGAnTTCGG GTGTTACAAA CTCTCGTGGT 300
 GTGACGGGCG GTGTGTACAA GACCCGGGAC GTATTACCT GGCAGCTTgn CTGGGTTTAC 360
 nT 362

(2) INFORMATION FOR SEQ ID NO: 4148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4148:

CACCATACAT GCGAAATGGA CAGCAGATTC AAAATTGAA AATGATGAAC GATTCAGTGG 60
 TTACGGCAAG CTTGCGCCAA AATCCAAAGC AGACTTTGCC TTTATTCAAC ACATGGTACA 120
 45 TTACCTAGAC GATGAAGGTA CCATGGCAGT CGTACTCCCA CATGGTGTAT TATTCCGTGG 180
 TGCCGCAGAA GGTGTGATTC GTCGCTATTT AATAGAAGAA AAGAACTACT TAGAAGCCGT 240
 GATTGGGTTA CAGCCAATAT TTTCTATGGG nCAAGTATTC CAACATGTAT TTAGTATTAA 300
 50 AAATGTCGCC ACAAGACGCC ACGTACTATT ATCGATGCAT CCAATGATTT GAAAAGGAAA 360
 AATCAAACCA TTAAGCGTGC CAAGCGACGA TATnGChCTA 400

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4149:

10 CAGCTATTGA TATCGATTAC CATACTGCTG TGGATAGCGA CAGGTTACAG TTGGAGGATA 60
 CACTGAGTCC TCTGAGGAAT CAAATCCAAT TGACTTTGAA GAATCTACAC ATGAAAATTC 120
 15 AAAACATCAC GCTGATGTTG TTGAATATGA AGAAGATACA AACCAGGTG GTGGTCAGGT 180
 TACTACTGAG TCTAACTTAG TTGAATTTGA CGAAGAGTCT ACAAAGGTA TTGTAAGTGG 240
 CGCnTGAGCG ATCATAACAAG AGTTGAAGAT ACGAAGAATA TACTCTGAAG TAATCTGATT 300
 20 GAATAGTGGA TGAATACCTG AAGAGCATGn TCAGCACAAG ACCAGTCGAG GAATnACTAA 360
 AACCATCATC ATATTnCAT CTGGTTAGGA CTGAAATGGC 400

(2) INFORMATION FOR SEQ ID NO: 4150:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4150:

35 AAGGACGACA TTAGACGAAT CATCTGGAAA GATAATCAAA GAAGGTAATA ATCCTGTAGT 60
 CGAAAATGTT GTCTCTCTTG AGTGGATCCT GAGTACGACG GAGCACGTGA AATCCGTCG 120
 GAATCTGGGA GGACCATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCACT 180
 40 ACCGTGCAGG AGAAGGTGAA AAGCACCCCG GAAGGAGTTG AAATAGAACC TGAAACCGTG 240
 TGCTTACAAG TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG 300
 GCGAGTTACG ATTTGATGCA AGTTAAGCAT AAATGTGGAG CCGTAGCAGA ACnnGTTnTG 360
 45 AATAGGCGTT A 371

(2) INFORMATION FOR SEQ ID NO: 4151:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4151:

TCAGCTTTTT TGATATGTAT TTTATAATGT ACAGCTCGTT GACnnTAATT TTCCTTATAT 60
 5 TAAGTGCCAT CAATACAAAA CCTAGCTCTC GTTTAACTTT ATTTATTCCT CGAACTGACA 120
 TTCGAGTGAA CCCAAAATAG CCTTCATAAA TCCAAAAGCA GGCTCTACAT CAATTTTTCT 180
 TTGACTATAG ATGTTTTTCG TTTCTGGTTC AGAAAGCTTT TGATTAATTT GGACTTTAAA 240
 10 GTATTCCCAA TTATAATTCT TCATGGATTT TCTTATTGGG ATTTCGAATT TGGTTTCATG 300
 CATTGATGTC TCAAAGAACA TGATGGAACA GTCCnCACa TTCCAGATAG TTTGGAAGTC 360
 15 TCGTTT 366

(2) INFORMATION FOR SEQ ID NO: 4152:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 20 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4152:

TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG CTACCATCGT CGCTAAAGAC 60
 CTTTCTTGAC TTGTGACAAT CGCTTGCTTC TTTCTCTCC TTCGGCTCTC GCTTACTCAT 120
 30 TTAGCTCTAC TAAACTCGTT GCGCTCTTTT CTCGTTTCGT CAGATTCAAA CGTTTTCACT 180
 TCGCCAAGCC ATTTTTCTTT GTGTTTACTT TTTATTTTGA CGTTTTAGAC ATAAAAAAAA 240
 35 GAGACCTTGC GGTCTCAATG CGGCTCATCG CATCCATTTT TTGCCTGGCA ACGTTCTACT 300
 CTAGCGGGAC GTAAGTGGCT ACCATCGACG CTAAGAACCT TTCCTGGACT TGGTGGACAA 360
 TCGCnTGCCT CCTTCCTCCT CCTCGGGCTC TCGGCTTACG 400

(2) INFORMATION FOR SEQ ID NO: 4153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4153:

TGATATTCCT GTACCACCTA TAATCGTTTT AATCGATGGG GGGACGCATA GGnATAGGCG 60
 ACGTGCGATT GGATTGCACG TCTAAGCAGT AAGGCTGAGT ATTAGGCAAA TCCGGTACTC 120

CCGAGAAAAG CCTCTAGATA GAAAATAGGT GCCCGTACCG CAAACCGACA CAGGTAGTTC 240
 AAGATGAGAT TCTAAGGTGG AGCGAGCGAA CTCTCGTTTA AGGACTCGGG CAAATGGACC 300
 5 CCGTTACTTC GGGGAGAnGG GTGCTCTTTA nGGGTTTACG CCCAGAAGAG CCGCATTGAA 360
 TAAGGCCCAA GCGnTGTTTT ATCCAAAACA CGGTCTCTGC 400

(2) INFORMATION FOR SEQ ID NO: 4154:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4154:

20 TTTTAGCAAT CATTTTAACA GTCAGTCATA TTAAAGGCTG GCTAACGATT GTTATCTnGT 60
 nCAGATTTGT AAGTTAAGAT TTCTTGTAAT GTGTATGCAG CACCATATGC TTCAAGTGCC 120
 CATACCTCCA TCTACCAAA ACGTTGTCCA CCGAATTGCG CTTTACCGCC AAGTGGTTGT 180
 25 TGTGTAACAA GTGAATATGG TCCTGTTGAA CGCGCATGTA ATTTATCATC AACCATGTGC 240
 GCAAGTTTCA ACATGTACAT TACACCTACT GAAATACGGT TATCGAATGG TTCACCTGTA 300
 CGTCCATCAT AAAGTACAGT TTTACCATCA CGAGCCATAC CAGCTTCTTC AATTGTTGGA 360
 30 CCATACATCG TCATCGTTTG CACCGTCAAA TACTGGTGGA 400

(2) INFORMATION FOR SEQ ID NO: 4155:

- (i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4155:

GATCCGAAGT TACCAACAGG AGAGAAAGAG GAAGTTCCAG GTAAACCAGG AATTAAGAAT 60
 45 CCAGAAACAG GAGATGTAGT TAGACCACCG GTCGATAGCG TAACAAAATA TGGACCTGTA 120
 AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCG AGAAAGAACG TAAATTTAAT 180
 50 CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG TGAGAAGACA 240
 ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA AGGTGAATCG 300
 AAAGAAGAAA TCACAnAAGT CCAGTTAATG AATTAACAGA TTCGGTGGCG AGAAATACCG 360

(2) INFORMATION FOR SEQ ID NO: 4156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4156:

CAAAGTGACA GGTGGTGCAT GGTGTGCGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60
 CCGCAACGAG CGCAACCCTT AAGCTTAGTT GCCATCATT AAGTTGGGCAC TCTAAGTTGA 120
 CTGCCGGTGA CAAACCGGG GAAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180
 TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG CGAGTGCAAG 240
 CAAATCCCAT AAAGTTGTTC TCAGTTCGGA TTGTAGTCTG CAACTCGACT ACATGAAGCT 300
 GGGAAATCGCT AGTAATCGTT AGATCCAGCA TGGCTAACGG TGGAAATACGT TTCCCGGGGT 360
 CCTTGTTACA CACCGCCCGT 380

(2) INFORMATION FOR SEQ ID NO: 4157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4157:

TGGAGAAGGA CCCAAAAATG TTGCCGTTTC AAGGTTATGT TTTACAACAT TTCGAACTTA 60
 TGGATGATGG ATTCTGCCAA GTTAAAATAA CTGAAGATGT ATTGGAGCAA TTCGGTATTC 120
 AGCCAAATGA AGCATCTCAG TTGTTAATA CAATTGCTGA CATCAAAGGC TTGAAAATAT 180
 GGGTATTTGC AGTCGATGGA AGGTAATGAA ATCAGATGTC GATTACGTTC TAAAGGGCAA 240
 TTGATTATT AATGATATTG CGCAGATTTT GGTGGCGGTG GTCATCCGAA TCGTCAGGA 300
 GTTTCAGTGG ACCAGCTGGG GTGGAAATTGA GCCACTTGCT ACCAGCTTTA CGGCACCAAA 360
 ACTTAACTTA TAGGAAGGGG CCCATTCCAT CCAGGTGGGC 400

(2) INFORMATION FOR SEQ ID NO: 4158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4158:

5 AAATCTCTGG GATCAAATCT TACTTACAGC TCCCCAAAGn CATATCGTCG TTAGTAACGT 60
 CCTTCATCGG CTTCTAGTGC CAAGGCATCC ACCGTGCGCC CTTAATAACT TAATCTATGT 120
 TTCCACCATT TTTATAAGTC AAACGTTAAC ATGAAGTTAC GTTCTTTTAT AAAAAGATTT 180
 10 AAACGCGTTA TTAATCTTGT GAGTGTCTT TCGAACACTA GCGATTATTT CTTATGAATT 240
 CAAGCTTATT TAAAACTCTT TATTCACCTG GTTTTGCTTG GTAAAATCTA TATTTTACTT 300
 ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGn n 351

(2) INFORMATION FOR SEQ ID NO: 4159:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 420 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4159:

25 AGTTAAAGGA ACTTTTAAAG TGGTTGGCCG CCGTnATTGC CTTCTnACC TTTTGTCTCT 60
 TCTCTGtTA CTTTTTCTGT CCCTGGTGCT AAATCnGGAT TAAATTTACG TTCTTTCTTG 120
 30 AATGGAATyT CTTCTTTTTC TACAATCGAG TCTCCTTTTA CAGGTCCATA TTTTGTACG 180
 CTATCGACCG GTGGTCTAAC TACGTCTCCT GTTTCTGGAT TCTTAATTCC TGGTTTACCT 240
 GGAACTTCyT CTTTCTCTCC TGTGGTAAC TTCGGATCAA ATTCGTCTCG ATGACCTGGT 300
 35 GTTATCGTTT CTGGTCCGTA TTCTGTTAAT TCATTAAATCG GATCTTTTGT GATTTCTTCT 360
 TTTGGTTCAC CnTTnACGAA TAATnACTCC AGTAAAGGAT TTTTAAAGTG TTGGTGTCGT 420

(2) INFORMATION FOR SEQ ID NO: 4160:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4160:

50 ACGATAATGG TGACGGGTTA CAAAGCCAAC ACAGCTAGGG TAGTATCCCA CCAGCGTCCT 60
 CCACGTAATC TAGCGCTCAC GTTTCAAAGG CTCCTACCTA TCCTGTACAA GCTGTGCCGA 120

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TGCATCTTCA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAnTCGT 240
TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAnT TTCGCTACCT TAGGACCGTT 300
5 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAGAAAn TAACCACTC 359

(2) INFORMATION FOR SEQ ID NO: 4161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 351 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4161:

ATTGACTAAG GTTTCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA 60
20 GGCCGGnAAC GGTAGGGCGA TGGATAACAG GTTGATATTC CTGTACCACC TATAATCGTT 120
TTAATCGATG GGGGGACGCA TAGGGATAGG CGAACGTGTC GATTGGATTG CACGTCTAAG 180
CAGTAAGGCT GAGTATTAGG CAAATCCGGT ACTCGTTAAG GCTGGAGCTG TGATGGGGAG 240
25 AAGACATTGT GTCTTCGAGT CGTTGATTTC AACTGCCGA GAAAAGCCTC TAGATAGAAA 300
ATAGGTGCCC GTGACCGCAA ACCGACACAG GTAGTnCAAG ATGAGAAAnTC T 351

(2) INFORMATION FOR SEQ ID NO: 4162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4162:

AnCGTCCTGC TTTGCACGCC AGAGGTCAGC GGTTCGATCC CGCTAGTCTC CACCATTAT 60
TTTTTACACG ATGAACATTG AAAACTGAAT GACAATATGT CAACGTTAAT TCCAAAAAAC 120
GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT AATCAAACAT CATAATTTTT 180
45 ATGGAGAGTT TGATCCTGGC TCAGGATGAA CGCTGGCGGC GTGCCTAATA CATGCAAGTC 240
GAGCGAACGG ACGAGAAGCT TGCTTCTCTG ATGTTAGCGG CGGACGGGTG AGTAACACGT 300
GGATAACCTA CCTATAAGAC TGGGGATAAC TTCGGGGAAC CGGAGCCAAT ACCGGATAAT 360
50 AnTTTGAACC GCATnGGTCC AnaAGTGAAA GACCGGCTTG 400

(2) INFORMATION FOR SEQ ID NO: 4163:

(A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4163:

10 ATTTTATATA TGAAATAATC TGGGACAACA TTCATAAATC TTATTGTCGT CCATTTTTTTT 60
 AAAATAATAC CAATCTCATT TTAAATTCT AAAGTTGGTT TCGTATAATA CGCTCTTAAA 120
 TCTTTAAATT TAGGATTTAT TTCTGTTGGT ACTTGTTTTG TGGTTGGCGA TTGTGGTGTG 180
 15 TCTGATTTAG TAGATTGCAT TGGTTGTGGC GTGTTTGTG ATGGAGGTGT TGTCACTTTA 240
 GTTGnAAGGC GGTGTTGTCG CATTGCTGT TTGTTGCGGT GCTTCTACTT TnATTGCAGG 300
 CGGTGTTGTC GCGTTTGGTT TTGnATGCGG TGCTTCTATT TT 342

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(2) INFORMATION FOR SEQ ID NO: 4164:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4164:

TCACGACACG AGCTGACGAC AACCATGCAC CACCTGTAC TTTGTCCCC GAGGAAGGGC 60
 TCTATCTCTA GAGTTGTCAA AGGATGTCAA GATTGTGTAA GGTTCCTCGC GTTGCTTCGA 120
 35 ATTAAACCAC ATGCTCCACC GCTTGTGCGG TTCCCCGTCA ATTCCTTTGA GTTCAACCT 180
 TGCGGTGTA CTCCCAGGC GGAGTGCTTA ATGCGTTAnT GCCAGCACTA AAGGGGCGGA 240
 AACCCCCTAA AACTTAGCA CTCCATCGTT TACGGCGTGG AACTACCAGG GTATCTAATC 300
 40 CTGTTTGATC CCCACGCTTT CGCACATCAG GTCATTAACA GACCAGAAAT CGCTTGCCCA 360
 nGGGGGTnCC nCCAAAACCT TGGGGATTTA ACGGTAAAAA 400

45 (2) INFORMATION FOR SEQ ID NO: 4165:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4165:

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GCATTAATTT CATGTGTACC TTCGTACGTG TAAATCGCTT CTGCATCAGA GAAGAAACGT 120
 GCAATATCAT AATCGTCAGC TAGTATGCCA TTACCACCTG TAATACCGCG GCCCATAGCT 180
 5 ACTGTCTCAC GCAAACGTAA GGCATTCATC ATCTTCGCCG TTGAAGTTGC AACCTCGTCA 240
 TATTACCAT GTGCTTGCAT ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGAGCTAAA 300
 10 TTAnCTTGCA TCATTGCTAG CTTTCCTGTA TTAACGGATA TTAATAATnG GTTGCCGAAT 360
 GCTTACGCTC AGGGACnTAA CnAAGTGGCA CGTAAGCGGC 400

(2) INFORMATION FOR SEQ ID NO: 4166:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4166:

AAAGTTCTTT GGAAATAGTA ACGTTGAAGT TGTACTCACT GGTGATACAT TTGATCACTG 60
 25 TTTAGCTGAA GCTTTAACTT ATACAAGTGA ACATCAAATG AACTTTATAG ATCCATTCAA 120
 TAATGTTTCA ACAATTTCTG GACAAGGTAC GCTTGCTAAA GAAATGCTAG AACAAGCAAA 180
 30 GTCTGACAAT GTTAACTTTG ATTATCTATT TGCCGCAATT GGTGGTGGCG GTTTAATTTT 240
 AGGTATTAGT ACTTACTTTA AAACCTATTC ACCTACCACG GAAAATTATA GGTGTTGGAA 300
 CCTTCAGGTG GCAAGTAGTA TGGTATGGAA TCnGGTGGTG GGTAAATAAT CnGGTnGTC 360
 35 CACATTGGCC CTAATAACCG ATAAAATTTG GGGGGCCGGG 400

(2) INFORMATION FOR SEQ ID NO: 4167:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4167:

CTTATAATCC ACACCCTGAG CAAACGCTnC TTATGACAGA GTATTAAAAT AAGCCGATAA 60
 50 AGATACACAC CTTTACCGAC TATTTAAAAT AACTTCACC AATTCATTTT AATTTAATGG 120
 ATTGAAGTAA CTAAATTAAT ATTATGTTGT TCAATTAAAA GCTTCATACA AACCTAATCT 180
 ATTTGCACTC CACCGGTAAC ACCGAACACT TGTCCGGTTG TATAACTTGA TTCTTCTGGA 240

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GT TTTTGTGTA CCAAATGnTT GGGGATTTTA CTTnGTGGGT TGTCCACCAG AAATTTGT

358

(2) INFORMATION FOR SEQ ID NO: 4168:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4168:

15	TTTCTTGACC ATATGGACGT AAAGAGATGT TAGCATCACA ACGTAAAGAT CCCTCTTCCA	60
	TCTTAACGTC TGATACACCA GTGTATTGAA TAATTGAACG CAATTTTCT AAATATGCAT	120
	ATGCTTCTTT AGGTGAACGA ATATCTGGTT CAGATACGAT TTCAATTAGC GGTGTACCTT	180
20	GACGGTTCAA GTCAACTAAT GAATACTCAC CTTTATGTGT TGACTTACCA GCATCTTCTT	240
	CCATGTGGAA GACGAGTAAT ACCGATTCGT TTTGTTTCAC CGTCGACTTC GATATCGATA	300
	TATCCATTTT CACCAATTGG TTGATCAAAT TGAGAAhTTG AGAGCTTnTG GnTTAGCTGG	360
25	ATAGAAATAG TTCTTACGGT CAACTTAGAT CCGTTGCGAT	400

(2) INFORMATION FOR SEQ ID NO: 4169:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4169:

	ACCATGTTTG AATGAATCCA TTGGAATCAT TATTGAAGTA AATTAAGGAA TCTATAATGT	60
40	TCGTTAAATA AAACGTATCC CGTTGTGCTT CACACCCGAT AGATAGGGAT TTACAGATAA	120
	ATTGAGGTCT CTCCACGTC ATATTTGGAC CCATCGAAAA TTCGGGTTCT CAAATCATCG	180
	AACATAACAA AAGAAGCTAA GCAACATGTA GGCCGTTGTC ACTTAACTTC TGTTTTTTCC	240
45	GATGACAGCT TCTATTTAGA GAATGTCATG ATTATTTTAT ATTCACTTCA ATGTTATCAA	300
	TATTAGTGCC ATCTATGACA TCTGCCATGC GATTTTCTTG TAATTTTTTG TGCAATCAAC	360
50	GTGTACnTCC ACGGTTTTCA TTAAhAACA ATTTACCGGA	400

(2) INFORMATION FOR SEQ ID NO: 4170:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 395 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4170:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA	60
10 TTCCTTGTCG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTGGGC ACTGTCTCAA	120
CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG ACAGGACGGA	180
AAGACCCCGT GGAGCTTTAC TGTAGCCTGA TATTGAAATT CGGCACAGCT TGTTACAGGA	240
15 TAGGTAAGGA GCCTTTGGAA ACGTGAGCGC TAnTTTACGT GGrAGGCGCT GGGTGGGGAT	300
ACTTACCCTA AGCTGTGTTG GCTTTCTAAC CCGCACCAnt TATCGTGGTG GGGAGACCAT	360
GGTCAAGCGG GGCATTTTGA ATGGGGGGCG GTTCG	395

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(2) INFORMATION FOR SEQ ID NO: 4171:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4171:

TACATTATAG CTTTAATCGT TTGAAGTATA GTTTGAAACC AGTAGTCACA GCTGTTCAAG	60
GTCGTGCCTT AGGCGGTGGC TGTGAGCTTG TACTTTACTC ACCTATTGTT GTCGCTGCAA	120
35 GTGAAACATA TATCGGTCTT GTTGAAGCAG GTGTTGGCTT ATTACCGAGT GGCGGTGGCC	180
TTGCAGAAAT GGCTGATCGC ATATTACGCA CATCGCATAA GTTTGATGAC AAACAAGCTT	240
CCATGACAAA AGTACTGACG AATATCGCAT TCGGAAnGCT CTACAAATGC CTTTGAGGCA	300
40 CGTCGTATGG GTATTTACCG TGGATACAGA TACGATnATT TCCAATACAG CACAACGnGT	360
CGAAGTGGCG C	371

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(2) INFORMATION FOR SEQ ID NO: 4172:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4172:

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GCTGAGCTAA GCCCCCATAA TAATTACAGT ATATCGGGAA GACAGGATTC GAACCTGCGA 120
 CCCCTTGGTC CCAAACCAAG TGCTCTACCA AGCTGAGCTA CTTCCCGTAT AATTAACGCG 180
 5 CCCGATAGGA GTCGAACCCA TAACCTCTTG ATCCGTAGTC AAACGCTCTA TCCAATTGAG 240
 CTACGGGCGC ATATGTTTTT ATTGAAAATn GTGCCGAGGA CChGAATGAA CCGGTACGTG 300
 ATCATTACCG CAGATTTTAA GTCCTGTGCG TCTGCCAGTT CCGCAnCCCC GACTATAAAA 360
 10 T 361

(2) INFORMATION FOR SEQ ID NO: 4173:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4173:

GTACAGATGC ATTGTTAAAC AATCAGTTGC AACAGCTGTT GAAACTGGTA GAGTATCTAA 60
 25 TGGTGATTTA ATCATTATTA CTGCTGGTGT ACCAACTGGT GAAACTGGAA CTACTAATAT 120
 GATGAAAATC CACCTAGTTG GTGACGAAAT TGCTAATGGT CAAGGTATTG GACGTGGATC 180
 AGTTGTTGGT ACTACGTTAG TTGCTGAAAC TGTTAAAGAT TTAGAAGGTA AAGATTTATC 240
 30 TGACAAAGTT ATCGTTACTA ACTCCATCGA TGAAACGTTT GTACCTTATG TAGAAAAAGC 300
 TTTAGGCTTA ATTACAGAAG AAATGGTATT nCACACCCAG TGCCATGGTT GGTTAGGAAA 360
 35 AGnAATCCCA CCGTTGTAnG 380

(2) INFORMATION FOR SEQ ID NO: 4174:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4174:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAG 60
 CTGAGCTGTG ATGGGGAGAA GACATTGAGT CTTCAAGTC GTTGATTTCa CACTGCCGAG 120
 50 AAAAGCCTCT AGATAGAAAA TAGGTGCCCG TACCGCAAAC CGACACAGGT AGTCAAGATG 180
 AGAATTCTAA GGTGGAGCGA GCGAACTCTC GTTTAAGGAA CTCGGGCAAA ATGGACCCCG 240

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GCCCAAGCGC TGTTTATCCA AAACACAGTC TCTGCTnAAC CGTAGGGGAT TGTATAGGGG 360
 CTTACGCCCTG CCCGGTGCCT GGAAGGTTTA AAAGGTGGT 400

5 (2) INFORMATION FOR SEQ ID NO: 4175:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4175:

AGCCATGGCT CAGCGAGGTA GGA CTACGACCGA TCGGTTAACA GCCGATAGCT 60
 CTACCACTGA GCTACTGTGG ATTAATATTA TGCCTGGCAA CGTTCTACTC TAGCGGAACG 120
 20 TAATTCGnAC TACCATCGAC GCTAAGGAGC TTAAC TTCTG TGTTCGGCAT GCGAACAGGT 180
 GTGACCTCCT TGCTATAGTC ACCAGACATA TGAnTGTAAT TTATACATTC AAAACTAGAT 240
 AGTAAGTAAA AGTGATTTTG CTTCGCAAAA CATTTATTTT GGATTAAGTC TTCGATCGAT 300
 25 TAGTATTCGT CAGCTCCACA TGTGCACCAT GCTTnCCACC TCGAACCT 348

(2) INFORMATION FOR SEQ ID NO: 4176:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4176:

CATTTTTTTA AAATAATACC AATCTCATT TTAAATTCTA AACTTGGTTT CGTATAATAC 60
 40 GCTCTTAAAT CTTTAAATTT AGGATTTATT TCTGTGGTA CTTGTTTTGT GGTGGCGAT 120
 TGTGGTGTGT CTGATTTAGT AGATTGCATT GGTGTGGCG TGTGTGTGA TGGAGGTGTT 180
 GTCACCTTAG TTGAAGGCGG TGTGTGCGCA TTTGCTGTT GTTGCGGTGC TTCTACTTTA 240
 45 GTTGAGGGCG GTGTGTGCG GTTTGGTTT GATTGCGGTG CTTCTATTTT AGTTGAGGGC 300
 GGTGTTGAnT GTGGTGCTTC CACTTTAGGG nAAGATnAGT GGTG 344

(2) INFORMATION FOR SEQ ID NO: 4177:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4177:

5 CAGAACCTTG nAATGAATCG CGATGGAATA TCTCTATCTG nAAACAGATT TCTTTTTGTC 60
 CGCCAATGGC CTTGGAATTG TTAAATAAA TCTATTTGCG CTTCTTTATC AATGTCATAA 120
 CCTAATGCTT TTAACCTTCTC TGAGAAGCGT GTTTACCAGA TAATTTTCCT AATGGAAGTT 180
 10 CAGTCGTGCT TACACCAACA AGTTGAGGTG TCATAATTTC ATATGTTTCA CGATGTTTTA 240
 ATACGCCATC TTGGTGAATA CCTGATTCAT GACTAAATGC ATTTGGCCAA CAATTGCTTT 300
 ATTTCTAGGC ACTCGAATAC CTGCATATCT TGAaATTAA TCCGAGGTTT TAGTTCCTCG 360
 15 AG 362

(2) INFORMATION FOR SEQ ID NO: 4178:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4178:

GGAGCTAATA CCGGATAATA TTTGAACCG CATGGTAAAG nTGGAAAGAC GGTCTTGCTG 60
 30 TCACCTATAG ATGGATCCGC GCTGCATTAG CTAGTTGGTA AGGTAACGGC TTACCAAGGC 120
 AACGATGCAT AGCCGACCTG AGAGGGTGAT CGGCCACACT GGAACGAGA CACGGTCCAG 180
 ACTCCTACGG GAGGCAGCAG TAGGGAATCT TCCGCAATGG GCGAACTTn ACGGAGCAAC 240
 35 GCCGCGTGAG TGATGAAGGT CTTGGGATCG TAAAACTCTG TTATTAGGGG AGGACATATG 300
 TGTAAGTAAC TGTGCACATT TTTGACGGTA CCTnATCAGG AAGCCACGGT TTAGTAGGGG 360
 CCCAGAAGCC CCGGTTAATA CGTGGGTGGG nAAGGGTTTT 400

(2) INFORMATION FOR SEQ ID NO: 4179:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4179:

50 GTTGTTTCAG CAGCGACACA GTGTATTCCA TTCTTAGAAA ATGATGACTC AAACCGTGCA 60

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GTTGGTACAG GTATGGAACA CGTTGCAGCA CGTGATTCTG GTGCGGCTAT TACAGCTAAG 180
 CACAGAGGTC GTGTTGAACA TGTGAATCT AATGAAATTC TTGTTTCGTCG TCTAGTTGGA 240
 5 AGAGAACGGC GGTGAACAT GAAAGGTGGA TTAAGATCGC TATCCATTAG CTAAATTTAA 300
 ACGTTCAAAC TCAGGTACAT GTTACAACCA ACGTCCAATC GTTGCCAGTT GGGAGATGTT 360
 GTTGGnnnTA C 371

(2) INFORMATION FOR SEQ ID NO: 4180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4180:

AAAGGGAATC GAATTTTCTT TCTCTTCCTC CGGGTACTAA GATGTTTCAG TTCTCCGGGT 60
 GTGCCTTCTG ATATGCTATG TATTCACATA TCGATAACAT GACATAACTC ATGCTGGGTT 120
 25 TCCCCATTCTG GAAATCTCTG GATCAAAGCT TACTTACAAC TCCCCAAAGC ATATCGTCGT 180
 TAGTAACGTC CTTTCATCGGC TTCTAATGCC AAnGCATCCA CCGTGCGCCC TTAATAACTT 240
 30 AATCTATGTT TCCACCATT TTTATAAGTCA AACGCTCACA TACGGCTTCG TTTTCATTAT 300
 nTnAAATGCT CATTTACATA AGTAAACTCT GCTTTAAAAT AATT 344

(2) INFORMATION FOR SEQ ID NO: 4181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 343 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4181:

CCGTGATCGG AAGGTGCGGC TGGATCACCT CCTTTCTAAG GATATATTCG GAACATCTTC 60
 TTCAGAAGAT CGGGAATAAC GTGACATATT GTATTCAGTT TTGAATGTTT GTTCATTCAA 120
 ATTAATGGGC CTATAGCTCA GCTGGTTAGA GCGCACGCCT GATAAGCGTG AGGTCGGTGG 180
 50 TTCGAGTCCA CTTAGGCCCA CCATTAATTT AATACCTATT TGGGGGCTTA GCTCAGCnGG 240
 GAGAGCGCCT GCTTTGCACG CnGAGGTCAG CGGTTTCGATC CCGCTAGTCT CCACCATTAT 300
 TTGTACATTG AAAACTAGAT AAGTGAnGTA AAAATATAGA TTT 343

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4182:

CAGAGCCAAC TCGTATGTGA TTTGTCGCG CCAATGTATG CATCATCAAA AGTTCTGGAC 60
 TACTACACGC AAACGCTGGT ACATTATGAT GTTCCGTAAA CCAAATTCGC TTAAAGCCAA 120
 GTCGATCTGC TAATTTTGCA AGTGCTCACTG AATCTTGCAA TGCCTTTTGT GCATCCTTAC 180
 CTTCATCTAT TAAGGCATAG TCTAATACGC TTAATTAAAC CAATCCGTCA TCTCCAAACT 240
 TATCCTGTCA TGTCAAACCG ACATAACATT TTAGCGTCTT AATACCATTG CCTCTTCATA 300
 TACCCACGTA TATGATAACG TTTTCAATAA CTTTATATCT TTCGCCTTAT TTnCTTTTCA 360
 TATCATATTT CAGACTACAA ATGCATCATA GTTAATTAAA 400

(2) INFORMATION FOR SEQ ID NO: 4183:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4183:

AAAGTATGAA AGATGGTAGT GACGCGGTTG GTGATTGGGC TGTATTGAAT GCACTCATTG 60
 ACACAGCTGC AGGTGGTTCA TGGATTTCAT TCCATCACGG TGGCGGTGTT GGCATGGGAT 120
 ATTCACTTCA TCGGGGTATG GTTGTGTAG CAGATGGATC AGAGCGTGCT GAAGGAAGAT 180
 TGGAACGTGT ATTGACGACT GACCCAGGTA TGGTGTGGCC CGACATGTTG nATGCTGGCT 240
 ATGACATCGC TATTCAAACA GCTAAAGAAA AAGGTATTCA nATTCCAATG ATTGGTGAAA 300
 GCAGGTGATA AGTAATGAAT GATTTAATAT TAATCAnATA GCAGAnTATT TTTACCGGGT 360
 CCAACAGATA AACCTTTGAA GGGTTAGGTA TTAGATGCAT 400

(2) INFORMATION FOR SEQ ID NO: 4184:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4184:

TTCCCTGTGC ATCGGCATCA CTATTATTAG CATGACTCAA TTATTGGCAT CACAATATGT 60
 5 CATTGCAGTT ATCATTGGTT TCGTCATATG TCGGATAGGT AATGGTTTAG TCGCAACACC 120
 TGGACTTACG ATTGCAATTT TCAGTATGCC TAATGAnAAA GTTGGTTTAG CTACAGGATT 180
 ATATAAAATG AGTGGTACAT TAGGTGGCTC CTTTGGTATA GCACTAAGTA CTACAGTTTT 240
 10 CAGTATGTGA CAACTAAACT ATGCACCAAG TGTAGCTGCA ACCGTAACAT TTATAGTCAG 300
 CATTGTATTG ATGnTCCTTG GGThCATTGT CTGCATACAT GA 342

(2) INFORMATION FOR SEQ ID NO: 4185:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4185:

25 AAGCATACTC TGAAGCGGTG AACAAAAATA GAACAGATCA CATTAGACAT TTACTTGAAT 60
 TTAAAGCATG TACACCGATT GACATCGACC AAGTTGAACC GGTAAGTGAC ATTGTCAAAC 120
 GCTTTAATAC AGGGGCGATG AGTTATGGAT CGATTTGAGC GGAACACATG AAACGTTAGC 180
 30 ACAAGCCATG AACCAATTAG GTGGAAAGAG TAATACTGGT GAAGGTGGCG AnATGCAAAA 240
 CGTTATGAAG TACAAGTTGA TGGAAGCAAC AAAGTAAGTG CGATThAACA AGTTGCTTCT 300
 35 GGGCGTTTTG GTGTACTAGT GATTATTTAC CACCTGCCAA GGAATTCCAA TTAnACTTGC 360

(2) INFORMATION FOR SEQ ID NO: 4186:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4186:

45 CCCAAGCGGA ATTCTAAAAT GATCGTCGCT CCATTCTTCA TTTTAATAAA TCCAAACGCA 60
 50 GAATCTTCAA CTGTAAATTC ATCTGGATTC CATGAACCCC AAGCGTTTGC CGCATGATGC 120
 TGTTTATTTA ATTTATGGAA TGTTGAACCC ATCACTGATT CTGGTTCATA ATTATCCATC 180
 ATCCATAACG TTAAATCTAA AGCGTGTGTA CCGATATCGA TTAATGGTCC TCCACCTTGG 240

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nCTTTCCGAA GTTAAATGTC TCCTAAGTCG CCACGTTGGC GCTGCCTGGA TGGAAAATTG 360
 GACGATCTGC TCGGGAAACG AATTGGGATA AAcnGATGGG 400

5 (2) INFORMATION FOR SEQ ID NO: 4187:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4187:

GAATCATCTG GCAACChCCC CCAAGAAGG TAATAATCCT GTAGTCGAAA ATGTTGTCTC 60
 TCTTGAGTGG ATCCTGAGTA CGACGGAGCA CGTGAAATTC CGTCGGAATC TGGGAGGACC 120
 20 ATCTCCTAAG GCTAAATACT CTCTAGTGAC CGATAGTGAA CCAGTACCGT GAGGGAAAGG 180
 TGAAAAGCAC CCCGGAAGGG ATGTGAAATA GAACCTGAAA CCGTGTGCTT ACAAGTAGTC 240
 AGAGCCCGTT AATGGGTGAT GGC GTGCCTT TTGTAGAATG AACCGGCGAG TTACGATTG 300
 25 ATGCAAnGTT AAGCAGTACA TGTGGAGCCG TAGCGAAAGC GAnGTCTGA 349

(2) INFORMATION FOR SEQ ID NO: 4188:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4188:

TGGATCCTGA GTACGACGGA GCACGTGAAA TTCCGTCGGA ATCTGGGAGG ACCATCTCCT 60
 40 AAGGCTAAAT ACTCTCTAGT GACCGATAGT GAACCACTAC CGTGAGGGAA AGGTGAAAAG 120
 CACCCCGGAA GGGGAGTGAn ATAGAACCTG AAACCGTGTG CTTACAAGTA GTCAGAGCCC 180
 GTTAATGGGT GATGGCGTGC CTTTGTGTA ATGAACCGGC GAGTTACGAT TTGATGCAAG 240
 45 GTTAAGCAGT AAATGTGGAn CCGTAGCGAA ACGAGTCTGA ATAGGGCGTT TAGTATTTGG 300
 TCGTAGACCC GAAACCAGGT GATCTACCCT nGGTCA 336

50 (2) INFORMATION FOR SEQ ID NO: 4189:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4189:

5 CAAAGGATGT TAAGAAATAC AATTTATTAC CCAGCATTTA ATAATGGTGC TATAGAAGGA 60
 ATTAATAATA AGATAAAATT AATCAAGTGA ATTTCTTTTG GTTACAGAAA TTCAACAAC 120
 TTTAAAGCAC GTATAATGAT GATTTTCAGC TTGTACAAAG GAGAAAAAAA GAAGACAACC 180
 10 AAGCCCAATA ATGGACTGGC CGCCTAATAA TAAAAGCTCT AAAAGTTGTA TTTTAAAAAT 240
 AGTTCTTTAA ATTATATACC CACCACATTT GGTGGAGGAC CTAAAAAAA GCACCTCCCC 300
 AAAAATGGGA AAGTGCAAGT AGTGAGCCnT AGGAGGGTTC GGACCCTCTn nCCCCTCT 358

15 (2) INFORMATION FOR SEQ ID NO: 4190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4190:

TCACCAAGTT GAGCAAAGAA GATGTTCTGC GTACCTTGAA CTAAGTGCCC TTTGACTTCT 60
 AAnGTACCAC CAAGTGCCGT CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT 120
 30 GGACCTAACA ATCTTAAGAT GAAGCCATAA ACAAAGTAC CGATGGCACC TGTTTTCGTT 180
 ACAAATCCAC CAACATGATA AATGCCGGCT TGTATGCTTG GCCAAATGAA AAACATCAAT 240
 ACACCTAAAA AGATTGCGGC AAATGCTGTG ACAATAGGGA CAnATGTAGA GCCACCAAAG 300
 35 AAACCTAAAT ACGGTGGTAA TACCATTTGT GnTATTTGTT GTGAAGTATT GCGGTCATAA 360
 TA 362

40 (2) INFORMATION FOR SEQ ID NO: 4191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4191:

TGATCACCCA TGTTCTGGAC TCCCAATTGA AATTGAATTG GGCATTCGGA GTTTGTCTGG 60
 nATTTCGGTAA CCCGnGCAGG GTCCCCTCGT GCCAAACAGT GCTCTACCTC CAATAATCAT 120

55

1 nATTTCTCCG CTAACCTCAG TTCATCCGCT CACTTTTCAA CGTAAGTCGG TTCGGTCTCTC 240
 CATTCAAGTGT TACCTGAACT TCAACCTGAC CAAGGTAGAT CACCTGGTTT CGGGTCTACG 300
 5 ACCAAATACT AAAGCCCTA TTCAGACTCG CTTTCGCTAA GGCTCCACAT TTAAGTCTTA 360
 AC 362

(2) INFORMATION FOR SEQ ID NO: 4192:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4192:

20 CGTGTATTAT GCCTTCTACA TTGGCCATTA TGAAACTTA TTATCAGGGT GCTGAACGTC 60
 AGCGTGCCTT AAGTTATTGG TCTATCGGTT CTTGGGGTGG CAGTGGTATC TGTTCACTCT 120
 TCGGTGGTGC AGTTGCGACA ACTATGGGTT GGAGATGGAT TTTCATCTTC TCAATTATCG 180
 25 TTGCCGTACT TTCAATGTTA CTCATCAAAG GGACGCCTGA AACGAAATCA GAAATTACCA 240
 ATACACATAA ATTTGACGTT GCAGGGCTAA TTGTTCTAGT AGTATGTTGC TAAGTTAAAC 300
 GTTGTCAATTA CTAAAGGTGC AGCACTTGGn TACACATCAT TATGGGTCTT GGGTTGAATG 360
 30 CCAATCGGAA ATTGTAGCAT CnTTAATTTC CTAAAAGGTG 400

(2) INFORMATION FOR SEQ ID NO: 4193:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 373 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4193:

45 AATCCCATGG ACCCTCAAAT TCTTTATCTA AATAGTACCC TAATGAAGTT TTTCTGTGCA 60
 TGTGATTAAT TTCATGTAAA CCGATGACAC CAACTAGCGT TCCTTCATAC CAAATGCCAC 120
 ACTGAAATCC ATTACCATCA GCAAATTGCA AAAGTCCTCT TTTAATAAAT GCACGCGTAT 180
 50 CTGATGGTTG CTCAGTTGCA TCTACCCAAG GTAACCATTC CCTAAGTGAA TTTCTTGAAC 240
 GATTGACTAA ATTGAAAAGC GCTTCTGTGT CATGAGCTTC TAAAATTTTA ATGTTATTGT 300
 TCAATCACTT TCATTCCAAA CATACnATCA CATCCTCATT CATThTCATA TAATCCGnA 360
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(2) INFORMATION FOR SEQ ID NO: 4194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4194:

ACAAAGGACG ACATTAGACG AATCATCTGG AAAGAGAATC AAAGGTAATA ATCCTGTAGT 60
 CGAAAATGTT GTCTCGAGTG GATCCTGAGT ACGACGGAGC ACGTGAAATT CCGTCGGAAT 120
 CTnGGAGGAC CATCTCCTAA GGCTAAATAC TCTCTAGTGA CCGATAGTGA ACCAGTACCG 180
 TGAGGAAAGG TGAAAAGCAC CCCGGAAGGG AGGTGTAAAT AGAACCTGAA ACCGTGTGCT 240
 TACAAGTAGT cAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGAAT GGAACCGGCG 300
 AGTTtACGAT TTGgATTGCA AGGTTAAGCA GTAAATGTGG GAGCCGTA 348

(2) INFORMATION FOR SEQ ID NO: 4195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4195:

AAGGCAGATG CTCTCCCAGC TGAGCTAATT CTCCGATTTA AAAGTGCCTG GCAACGTTCT 60
 ACTCTAGCGG AAnTAAGTnG GACTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCGG 120
 CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180
 TTCAAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAAG 240
 TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGAACCTAT 300
 TAACCTCATC ATCTTTGAGG GATCTTATAA nCGAGTTGGG 340

(2) INFORMATION FOR SEQ ID NO: 4196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAAATTAA TGAAAGATAC AGTAGGTGCT 60
 GATGTAGAAG TAAAAGCATC AGGTGGCGTA CGTAATTTAG AAGATTTCAA TAAAATGGTT 120
 5 GAAGCAGGTG CGACACGTAT TGGTGCGAGC GChGTGTTCA AATTATGCAA GGTTTAGAAG 180
 CAGATTCAGA TTAATAATAT ATATnAATnT TGGGAGTGAT AGCTATGACA AGACCATTTA 240
 ATCGTGTA TTTAATCGTA ATGGATTGAG TAGGTATTGG TGAAGCGCCA GACGCAGCTG 300
 10 ATTTTTTAAAG ATGGAGGTTT ACATACTTTT A 331

(2) INFORMATION FOR SEQ ID NO: 4197:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4197:

GTAGACGTCC CGATAGCCGT TACGCATGGT TACGATGTGT ATTGGTGTCG GCATGGGTGC 60
 25 AGCTGCTATA TTTGAATATG TCGTTAGAA TGGTTGATTT TGGATGAAGC GGATTCGTTT 120
 TGTATTGAA TGAAGTAGGC TGAAGTTGAA GCCAGTTGAA GTTGAAGCGG GTTGAAGCAA 180
 30 TTTCGTTTTA TTGAATGAAG CTGTGTGAAA TATAGTGATT GAACAAAAAA AGTGGTTTTAA 240
 TGGGATGGTG GTTATTTCCG TTTTAGAATT TAACATTTAC ACGTCTAATT TTAAATCATT 300
 GTTTTAAATT TTATGAATCG AAGCCCTTTG GATTTAATn TATTGCTAAT GChAGTAACT 360
 35 nATCTGATTG T 371

(2) INFORMATION FOR SEQ ID NO: 4198:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4198:

GCGACCCCAA CCTTGGCAAG GTTGThATTC TACCGCTGAA CTACTTCTGC ATATGCGGGT 60
 50 GAAGGGAGTC GAACCCCCAC GCCGTAAGCT nAGnATCCTA AGTCTAGTGC GTCTGCCAAT 120
 TCCGCCACAC CCGCAAATGG TGAGCCATAG AGGATTCGAA CCTCTGACCC TCTGATTAAA 180
 AGTCAGATGC TCTACCAACT GAGCTAATGG CTCTTCCATG GTGCCGGCCA GAGGACTTGA 240

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TAAGAATAAA TGGTGGAGAA TGACGGGTTG GnACCGTCGA CCCTGTGCTT GTTAAGGCAG 360
 ATGGTTTTCC CACTGGGGTA AATTTTCCGA TTTAAAAATG 400

(2) INFORMATION FOR SEQ ID NO: 4199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4199:

ATCAGTTGCT GTTGCGCCTT GTGTAATGA ATTTACTAGT CGTACACCAA TAACCTCTGG 60
 AATTGGGAAA TAAGAAGGTT GTCCAAGCAT TCCAGCTTCA GCTTCAATAC CACCAACACC 120
 CCATCCTAGT ACGCCAATAC CATTATCAT TGTGTATGT GAATCAGTAC CAACTAATGT 180
 ATCTGGAAAT GCAGTTTTTT CACCATCTAC ATCACGAACA TGTACAACAC TTGCTAAATA 240
 TTCTAAGTTA ACTTGGTGAA CTATTCCAGT TGCAGGAGGG AACTGCATTG TAATTATCAA 300
 ATGCTTTCGG TTGGCCCAAT TAAAAAACT GGATAACGTT CATnGTTACG TTCCAATTCC 360
 TAATTTCCnA ATTACGGTTC CAnGAGCTTC TGGGATTTTG 400

(2) INFORMATION FOR SEQ ID NO: 4200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4200:

CAACCTTTAT TGGTAAAAAC ACCCCAGCCA GGCACTTTAC GCCTACGCAT CGCTTGTACA 60
 CGTGCTACTA nAGGTTTACC AACCACACCT GATTCAATTG CTTTTTTAGC AGTAATTGCC 120
 ACATCTGTGT GACGATAATG ATATGCGACA GTTAATAATT TGTGATTTTT ATTAGCCGCT 180
 TCAATCATGC GATCACACTC TTCCGTCGTC ATCGCCATTG GCTTTTCACA CAATACATGG 240
 CACACCATGG TTCAATGChT CTATAGAAAG ATCAGCAGGA ATTTATTAGG TGTACAAATG 300
 ACCCATCAAC AAGTTTAAAC AGCTCGCTAG GTGnC 335

(2) INFORMATION FOR SEQ ID NO: 4201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 370 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4201:

	ATGATGTGGC GGTGGTGAAA TCAGACCGAT ACCTGGCGTT GACCCTCTTG TCTTCGCAAT	60
10	CCACGGATAT ACCTTAGTAC CAGGTAATTG ACCACCTTCA CCAGGCTTTG CACCTTGCGC	120
	AACTTTAATT TGAATTTCTT TGGCATGTTG TAAATAATCA CTAGTTACAC CAAAACGCCC	180
	AGAAGCAACT TGTTTAATCG CACTTACTTT GTTGCTTCCA TCAACTTGTA CTTCATAACG	240
15	TTTTGCATCT TCGGCAACTT CACCACTATT ACTCTTTCCA nCTAATTGGG TCATGGGCTG	300
	TGCTAACGTT TCATGTGCTT CCGnTGnAAT CGATCCATAA CTCATCGGCC CCGTATTAAA	360
	GCGGTTGGAC	370

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(2) INFORMATION FOR SEQ ID NO: 4202:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4202:

	CAGCTAGCGA CTTACCTTGA CGTTTTGnGT ATTCAATTCCA GCTTTGTnGG AATGAGtCGG	60
	gATATAAGCA TCTTTAGATA ATGCACCATC AACTAATGGA TATTTATGTC CAGTTGGaGC	120
35	CAGAAATCAT AAACGTCTTC AGTGTAGCA ACAGCATCTT CaTTTAATGC CAAAATGCTT	180
	GGaTTAgTGC AATAACCATC GCAACTGnGC CanACCTTGT GTTGGCTCGC CGCCTGAATT	240
	CAATCCATAA CGTGCTGTAT CTGTAGCAAT AACTAATACT TTTTCATTCG GTCTAGTTGC	300
40	TAAATAATCT TTAGCTAATT GAATTGCTGG TGTTCAGCA TAACAAGCTT CTTTCATTTC	360
	AAAGCAGCGT GCAAAAGGTT	380

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(2) INFORMATION FOR SEQ ID NO: 4203:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4203:

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GACATGTCAC CAAGAGCATT AGAAGAAGTT ATTTACTTTG CTTCTTATGT TGTGTAGAT 120
 CCAGGTCCAA CTGGTTTAGA AAAGAAAAC TTTATATCTG AAGCTGAATT CAGAGATTAT 180
 5 TATGATAAAT ACCCAGGTCA ATTCGTTGCA AAAATGGGTG CAGAAGGTAT TAAAGATTTA 240
 CTTGGAAGAG ATTGATCTTG ACGAGGAACT TAAATTGTTA CCGATGAGT TGGGAATCAG 300
 CTACTGGGTC CAAAGACTTA CTCCGTGGCA ATTAACGGTT TAGAAGTTGT TnGAATCATC 360
 10 CCGTAATCCA GGGTACCACC CTCCnnGGnT GGATTTAGGA 400

(2) INFORMATION FOR SEQ ID NO: 4204:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4204:

AAATTCTTCC GCCCTGTAAT TCCTTAACCG CTTCAACGGC ATCGTnAATn TCTTACATTT 60
 25 AGATAAAGAT GCATTGCAAG ATATCGTCAA CTTATTATTA GACGATGTAC AAGTTACATT 120
 AGACAAAAAA GGTATTACGA TGGACGTTTC TCAAGATGCG AAAGATTGGT TAATTGAnGA 180
 AGGCTATGAT GAAGAATTAG GTGCACGTCC ATTAAGACGT ATTGTTGAAC AGCAAGTACG 240
 30 TGACAAAATT ACAGATTACT ATTTAGATCA TACAGACGTT AAACATGTGG ATATAGATGT 300
 TGAGGATAAC GAATTAGTCG TAAAAGGTA 329

35 (2) INFORMATION FOR SEQ ID NO: 4205:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4205:

45 GGTAAACAAA AAACCTCCCT TTGGAAGCGA ATTATGGAGC GGAAGATAGG ATTTACACCT 60
 ATACCTCGTT CCGGGAAGGG CTGTTTCTAA AAGTTGAACT ACTCCGCAA ATATTAAATT 120
 50 ATGGAGCGGA AGATAGGATT TACACCTATA CCTCATTCCA GGAAGGAATG TATTCTAAGA 180
 GTTGAAATAC TCCCGCATT TATTAAATT ATGGAGCGGA AGTAGGATTT GCACCTATAC 240
 CTCGTTCCGG GAAGGAGCTG TTTCTAAAAG TTGAACTACT ACCGCATAAA CCTGGTGGCG 300

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(2) INFORMATION FOR SEQ ID NO: 4206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4206:

TACTTTGTGA ATCCAGAAAA CTTTGAGGAT GTCACATAA GTGTGAATAT TACATTCCCA 60
 AATCCAAATC AATATAAAGT AGAGTTTAAT ACGCCTGATG ATCAAATTAC AACACCGTAT 120
 ATAGTAGTTG TTAATGGTCA TATTGATCCG AATAGCAAAG GTGATTTAGC TTTACGTTCA 180
 ACTTTATATG GGTATAACTC GAATATAATT TGGCGCTCTA TGTCATGGGA CAACGAnnAG 240
 CATTTAATAA CGGATCAGGT TCTGGTGACG GTATCGATAA ACCAGTTGTT CCTGAACACC 300
 TGATGAGCCT GGTGAAATTG AACCAATCCA GGGATCAGAT CTGACCCAGG TCAGATCTGG 360
 CAGCGATCTA ATCAGnAGCG GTCAGATCGG GnAGGATCAC 400

(2) INFORMATION FOR SEQ ID NO: 4207:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4207:

AAAAAGTTGA GAAAAATGTT TGAATCAGCA AACGTTGTGC AATCGAAATT TCCACACCAT 60
 CAAAACCTGC TTTAATCGCG CGTAATGTAG CATCGCnGwk ACTGCTGAAT GATGCTATTG 120
 ATTTTCTCAT GAGACATGGC GATAACATCG TGTTtCAATC GGTGAATGCA ATGwCATAGG 180
 GCTTGGTCCA TACACCTTTC CAAAATTAA AATGGCTTGA TTTGAAAAAC GACCAGCATG 240
 CGCTACTGGG ATAATAGCGA GGCTACCATG TTGTTTCATC GTAGATCCCA TGTTAGTTAA 300
 TCCAGGGATA CAACCATCAT GATCAATATT AAAnCATATC CAACCATTGA CCATAAGGTC 360
 AATGTAACAC GCCGGTGA CT CATCCAGCT GAATAGACGC GT 402

(2) INFORMATION FOR SEQ ID NO: 4208:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4208:

5 GAAGAGTTGC AGCAGCAGAT ACAATTTATC CATTCACTCA AGCTGAAAAT GTTTGGTTAC 60
 CAAACAAAAA TGACATCATC GAAAAAGCAA AAGAACTTT AGAATTTTAA TACATTTTAA 120
 AAGTTAACGA ATTAGCCGTG ATTTTAGTCT CATTGATTAA AATGAAATnG TTAATTTACG 180
 10 AAATCTTAGG AGGGCAAAAA CGTGGGCATT TGAATTTAGA TTACCCGATA TCGGGGGAAG 240
 GTATCCACGA AGGTGAAATT GTAAATGGT TTGTTAAAGC TGGAGGATAC TATnGGAAGA 300
 AGACGATGTT TTAGCTGGAG GTACAAAACC GATAAATCAG TAGTAGAAAT CCCCATCCAC 360
 15 CAGCATCTGG TACnGGTAAG 380

(2) INFORMATION FOR SEQ ID NO: 4209:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4209:

AATAAACCTC AGGCTATTCA ATGGCATACA AATTTAACGA ATGAGCGATT CACTACTATC 60
 30 GCACATCGTG GCGCAAGTGG CTATGCACCC GAGCATACGT TTCAAGCATA TGATAAGAGT 120
 CATAATGAGT TAAAAGCATC TTATATCGAA ATTGATTAC AACGTACCAA AGATGGCCAT 180
 TTAGTTGCTA TGCATGATGA AACTGTTAAC CGTACAACAA ATGGACACGG TAAAGTTGAG 240
 35 GATTATACCC nTGATGAATT AnAACAGTTA GATGCAGGAA GTTGGTTAAT AAAAAATATC 300
 CnAAATACGC CAGAGCAGTA TTAAATGCT AAAGTACCAC TTAGGTGGAA TTTAGGACGT 360
 ATTGGCCCGA TGCCAACnTT TATATTGAAC CAAGCACCTG 400

(2) INFORMATION FOR SEQ ID NO: 4210:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4210:

50 GCCCAACC ACAAAGGCTG TAGGCTACAA ATATGGAGAC GGCGGGATTT GAACCCGCGT 60

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AAAAGTGATA AACAAACCAAC ATGATGCTAG TTTGATTAAG TTTCTTCTAA ACAGACTTCA 180
AACGGCATnG TTAGCATATC CTATTAAGGT TGAATCGCGT TAACAGCACA TAGGAAATGC 240
5 TGTTAGGCGA TGCAGAGTGC GATTAGGCAG CTA CTGCGAA ATTATTGTnT GATTTGCCAG 300
TTATTATnAA CTGTGTGGTG TTGATGACGA 330

(2) INFORMATION FOR SEQ ID NO: 4211:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4211:

AAATCATCTT ATGACTGCTT TTTATTATAC TTTACATTTT TCGTTTCGTC AGATTCAAAC 60
GTTTTCACTT CGCCAAGCCA TCTTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT 120
AAAAAAGAG ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTG CCTGGCAACG 180
25 TTCTACTCTA GCGGAACGTA AGTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCnGTG 240
TTCGGCATGG GAACAGGTGT GACCTCCTTG CTATAGTCAC CAGACATATG AATGTAAATT 300
ATACATTCAA AACTAGATAG nAAGTAAAAG TGATTTTGC 339

(2) INFORMATION FOR SEQ ID NO: 4212:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 334 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4212:

GCGATGGTTG AAACATTGAC TGATATTAAA GAGTTTATGA ACCAAGTTGA GTCGCATAGC 60
TAGTATGAAA CGTGGTGTGC GCATGGGAAC TATCAAGCTT TGAAGATGTG GTACTACATG 120
45 CGTTGAATTA GGGATCGGTA CTTTATATGA AGACGTGCTG CTTCCATTAA ATGAGTGATG 180
CGATTTTGGC ATGAAGGTCA CCTnAAATGT ACATTGTTGT AATAAAATTG CCTATAAAAT 240
TTTTAGCACA TAAAATAAGA GGGGCCAnCC ATTTTAGACT ATAACAACGG TTGGCTCTTT 300
50 GAATTGTAAA AAGAAAACCA TACGCTATGn TATT 334

(2) INFORMATION FOR SEQ ID NO: 4213:

(A) LENGTH: 332 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4213:

10 CTATGATTTC ACCGAGTCTC TCGTTGAGAC AGTGCCCAAA TCGTTACGCC TTTCGTGCGG 60
 GTCGTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT ATAGTTACGC CGCCGTTTAC 120
 TGGGGCTTCG ATTCGTAGCT TCGCAGAGTA nACCCACTCC TCTTAACCTT CCAGCACCGG 180
 15 GCAGGCGTCA CCCTATACAT CACCTTACGG TTTAGCAGAG ACCTGTGTTT TTGATAAACA 240
 GTCGCTTGGG CCTATTCACT GCGGCTCTTC TGGGGCGTTA ACCCTAAAGA GCACCCCTTC 300
 TnCCGAAGTT TACGGGGTCA nTTTGCCGAG TT 332

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(2) INFORMATION FOR SEQ ID NO: 4214:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4214:

CGCCTGGCAA CGTTCTACTC TAGCGGAACG TAAGTTGGCT ACCATCGTCG CTAAAGACCT 60
 TTCTTGACTT GTGACAATCG CTTGCTTCTT TCCTCTCCTT CGGCTCTCGC TTACTCATT 120
 35 AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC 180
 GCCAAGCCAT TTTTCTTTGT GTTTACTTTT TAnTTTGACG TTTTAGACAT AAAAAAAGA 240
 GACCTTGCGG TCTCAATGCG GCTCATCGCA TCCATTTTTT GCCTGGGCAA CGTTCTACTC 300
 40 TAGCGGAACG TAAGTTGGGT ACCATCGACG CTAAGAACCT TCTTGGA nTG TGGACAACGn 360
 TGG 363

45

(2) INFORMATION FOR SEQ ID NO: 4215:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4215:

TTATTTGTAT TGTATAGAGA GAAATAAAAA GAAACCTTGT TTTACAAGGT TTCTAATACG 120
 TTATGTTATG TAAATAACAG TTAATTATAC CGGTGGTCGG GGTCGAACCG AACTCCACA 180
 5 AGTGAACCG GGATTTTGAG TCCCGCGCGT CTGCCAATTC CGCCACACCG GCTTAATGGT 240
 AAACAAAAAA CTTCCTTTG GAAGCAATTA TGGAGCGGAA GATAGGATTT ACACCTATAC 300
 CTCGTTCCGG GAAGGACGTG TTCTAAAAGT TGACTION 338
 10

(2) INFORMATION FOR SEQ ID NO: 4216:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4216:

ACGGTGATCC CATAATGCTT GAACATCAAT TTCATCCATT AATGTTACAT GAGGTGCAGT 60
 ATGCTTAGAG TTAACCATTG CTTTCGCAAT TGCTCTACGC ATAGCAGGGA TTTTTCAGT 120
 25 TGTTCCTGGG AAGTCGCCTT CTAATGTTAC TGCTGCAGGT GCTGCAGGAG TTTCAGCAAC 180
 TTCTTCACTT GTAGCTGAAG CAGCTGATTC ATTTGAAGCT GTTGGTGCAC CACCATTTAA 240
 GTATGCATCT ACATCTTCTT TTGTAATACG ACCATTTTTC CCAGATCCAG AAATGCTTTT 300
 30 AATGnTAACA CCTnTTTCAC GTGCGTATTA CGACTGAAGG CATGCCTTAA CAGTCnGGTT 360
 CACCACTCTC AGTTGAGAGC ACAGGGCTGC nCGCTGGCGC 400

(2) INFORMATION FOR SEQ ID NO: 4217:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4217:

45 AGGGAATCGA ATTTTCTTTC TCTTCCTCCG GGTACTAAGA TGTTTCAGTT CTCCGGGTGT 60
 GCCTTCTGAT ATGCTATGTA TTCACATATC GATAACATGA CATAACTCAT GCTGGGTTTC 120
 50 CCCATTCGGA AATCTCTGGA TCAAAGCTTA CTTACAGCTC CCCAAAGCAT ATCGTCGTTA 180
 GTAACGTCCT TCATCGGCTT CTAGTGCCAA GGCATCCACC GTGCGCCCTT AATAACTTAA 240
 TCTATGTTTC CATCCTACAG GAAACGCGTT ATTAATCTTG TGAGTGnCT TTCGAACATA 300

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(2) INFORMATION FOR SEQ ID NO: 4218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4218:

```

GGCGCCCTCG TGCCAAACAG TGCTCTACCT CCAATAATCA TCACTTGAnG CTAGCCCTAA      60
AGCTATTTTCG GAGAGAACCA GCTATCTCCA GGTTCGATTG GAATTTCTCC GCTACCCTCA      120
GTTTCATCCGC TCACTTTTCA ACGTAATCGG TTCGGTCCTC CAnTCAGTGT TACCTGAACT      180
TCAACCTGGA CCAAGGGTAG ATCACCTGGn TTCGGGTCTA CGACCAAATA CTAAACGCCC      240
TATTCAGACT CGCTTTTCGCT GACGGCTCCA CATTTACTGC TTAACCTTGC ATCAAATCGT      300
AACTCGCCGG TTGCATTCTA CAAAAGGCAC GCCATGCACC CATTAA      345

```

(2) INFORMATION FOR SEQ ID NO: 4219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4219:

```

TCTTATGACT GCTTTTTATT ATACTTTACA TTTCTCGTTT CGTCAGATTG AAACGTTTTT      60
ACTTCGCCAA GCCATCTTTC TTTGTGTTTG CTTTTATTTT GACGTTTTAG ACATAAAAAA      120
AGAGACCTTG CGGTCTCAAT GCGGCTCATC GCATCCACTT TTTGCCTGGC AACGTTCTAC      180
TCTAGCGGAA CGTAAAGTTC GnACTACCAT CGACGCTAAG GAGCTTAACT TCTGTGTTTCG      240
GCATGGGAAC AGGTGTGACC TCCTTGCTAT AGTCACCAGA CATATGGAAT GTAAATTATA      300
CATTCAAAAC TAGATAGTAA GTAAAGTGGn TTTGCTTCGC AAACnTTAT TTTGGTTAGT      360
CTTCGTC      367

```

(2) INFORMATION FOR SEQ ID NO: 4220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4220:

5 AAGAGCCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCACTT 60
 ACTCATTTAG CTCTACTAAA CTCGTTGCGT TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 120
 TTCACCTTCG CAAGCCATTT TTCTTTGTGT TTGCTTTTAA TTTTGACGTT TTAGACATAA 180
 10 nAAAAAGAGA CCTTGC GGTC TCAATGCGGC TCATCGCATC CATTTTTTCG CTGGCAACGT 240
 TCACTCTAGC GGAAnTAAGT CGAACTACCA TCGACGCTAA GGAGCTTAAC TTTCTGTGTT 300
 CGGCATGGGA ACAGGTGTGA CCCCnTGGC TATAGTCACC AG 342

15 (2) INFORMATION FOR SEQ ID NO: 4221:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4221:

25 ACCGGATGAC AGCCCCAGGA TCGATGAGC CGACATCGAG GTGCCAAACC TCCCCGTCGA 60
 TGTGAACTCT TGGGGGAGAT AAGctGTTAT CCCC GGGTA GCTTTTATCC gTTGAGCGAT 120
 GGCCCTTCCA TGCGGAACCA CCGGATCACT AAGTCCGTCT TTCGACCCTG CTCGACTTGT 180
 30 AGGTCTCGCA GTCAAGCTCC CTTATGCCTT TACTCTAT GAATGATTTC CAACCATTCT 240
 GAGGGAACCT TTTGAGCGCC TCCGTTACCT TTTAnGAGGC GACCGCCCCA GTCAAATGCG 300
 35 CCGCCTGACA CTGTCTCnCA CCACGATAAG TGGCGnG 337

(2) INFORMATION FOR SEQ ID NO: 4222:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4222:

GGCGCTTGAC TAAAAAGAAA TTGTACATTG AAAACTAGAT AAGTAAGTAA AATATAGATT 60
 50 TTACCAAGCA AAACCGAGTG AATAAGAGT TTAAATAAG CTTGAATTCA TAAGAAATAA 120
 TCGCTAGTGT TCGAAAGACA TCCACCAAGn TTAATAACGC GTTTAAATCT TTTTATAAAA 180
 GAAAACGTTT AGCAGACAAT GAGTTAAATT ATTTTAAAGC AGAGTTTACT TATGTAAATG 240

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ACATAGATTA AGTTATTAAG GGCGCACGGT GGGTGCCnTG GCACTTAGAA GCCGCTGAAG 360
G 361

5 (2) INFORMATION FOR SEQ ID NO: 4223:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4223:

CGGTAGAATA CAACCTTGCC AAGGTTGGCG TCGCGGGTTC GAATCCCGTC TTCTGCTCCA 60
TTATTTTGCC GGGGTGGCGG AACTGGCAGA CGCACAGGAC TTAAAATCCT GCGGTGAGAG 120
20 ATCACCGTAC CGGTTGATT CCGGTCCTCG GCACCATTTT AGCGCCCGTA GCTCAATTGG 180
ATAGAGCGTT TGAACGGA TCAAGAGGTT ATGGGTTTCA CTCCTATCGG GCGCGCCATT 240
TTTAAATTAA TTGAATAACG GGAAGTTAGC TCAGCTTGGT AGAGCACTTG GTTTGGGGAC 300
25 CAAGGGTCGC AGTTCGAATC CTGTCTTCCC GATTACTCnT AAnTCCATTT AnGGGGGCTA 360
GCTCAGTGGG GAGAGCGCTG CTTGCACGCA GGAGGTCACG 400

30 (2) INFORMATION FOR SEQ ID NO: 4224:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4224:

40 CATAATATAC TCTTAAGTGT AAAGGGGAAT TTCCTGGGTA ATAATTCGCG TGTGCACCTT 60
GAGTGACTTC TACCATTTTA TAGTCAAATT GCTTTAGTTC GTTTGGTTTA ACGCCGACAC 120
TCGCAAATGT ATAATCAAAG AACTTCACAA TATTGTTGCC TAAGAAGCCT TTGAATTCAA 180
45 TAGTGTCAAT TCCAGCAATT TGTTCGGCAA CAATACTTGC TGCACGGGTG AGCGCCCCCA 240
GnCAAAAGGA CCACTAGCCG GTAGAATCGA CATGTCGATA ATGTGATGGT TGCCAATAAT 300
CGCCTATTGC ATAATGTTTG GACCATTGGT TCCAAATTTA TCGTTACCGG TATGAAACCT 360
50 TTCGATCCAG TTGGATAATT GAACTTCGnA AATTTGATTG 400

(2) INFORMATION FOR SEQ ID NO: 4225:

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(A) LENGTH: 328 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4225:

GGGTTCAATT TCTGCATACC AATCGATGCC AGCTCTATTT CTGACAATAT CCATATATTT 60
 TGAAATTTTC TCTAATTCTT TGCCACTAAC CTTTTACCA TTCAACCAAA ATTGATCCTG 120
 TGTTAACTGG TCGTTAAAAG TGACTTTCGT TTCAGTGTA AATTTTCTA ATGTAACAGA 180
 TATGCTATTA TTCATTGGAA TGATTAGTGC TTCATCTTTT TTACCCCAAT ATTTTATnAG 240
 TGCAATATTC GTATGTGCAC GTGCTTTGCC ACTnnTAATC AACGCATTAA CCTCCTAAAT 300
 TCTCAATCCA AGTATGTGCT GCACCAGC 328

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(2) INFORMATION FOR SEQ ID NO: 4226:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4226:

TGACGGGTTT GAACCGCCGA CCCTCTGCTT GTAAGGCAGA TGCTCTCCA GCTGAGCTAA 60
 TTCTCCGATT TAAAACTGCC TGGCAACGTT CTA CTCTAGC GGAAnGTAAG TTCGnACTAC 120
 CATCGACGCT AAGGAGCTTA ACTnCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180
 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT AAGTAAAAGT 240
 GATTTTGCTT CGCAAAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 300
 TCCACATGTC ACCATGCTTC CACCT 325

40

(2) INFORMATION FOR SEQ ID NO: 4227:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4227:

GCGCAACTCA CACAACAAGG TGGCAATCAC TCTGAACAAA GTGCGGCAAn TTnTTCAACA 60

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AACCTTACGC AAGAAGCACG TGACGGTTTA TTAGATCCAG TCATTGGTCG TGGATAAAGA 180
 AATTCAAGnA ACTGCTGAAG TTTTAAGTAG ACGAACTAAA AACAACTCCTA TATTAGTTGG 240
 5 AGAAGCTGGT GTTGGTAAAA CTGCGATTGT TGGAAGGTTT AGCACAGGCA ATCGTTGGAA 300
 GGAAATGTAC CAGCAGCAAT CAAAGACAAA G 331

(2) INFORMATION FOR SEQ ID NO: 4228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4228:

AGAGGTCCGT TGCCTTACCG CTTGGCTATA GCCATTAATA ATAAGGGCGG CTGAAGGGGA 60
 TCGAACCCCTC GAATGTCGGA ACCACAATCC GATGTGTAA CnCTTCACCA CAGCCGCCAT 120
 GGCAGGGGCA GTAGGAATCG AACCCACACC AAAGTTTGG AGACCTCTAT TCTACCGTTG 180
 25 AACTATGCCC CTATTAAAA TAATAAATGG AGGGGGCAG ATTGGAAGTG CCGAACCCGA 240
 AGAGCGGATT TACAGTCCGC CGCGTTTAnC CACTTCGCTA CCCCTCCATA AATGGTGCCG 300
 GCCAGAGGAC TTGnAACCCC CAACCTAATG GTT 333

(2) INFORMATION FOR SEQ ID NO: 4229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4229:

CTCTTACTTT GTAAACCAAA TCTTAAATTA AAATATTGAA AATGCAATGn ATCCTTAATA 60
 TTTTATTAAA CCTATAATTA CTTATTAAAA ATAACACACA ATATTCATAA AGTTTTAAAA 120
 45 ATATTCTGTT TTATCACCTA CTATTAGTGG AAAAGTACAA TTGCAATTGT ATATAGTTTG 180
 CATAACGCTT CAAAAGTAAT TTCTTTTTTG TTTAGTTCAA AAAAATTTAG AGGTGATGTT 240
 ATATGAATAA CGGTTTTTTC AATAGCGACT TTGATTCAAT TTTTCGAGGA TGATGAAAGA 300
 50 TATGCAAGGT TCAAATCAAG TCGGAAACAA AAGTACTATA TTnATGGTAA GGAGTTTCAC 360
 CTGAGGACTG GCGCAACTnC ACACACCAGG TGGCCATCAC 400

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4230:

10 CATTAACGGG CTCTGACTAC TTGTAAGCAC ACGGTTTCAG GTTCTATTTT ACTCCCCCTTC 60
 CGGGGTGCTT TTCACCTTTC CCTCACGGTA CTGGTTCAC TCGGTCAC T AGAGAGTATT 120
 15 TAGCCTTAGG AGATGGTCCT CCCAGATTCC GACGGAATTT CACGTGCTCC GTCGTA CTCA 180
 GGATCCACTC AAGAGAGACA ACATTTTCGA CTACAGGATT ATTACCTTCT TTGATTCATC 240
 TTTcCAGATG ATTcGTCTAA TGTCGTCTT TGTAAC TCCG TATAGAGTGT CCTAsAACCC 300
 20 CAACAAGCAA GCTTGTTGGT TTGGGnTCTT GCCGTTTCG 339

(2) INFORMATION FOR SEQ ID NO: 4231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 349 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4231:

30 GAAGTCATAT GCATACACTT GGTTATCATT ATTCATACGT TCAATCGCAT CTGTAACTG 60
 35 AATTTcGTTA CCTGCGCCTT CTTTTTGCGT TTTTAAATAA TCGAAAATTT CAGGCGTTAA 120
 TACATAACGT CCCATAATAG CTAGGnTTGA TGGTGCCGTA CCTTGTGCTG GCTTTTCAAC 180
 AAAC TTTTTC ACTTCAGACT GACGTCCGTh TTTAGTTAAT GGGTCAATAA TTCCATAACG 240
 40 ATGAGTATCT GCTTCCGGAA CTTCTTGGAC ACCTATAACT GAGTGCCCTG ThTCTTCATA 300
 AACGTCAATC AACTGTTTCA CTGCTGGCAC TTCAGAGTCA ACAATATCG 349

(2) INFORMATION FOR SEQ ID NO: 4232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4232:

CCAGGATGCG ATGACCGACA TCGAkGTGCC AAACCTCCCC GTCGATGTGA ACTCTTGGGG 120
 GAGATAAGCC TGTTATCCCC GGGGTAGCTT TTATCCGTTG aGCGATGGCC CTTCCATGCG 180
 5 GAACCACCGG ATCACTAAGT CCGTCTTTTCG ACCCTGCTCG ACTTGTAGGT CTCGCAkTCA 240
 AGCTCCCTTA TGcCTTTACA CTCTATGAAT GATTTCCAAC CATTCTGAGG GAACTTTGaG 300
 10 CGCCTCCGTT ACCTTTTAGG AGGCGACCGC CCAGTCAAAC TGCCCGCCTG ACACTGTCTC 360
 CCACCACGAT AAGGTCG 377

(2) INFORMATION FOR SEQ ID NO: 4233:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4233:

GGCTAGCCTC AAGTGATGAT TATTGGAGGT AGAGCACTGT TTGGACGAAG GGCCCCCTCTC 60
 25 GGGTTACCGA AGTTCAGACA AACTCCGAAT GCCAATTAAG TTAACTTGG GAGTCAGAAC 120
 ATGGGTGATA AGGTCCGTGT TCGAAAGGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA 180
 AATATATGTT AAGTGGA AAA GGATGTGGCG TGGCCCAGAC AACTAGGATG TTGGCTTAGG 240
 30 AAGCAGCCGT CATTTAaAGA GTGCGTAATA GCGCACTAGT CGAGTGACAC TGGGGGGAAA 300
 GGGTACCGGG GCTGAACATA TTACCGAAGC TGGTGGGTTG TCCTTTGGAC AnTTn 355

35 (2) INFORMATION FOR SEQ ID NO: 4234:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4234:

45 ATCCGCCTCC CGCAATATTT TATAGGTCTC GTAGTGTAGC GnTTAACACG CCTGCCTGTC 60
 ACGCAGAGAT CGCGGGTTCG ATTCCCGTCG AGACCGCCAT CATTACATTT TTATTATGGT 120
 TCAGTAGCTC AGTTGGTAGA GCAATGGATT GAAGCTCCAT GTGTCGGCAG TTCGACTCTG 180
 50 TCCTGAACCA TTTCTTAGCC GGCTAGCTC AATTGGTAGA GCAACTGACT TGTAAATCAGT 240
 AGGTTGGGGG TTCAAGTCCT CTGGCCGGCA CCATTTATGG AGGGGTAACG AnTGGGCTAA 300

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TTAATAATTT TAATAAGGGG CATAnTTCAA CGGTAnAATA

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(2) INFORMATION FOR SEQ ID NO: 4235:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4235:

ATGCCATGTT CACCTTGTTT AAAATCAAGG TTTGTAATGT TTCCTTGTTT CACGATAATA 60
 GCGTAATAT CACTCTTTCG ATGATTGCGG ATGTAGTCTA AATCAAAGTT GATTAATAAA 120
 TCACCTTCTT TAACTnTTG ACCTTCCTCA ACATGTAAAG TAAAGCCTTC TCCGTTTAAT 180
 TTAACAGTGT CTAAACCGAT GTGGATTAAAT AGTTCTAAAC CACTATCTGA TACAAGACCA 240
 ATTGCATGnT TTGTGGGAA AATCATTTGT ACTTTACCGT TGAATGGTGC ACGAACTTCA 300
 CCTTGTGAGG TTTGATAGCG ATACCGTCAC CCATGCATTT T 341

(2) INFORMATION FOR SEQ ID NO: 4236:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4236:

GTTGATGCAG CCCGTTGAGC TCTAAACCAA CTGAGCTAAA GGTCTTAAAT ATAATTTTAC 60
 AACTAATAAA TAGTGGCGGT GGAGGGGATC GAACCCCGA CCTCACGGT ATGAACCGTA 120
 CGCTCTAGCC AGCTGAGCTA CACCGCCTTA TATAGTTTGT AAATAATATG GTGGAGACTA 180
 GCGGGATCGA ACCGCTGGAC CTCCTGCGTG CAAAGCAGGC GCTCTCCAG CTGAGCTAAG 240
 CCCCCATAAT AATTACAGTA TATCGGGAAG ACAGGATTCG AACCTGCGAC CCCTTGGTCC 300
 CAAACCAAGT GCTCTACCAA GCTGAGCTAC TTCCCGTATA ATTAACGnGC CCGTAGGAGT 360
 TGAACCCATG AACCTnTTGA TCCnTAGTnC AAACGGTCTA 400

(2) INFORMATION FOR SEQ ID NO: 4237:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 376 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4237:

5 nAnTTCTTGA CCTGACATCA CCTGAAATTG AATGGACATG GTCCACCAGG TCATATACTC 60
 TAATCCATGG GTCGCCGATA CCTTCAACGn ACAACATCTA CACCACTATT TCTAATACAG 120
 AATCTTTCTC CTGCACTACC GTTAATAAAT GCCTTACCAC TTGTCGCACC ATAGAATGAG 180
 10 ACGTTACCAG CAATAATTTT ATTTTGTCTG TCTTCAAAAG GTGCTTTGAC AATGACCGTA 240
 CCACCAGATA ATCCTTTTACC AACATAGTCA TTCGCATCTC CAGTATGATG AATCATTAAAG 300
 CCTTTCGGTG CATATGCTGC AAGACTTTGA CCAGCATGAC CATTCGTATA AACATTAAAT 360
 15 GTATTTTCAG GAAGTC 376

(2) INFORMATION FOR SEQ ID NO: 4238:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4238:

25 CGATTTAAAG CTAAGCCCAT TTTGCTCTT TCTCCATAGC CTAACCAAGC AATACGTGAT 60
 GGTAGTCCTT GATATGAAAT TTTTCTTCA GCTAAATCAA GCCATCTTAA TAACTTTTCA 120
 30 TTTTCTGGGA AAAGTTTGGC CATTTCTTCA TCCGCACGCT CGATATCTTT TGGATCACCA 180
 CTCAACGCAG CAAAGCGGAA TGGCCCTTTA CCTTCACAGA ATAATGGTCT AATGTAAGCT 240
 35 GGTACAAAAG CTGGGAAGTC AnAAAGCATT TTCACTCCG TATTGAAGGC TACTTGACGA 300
 TATGnTACCA TAATCAATGC TACAGCGCCA CGTTG 335

(2) INFORMATION FOR SEQ ID NO: 4239:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4239:

45 CCACAnTTAC AAGCAACTAC TGAAGGCGCT GTATTTATTA AAGGTGGCGA CGGTTTTGAT 60
 50 TTCGGACACG TAGAAAGATT TATTCAAAAC CCGCCACATG GGGCAACGGT TGCATGGCAT 120

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TTACCTAATG GTCAAGGTAC GCGTAATGTT GAAGTTCCAG TCAAAGTTTA TCCAGTTGCT 240
 AATGCAAAGG CGCCATCACG TGATGTGAAA GGTCAAAATT TGCTGTTGGA CGGATGCGAT 300
 5 GAACTACATT ACATTTGTCC AnTACAACAC AGATnGTATC ACTGCAGC 348

(2) INFORMATION FOR SEQ ID NO: 4240:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 395 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4240:

TTGATGTTAA AGATTTAGCA AGGGGCGAGA GAACTGGAGA AGAGGTTGCC AAACGAATGG 60
 AACGTGCTTC TGTATTGGCC CAAGTAGATA TTCATCGTGC AGCAACACAT AATAAAGGTG 120
 TTATGAATGG CATACTGCT GTTGTTTTAG CAACAGGAAA TGATACGCGT GGTGCAGAAG 180
 CAAGTGCACA TGCATTACGC GAGTTCGTGA CGGACAGTAT CGTGGTATTG CTACATGGCG 240
 25 TTACGATCAA GATCGTTCAA CGATTTGATT GGTACATTGG AAGTGCCTAT GACATTGGCA 300
 ATCGTTGGCG GTGGGTACAA AAGTATTACC AATTGCTAAG CCTTCATTAG GAGnTACTAA 360
 ATGGTAGAGT CCGCCCCAAG AATTAnGnCC CTGTA 395

(2) INFORMATION FOR SEQ ID NO: 4241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4241:

ACTAATGATT TATTATGTAG TGGTTCTTTG TCATTAGCCA CAGCTATTGT GTACTTAAAA 60
 ATAGGAATGC ATGAGTGCAA CTCTAnAnGn AGCATACTAA TTTCTAAAGA AAAAGTATTT 120
 CTTTATGTTG GGGCCCCGCC AACTTGCATT GTTTGTAGAA TTTCTTTTCG AAATTCTTTA 180
 45 TGTTGGGGCC CCGCCAACTT GCATTGTTTG TAGAATTCTT TTTGAAATT CTTTATGTTG 240
 GGGCCCCGCC AACTAATTCC AATATATCAT TGTAGAGCTT AGGTCATTGA TTTTGGCTC 300
 50 GGACTTTTAT GGCGATATGA ACCATGTAAA T 331

(2) INFORMATION FOR SEQ ID NO: 4242:

(A) LENGTH: 389 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4242:

10	TGCATTGCAT TATTGTACTG CGTAATTGTA CCTGGCTTTT TACCTTCAGT GCTTACTGGA	60
	TCATCTAAAT GATTTTTAGC TGTGATTAAAC TCACGTTTAT CCGCTTTTGT GAAAATGGAC	120
	TCTTGACTT CTTCAGTACT ACCATCATTG TAAGTTACTG TCACAGGAAT CGTCGTTGTG	180
15	CTACCACCAG CTAAATTAGT AGGCATTGCT GTGCCATTTT TAATCGTTGC AGTACGTTTA	240
	TTAGCAACTT GAACTGCATT GTTAATTTCA GCTGCTGTTA CATTTGAACC ATAATCTTTC	300
	ACAAATTnCAG TTGTGTTGAC AGATGAGnGG CGGTGCAGTA AGGACTGGAT ACACTACGAG	360
20	TGACCGGACT GCTTCGGGnA ATGTGATGA	389

(2) INFORMATION FOR SEQ ID NO: 4243:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4243:

35	ATACGCATGT TAACGATCGA ATGCTTAATG TCCCGGAAA TAAATCTATC ATAAGTTACT	60
	TTAATGAAGT TGTCTCACGA CAAGGTAATC ATGTTGCGCT ATCATGAATG ATTTGACAAT	120
	GACGTATGAA CATTACGCAA CTATGTGGAT GCCATTGCGC ACATGCTCCT ATCAAATGGT	180
40	GTGGGCAATG GTCAACGGGT TGCCTTGTTT ACAGAACGTh TTTTGAAAT GATTGCGGCG	240
	ATGTTGGCGA CAGTTAAAGT AGGTGCATCT TATATACCTA TCGATATTGA TTTTCCGAAT	300
	AAACGACAAG GTGCAATTTT GG	322

(2) INFORMATION FOR SEQ ID NO: 4244:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4244:

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CAGTTCTCCG GGTGTGCCTT CTGTATATGC TATGTATTCA CATATCGATA ACATGACATA 120
 ACTCATGCTG GGTTCCTCCA TTCGGAAATC TCTGGATCAA AGCTTACTTA CAGCTCCCCA 180
 5 AAGCATATCG TCGTTAGTAA CGTCCTTCAT TGGCTTCTAG TGCCAAGGCA TCCACCGTGC 240
 GCCCTTAATA ACTTAATCTA TGTTCACC ACCATTTATAA GTCAAACGTT AACATGAAGT 300
 10 TACGTTCTTT TATAAAAAGA TTAAACGCG TTATTAATC 339

(2) INFORMATION FOR SEQ ID NO: 4245:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4245:

CCATTAAACGG GCTCTGACTA CTTGTAAGCA CACGGTTTCA GGTTCATTTT CACTCCCCCTT 60
 CCGGGGTGCT TTTCACCTTT CCCTCACGGT ACTGGTTCAC TATCGGTCAC TAGAGAGTAT 120
 25 TTAGCCTTAC GAGATGGTCC TCCCAGATTC CGACGGAATT TCACGTGCTC CGTCGTACTC 180
 AGGATCCACT CAAGACAGAC AACATTTTCG ACTACAGGGA TTATTACCTT CTTTGGATTC 240
 30 ATCTTTCCAG ATGATTCGTC TAATGTCGTC CTTTGTAACCT CCGTATAGAG TGTCTACAA 300
 CCCCACAAG CAAGCTTGTG GGTnTTGGGC nACTTCCCGG TTTCGGTTCG GCCGChAA 358

(2) INFORMATION FOR SEQ ID NO: 4246:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4246:

45 AAAGAGACCT TGCGGTTAGA TGCGGCTCAT CGCATCCATT TTTGCCTGG CAACGTTCTA 60
 CTCTAGCGGA ACGTAAGTnG AnCTACCATC GACGCTAAGG AGCTTAACTT CTGTGTTCCG 120
 CATGGGAACA GGTGTGACCT CCTTGCTATA GTCACCAGAC ATATGAATGT AATTTATACA 180
 50 TTCAAACTA GATAGTAAGT AAAAGTGATT TTGCTTCGCA AAACATTTAT TTTGATTAAAG 240
 TCTTCGATCG ATTAGTATTC GTCAGCTCCA CATGTCACCA TGCTTCCACC TCGGAACCTA 300
 TTAACCTCAT GCATCTTTGA GGGGnGCTTG ATAACCGA 338
 55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4247:

CCCCGGGTAG CTTTTATCCG TTGAGCGATG GCCCTTCCAT GCGGAACCAC CGGATCACTA 60
 AGTCCGTCTT TCGACCCTGC TCGACTTGTA GGTCTCGCAG TCAAGCTCCC TTATGCCTTT 120
 ACACTCTATG AATGATTTCC AACCATTCTG AGGGAAC TTT GAGCGCCTCC GTTACCTTTT 180
 AGGAGGCGAC CGCCCAGTCA AACTGCCCCG C TGACACTGT CTCCCACCAC GATAAnGGCG 240
 GGGGTTAGAA AGCCAACACA GCTAGGGTAG TATCCCACCA GCGCTCCACG TAACTAnCGC 300
 TCACGTTTCA AAGnTCTACC TATCCTGTAC A 331

(2) INFORMATION FOR SEQ ID NO: 4248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4248:

ATAATCATAC AGATGGCAAT ACAACAGCAA CTGAGACAGT GTCAAACGCT AATAATAATG 60
 ATGTAGTGTC GAATAATACC GCATTAAATG TACCAACTAA AACAAATGAA AATGGTTCAG 120
 GAGGACATCT AACTTTAAAG GAAATTCAAG AAGATGTTTG TCATTCTTCA AATAAACCAG 180
 AGCTAGTTGC AATTGCTGAA CCAGCATGCT AATAGACCGA AAAAGAGAAG TAGACGTGCG 240
 GCACCGGCAG ATnCCTAAAT GCAACTTCCA GCCAGATCCA GCGGCTGCAG CGGTAnGGAA 300
 ACGGTGGTGC CACCAGTTTG CCAATTTACA GCGCCCATAT TACGCCAACA ACTGGTnCCC 360
 TAATGCCCAA T 371

(2) INFORMATION FOR SEQ ID NO: 4249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATTGCATGG CATAACATCG GCGATTAAAA GATGGACGTT TTGATGATGT ACAACAAGAC 60
 ATTGAAGCAG TGGTGAAAGC TGCGAAGGTC ACACAGTAAA AGTGATTATT GAGACGGTAT 120
 5 TGTGACCA TGACGAAATT GTAAAAGCGA GTGAATTAAC AAAAGCGGCT GGTGCGGACT 180
 TCGTTAAAAC TTCAACAGGT TTTGCAGGTG GCGGTGCGAC TGCAGAAGAC GTTAATTAAT 240
 10 GAAAGATACA GTAGGTGCTG ATATAGAAGT AAAAGCTCAG GTGGCGTACG TATTnTAGAA 300
 GTTTCAATGA AnGGTTGAAG CAGGTGCGAC ACGTAnTGGT GCGAGCGCAG CGTTCAA 357

(2) INFORMATION FOR SEQ ID NO: 4250:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 352 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4250:

25 GAGCCCAAAC CAACAAGCTT GCTTGTGGG nGTTGTAGGA CACTCTATAC GGAGTTACAA 60
 AGGACGACAT TAGACGAATC ATCTGGAAAG ATGAATCAAA GAAGGTAATA ATCCTGTAGT 120
 CGAAAATGTT GTCTCTCTTG AGTGATCCT GAGTACGACG GAACACGTGA AATCCGTCG 180
 30 GAATCTGGGA GGACCATCTC CTAAGGCTGA ATACTCTCTA GTGACCGATA GTGAAGnAGT 240
 ACCGTGAGGG AAAGGTGAAA AGCACCCCGG GAAGGGGAAG TGAAATAGAA GCTGGAAACC 300
 GGTGTGCTTA CAAGGTAGTC AnAGCCCGTT AATGGGTGAT GGCGTGCCTT TT 352

(2) INFORMATION FOR SEQ ID NO: 4251:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4251:

45 CATTACTGC TTAACCTTGC ATCAnATCGT AACTCGCCGG TTCATTCTAC AAAAGGCACG 60
 CCATCACCCA TTAACGGGCT CTGACTACTT GTAAGCACAC GGTTTCAGGT TCTATTTTAC 120
 50 TCCCCTCCG GGGTGCTTTT CACCTTTCCC TCACGGTACT GGTTCACTAT CGGTCACTAG 180
 AGAGTATTTA GCCTTAGGAG ATGGTCCTCC CAGATTCCGA CGGAATTTCA CGTGCTCCGT 240
 55 CGTACTCAGG ATCCACTCAA GAGAGACAAC ATnTTCGACT ACAGGATTAT TACCTTCTTT 300

(2) INFORMATION FOR SEQ ID NO: 4252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4252:

TATTTGATAT TTTGTGCATT GCAGTCAAAC CATGGCGGAA ATTGAACCAA TACCATTGCT	60
AATTTTTTCT GTGTATGTAA GGGCTCTAAC ATATTCTTAA ATTGATCAAA TAGTTCTnGC	120
CTTGATCTG CAAATGTTTT GTAGTCTGCA TGCAATGTGA GTGCTTGATG AATTTTGACC	180
ACAAATTCAA ATGTATCAGG CGTTTCTTTT ATCCATTTCa ATATATTCTT TTCCGGTTGT	240
ATCGCATAGT ATGTCGCATC TAATTCGCAA CCGGAAAATG TCCAGCATAT GTTTTAAGGT	300
TATCGGTTTG GCGTTCTAAA TCTGCATATA ATGAATAGTG ATCACCCCAA CCTGTTTAAAT	360
CCGATGGTTA TCCAnATGAT GATCACCATG TCATCAnACC	400

(2) INFORMATION FOR SEQ ID NO: 4253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4253:

AAAGGTATCA AAGATGTTAA AGTTACTTTA TTAAATGAAA AAGGCGAAGT AATTGGnACA	60
ACTAAAACAG ATGAAAATGG TAAATACTGC TTTGATAATT TAGATAGCGG TAAATACAAA	120
GTTATTTTTG AnAAGCCTGC TGGCTTAAAC ACAAACAGTT ACAAATACAA CTGAAGATGA	180
TAAAGATGCA GATGGTGGCG AGTTGACGTA ACAATTACGG ATCATGATGA TTTCACTT	240
GATAACGGAT ACTTCGAGGG GATGACATCA GACAGCGATT CAGACTCCAG ATAGTGACTC	300
AGnCAGCGAC TCAGACTTCA GACAGCG	327

(2) INFORMATION FOR SEQ ID NO: 4254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4254:

5 AGATGACATT AAATAGCATC TCCTCGTGT GATTATTTTG GTTGGCTGAC CAATATTTAT 60
 TCTAGCACGT AGAGATGCAT TTTTGTGAC AATGGTAGAA CCTTTTCTGA ACCATACGCA 120
 TAGGATTGTn CnTTTTTACA ATTAAAGAGC CAACCGTTGT TATAGTCTAA CAATGGTTGC 180
 10 CCTCTTATTT TATGTGGCTA AAAATTTATA GGCAATTTTA TTACAACAAT GTACATTTAA 240
 GGTGACCTTC ATGCCAAAAT CGCATCACTC ATTTAATGGA AGCAGCACGT CTTCATATAA 300
 AGTACCGATC CCTAATTCCA ACGCATGTn 330

15 (2) INFORMATION FOR SEQ ID NO: 4255:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4255:

ATTAGTGATT GTAAAAAGT AAAACTATTC TTGGGAGTCG GACATAAATC AATGTCTAGA 60
 CTCTATAGTG TTGTATTTGG CAGTAGTTGA CGGGGCCCCA ACATAAAGAA ATACTTTTTC 120
 30 TTTAGAAATT AGTATTTCTT ATACATGAGT TTTACTCAGG ATATCCTATT TTAAATACA 180
 CATTAGCTGT GTTTAATGAT AAAGAACCAC TACATCATAA ATCTTTAATG GTTCTTTATC 240
 AATTCCTTCC CCCCTCTCAT GTTTTGTATC TTAAATCAA TATAATTC AAAGGGTCG 300
 35 AAGATATGAn ATCACATCTT CGACCCTTnn TTGTACTAAT TTAA 344

(2) INFORMATION FOR SEQ ID NO: 4256:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4256:

CCAGTAATAT CTAAATGAGT TGGATATTTA ACTTTTCGCAT TAATTTCAAT ATTAAATTGC 60
 50 GTTACCGCGA CAAGnCATnA CACAACATAC ATAATAAGAT TGGCTAAAAA GATATAGTTA 120
 AAGCTAAATT CTGCGACAAA GCCGCCATT GCAGCACCGA CAGCCACACC AATATTTTGC 180
 55 GCTAAGTATA TCGCATTAAA CGTTTGTCTT CCGCCATTG GCCACACTGC TCCAGCCATA 240

TACCAAGGCC ACCCGTGGAn AGA

323

(2) INFORMATION FOR SEQ ID NO: 4257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4257:

15 GCTGACTTTC CACCAGCCTC TGTGTTGGGG CCCC GACTAT TTTTGAAAAG AGCGTGTTAC 60
 ACGGTCATTG TTTTACAGTC AACTACTGCT AAAATAAAAT TAACGAGCTT AGGGCTTTGT 120
 TTTCTGTCCC AAGCTCGTTA AATCACATAT GATAATTAAT TATGCCCAAC CACGATATCT 180
 20 AGCTGCTTCT GCTGTACGTT TAATACCTAT GGATATATGC TGCAnTCTGC ATATCTATTT 240
 TTCGGTTTTG AGACAAATCG TAAATCGTAT CAAATGCCGC TTCTAATTTT TnCACGTGGC 300
 25 TTTTGCATTG AACTTCTTCT nGCAGGACCA ATAATAACCT TGGATTATTT TGTGACCCAT 360
 GCGGAGTGA 369

(2) INFORMATION FOR SEQ ID NO: 4258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 335 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4258:

40 CCTTTTCAA AATCATTGGA TGCATCGATA AATAGTACGT TGTCGTCTTG TTGGCGACAT 60
 TTTTAAATA CTAAAATACA TGTTGGAATA CTTGTCCCAT AGAAAATATT GGCTGGTAAC 120
 CCAATCACGG CTTCTAAGTA GTTCTTTTCT TCTATTAAAT AGCGACGAAT CACACCTTCT 180
 45 GCGGCACCAC GAATAATACA CCATGnGGAG TACGACGCCA nGTACCTTCA TCGTCTAGTA 240
 ATGTACCAGT GTTGAATAAA GCAAAGTCTG CTTTGATTTT GGCGCAACTT GCCGTAACCA 300
 CTGAATCGTT CATCATTTCA AATTTGAACT GCTGT 335

(2) INFORMATION FOR SEQ ID NO: 4259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4259:

5 ATTTGCTAC CTTACGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTGTA 60
 GCTTCGCAGC nACAACCACT CCTCTTAACC TTCCAGCACC GGCAGGCGT CACCCTATAC 120
 ATCACCTTAC GGTTTAGCAG AGACCTGTGT TTTTGATAAA CAGTCGCTTG GGCCTATTCA 180
 10 CTGCGGnTCT TCTGGGCGTT AACCTAAAG AGCACCCCTT CTCCGAAGT TACGGGGTCA 240
 TTTTGCCGAG TTCCTTAACG AGAGTTCGCT CGCTCACCTT AGAnTTCTCA TCTTGACTAC 300
 CTGTGTCGGT TTGCGGTACG GGCA 324

(2) INFORMATION FOR SEQ ID NO: 4260:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4260:

25 AAGCGGTTGT TAGACAATGC ATTAAGAAAA ATTAAAGCGG AGTTTACTTT TGTAATGAG 60
 CATTTGATTT TTTGAAAATA AAGCAGTATC GGGCGCTTGA CTAAAAAGAA ATTGTACATT 120
 30 GAAAACTAGA TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAGAG 180
 TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ACGAGCAAGA 240
 TTAATAACGC GTTTAAATCT TTTTATAAAA GAAAACGTTT AGCAGACAAT GAGTTAAntT 300
 35 ATTTTAAAGC AGAGTTTACT TATGTnAATG GAGCATTGAA AATnATGAAA ACGAGCCCGT 360
 ATGTGGAGCG TTTGGACTTA TAAAAATGGT GGGAAACATA 400

(2) INFORMATION FOR SEQ ID NO: 4261:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4261:

50 AATTAATGTG CGAGTTGGGG TGGGACGACG ATAAAGAAAT ACTTTTCTA TAGAAATTAG 60
 TATTCTTAT GCATGAGTTT TACTCAGTAA TTCCTATTTT TAAGnACACA TTAGCTGTGG 120

55

CTCCCCTGAG AAGTTTAAAA TTTTATATGT TGGCTTGTTA TGTTAAGGGA ATTAACATGG 240
 TTGTCCTTGTT TATATTATGT GATTCAAACA TTACTAGTCT TGGTAAATCT AATTCGTAAA 300
 5 ATGCTAAATC TAACCATCTA TTAAATTTAA AACC 334

(2) INFORMATION FOR SEQ ID NO: 4262:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4262:

TTTCGGTCAT ATTCAAACGT TTTCACCTCG CCAAGCCATT TTCTTTGTG TTTACTTTTT 60
 20 ATTTTGACGT TTAGGCATA AAAAAAAGAG ACCTTGGCGG TCTCAATGCG GCTCATCGCA 120
 TCCATTTTTT GCCTGGCAAC GTTCTACTCT AGCGGNAGTA ATTGGGCTAC CATCGTCGCT 180
 AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTCTCTTC CTCTCCTTCG GCTCTCGCTT 240
 25 ACTCATThAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTCGTCAGA TTCAAACGTT 300
 TTCACTTCGC CAAGCCATTT TTCTTTGTGT 330

30 (2) INFORMATION FOR SEQ ID NO: 4263:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4263:

40 GAGGTATACC CCGGGACGGC TGAAGGGGAT CGAACCCCTAC GAAATGTCGG AACCACAATC 60
 CGATGTGTTA CCACTTCACC ACAGCCGCCA TGGCAGGGGC AGTAGGAATC GAACCCACAC 120
 CAAAGGTTTT GGAGACCTCT ATTCTACCGT TGAAGTATGC CCCTATTAAA AATAATAAAT 180
 45 GGAGGGGGGC AGATTGGAAC TGCCGAACCC GAAGAGTCGG ATTTACAGTC CGCCGCGTTT 240
 AGCCACTTCG CTACCCCTCC ATAAATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 300
 50 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 339

(2) INFORMATION FOR SEQ ID NO: 4264:

(i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 351 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4264:

	GTATTTCAAA GTAAAATTAC ATGTTAATAC GTGnTTAATG GGCGAGACTC CTGAGGGAGC	60
10	AGTGCCAGTC GAAGCCGAGG CTGAGACGGC ACCCTAGGAA AGCGAGCATT CAATACGAGA	120
	TnTnATGAAA TAGAGAACAG CAGTAAGATA TTTTCTAATT GAAAATTATC TTAGTGCTGT	180
	TTTTTAGGGA TTTATGTCCC AGCCTCTTAC TCTAATTATA TTCACTATCA ATTAGACAAA	240
15	ATGGCCATTT TCAAATATCA CGCGTTGTTT CTGACCTTGA ATATATTTAT TATAATTCTC	300
	TTTTTGAAA ATCAGTTAAC ATTAATTTAG ATGTACCGTA TTTTAAACAC T	351

(2) INFORMATION FOR SEQ ID NO: 4265:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4265:

30	ATTTTCACTT TAAACCTGC TTCTTTGGCT TTTTGCATAT AATGTTGCGA TTGTTCTATT	60
	GTAAATACAC CTGTTTCACA GAAAATATCC GCAAAGTCTG CATATTGTTT TACTTCCGGA	120
	AGTAACGCAA TCATTTCTTC TAAAATGCC TCATTTGAAC TTGCCTCTTT AGGTACAGCA	180
35	TGAGGCCCTA GGAAAGTATG TTTCATGTCT AAATCATATT TCTCAGCTAA ACGnTTAGAC	240
	ACTTTCAATT GCTTCAGTTC ATTTTCTCTA TCTAATCCAT AAACCACTCT TGACTTTCAA	300
40	CTGCAGTCAC GCCGTGTTTn AATCCATAGT AAGACAAAnC ATGACT	346

(2) INFORMATION FOR SEQ ID NO: 4266:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 347 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4266:

	TCAAACGCTC TATCCAATTG AGCTACGGGC GCATATGTTT TTATTGAAAA TGGTGCCGAG	60
55	GACCGGAATC GAACCGGTAC GTGATCACTC ACCGCAGGAT TTAAAGTCCT GTGCGTCTGC	120

CCAACCTTGG CAAGGTTGTA TTCTACCGCT GAACTACTTC TGCATATGCG GGTGAAGGGA 240
 GTCGAACCCC CACGCCGTAA GGnTGAGATC CTAAGTCTAG TCGCTCTGCC AATTCGCCCA 300
 5 CACCCGCCAA TGGTGAGnCA TAGAGGnTTC GAACCTCTGA CCCTCTG 347

(2) INFORMATION FOR SEQ ID NO: 4267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4267:

GACTTGTCT CTTGGACCTA TATCATGTTT TTTATTTTCT AATGCAGGAT CTTTAATTGC 60
 20 ATCTTTAAGT GATTTCATCCG CTGCAGGATA GTTTTTTCGA GTGTTTGCTG GTTGCGTGAG 120
 GTnTGTGTTT GATTGTATC CTTAGGTGGC TGAGTTGTAG TTGCATTATT ATTTTGATTT 180
 TCCGAGATTT TATCTGAAGT ATTTGTATTT TCTGCTGCTT GTGCTTGATG TTGAGAAGTA 240
 25 ATTA AAAATA GTGTACTGAC AATGACCGAT GCAACGCCTA GAGTTGATTT TCTAATAGAA 300
 TAGGAAAGAC CnTnAATTTT GGGTGGATGT TTGTTCA 337

(2) INFORMATION FOR SEQ ID NO: 4268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4268:

ATACATGTTG GAATACTTGT CCCATAGAnA ATATTGGCTG GTAACCCAAT CACGGCTTCT 60
 AAGTAGTTCT TTTCTTCTAT TAAATAGCGA CGAATCACAC CTTCTGCGGC ACCACGGAAT 120
 45 AATACACCAT GTGGGAGTAC GACTGCCATG GTACCTTCAT CGTCTAGGTA ATGTACCATG 180
 TGTTGAATAA AGGGCAAAGT CTGCTTTGGG ATTTTGGCGC AACTTGGCCG TTAACCACTG 240
 GAATCGTTCA TCATTTTTC nATTTTGGAA TCTGGCTGGT TCCATTTTCG GCACTGGTAT 300
 50 GGTGGGGGTT TCGGCAATAA ACGGCATTCA AATGGTATTT GGCCTAAACA AGGCCGGGAT 360
 TTTTCCAATG GGGGTCATCA TTAAnGGGAT CnTCGAAGTT 400

(2) INFORMATION FOR SEQ ID NO: 4269:

(A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4269:

10 GGCTCATCGC ATCCTGGGGC TGTAAGCGGT CCCAAGGGTT GGGCTGTTCG CCCATTAAAG 60
 CGGTACGGAG CTGGGTTTCAG AACGTCGTGA GACAGTTTCG TCCCTATCCG TCGTGGGCGT 120
 AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG 180
 15 TACCAGTTGT CGTGCCAACG GCATAGCTGG GTAGCTATGT GTGGACGnGA TAAGTGCTGA 240
 nAGCATCTAA GCATGAnGCC CCCTCAAGAT GAGATTCCCA ACTTCGGTTA TAAGATCCCT 300
 CAAAGATGAT GAGGATATAG GTCGAGGTTG GAGCATGGTA CATGT 345

20

(2) INFORMATION FOR SEQ ID NO: 4270:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4270:

AAGAATTAAT TATACATTTT ATTAACATTT AAGTCAATAA CTTTTTTTAT CTTGTCCATT 60
 TTATTTTTTA ACCAAAATTT GATTAAAAA CTGCCTGGCA ACGTTCTACT CTAGCGGAAn 120
 35 TAAGTCGact ACCATCGACG CTAAGGAGCT TAACCTCTGT GTTCGGCATG GGAACAGGTG 180
 TGACCTCctT GCTATAGTCA CCAGACATAT GaATGTAATT TATACATTCA AAAGTAGATA 240
 GTAAGTAAAA GTGGATTTTG CTTGCAAAc ATTTATTTTG ATTAAGTCTT CGATCGATTA 300
 40 GTATTCGTCA GTCcCaCATG GTCACCAGCT TCCACCTCGA ACCTATTGGn CGCATCATCT 360
 CGCAGGGAnC 370

45

(2) INFORMATION FOR SEQ ID NO: 4271:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4271:

55

5 ATTAACAAAA GGCATTGATT TAGAAGGGCG GACATTTTTA CACAATTATG ATTGGCGTAA 120
 AGATAAAGAT GGCACATTAT TAAATACCAT CATTTCTGGT CCGGCACCTG TGGCACAATG 180
 10 GaTTAATTTA CAATATTATG CGTCGACAGT TGCGCCGCAT TTTTaCGGtA ATGGGAATAA 240
 AGCGACACAA ACCGTCACGT CAGTGTTGGT GTCATGCAAG GTAATGCGAG TGCATCTGAT 300
 GTAGGGCTTA TCATGGCCAA TCTGTTA 327

(2) INFORMATION FOR SEQ ID NO: 4272:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4272:

CATTCTTTAA ACTCTGTAAG TACTTCTTCA ATCTCAGGGG CATCTACTAA CATATCATCA 60
 GTAATATGCG TCAAATTGAT AATCGTTTCC GATAATCGTT CATGCGGATT ACTAAACCTT 120
 25 TCAAACCTTAT CGATGATTTC ACCGTTATGA ACTTTCACAG CTGCAAnTCG ATGATTTTAT 180
 CATACTGATT TGATAAACCA GTTGTCTCAA CGTCGAACAC AACATAAGTA GCATCTTTTA 240
 ATACGACATC TTGTGGGTTG TATGCAATCG GGAACACCAT CATCAACTAA CATACTTCC 300
 30 ATACCGGnAT ATCATTTTAA nGCCA 325

(2) INFORMATION FOR SEQ ID NO: 4273:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 357 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4273:

TCCGGCCTTG ACCTGAAGAA CACTTGTCTT GTCGTTAAGA TGA CTCTAGTA CTCTTATGTT 60
 45 TATTATCAAC CGTTAATAAA CTTACCATCA AGAGTGCACC TACCCATACT GACAGTGCAG 120
 TATAGAATGG TGTCATACCT GAACCATAAT CCTTAACTGG GAAAACATCA ACAGTCTTCT 180
 50 TATTAATAGG ATTTGCAATA ATACCGCTT GCTTTTCAA ATCATTCTTA AGTGTGTCGA 240
 TnAATTTGTC GACTGCATCA TCTnTGTCTA ATTTCTTGAA AATTTTGATT CGCTTTTTTC 300
 CAAATCCTTn TCCAACATCA GGCAATTTTA TTTTGAGAAA AATCAGCCAA ATCCGGA 357

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4274:

10 ACGTTAGCAC AAGCCATGAA CCAATTAGGT GGAAAGAGTA ATAGTGGTGA AGGTGGCGAA 60
 GATGCAAAAC GTTATGAAGT ACAAGTTGAT GGAAGCAACA AAGTAAGTGC GATTAAACAA 120
 15 GTTGCTTCTG GGCCTTTTGG TGTAAGTAGT GATTATTTAC AACATGCCAA AGAAATTCAA 180
 ATTAAAGTTG CGCAAGGTGC AAAGCCTGGT GAAGGTGGTC AATTACCTGG TACTAAGGTA 240
 TATCCGTGGA TTGCGAnGAC AAGAGGGTCA ACGCCAGGTA TCGGTCTGAT TTCACCACCG 300
 20 CCACATCATG ATATTTnATT CCATAnGAGG ATTTAGCCGC CACCTGATAC CTGGATTTTG 360
 GAAAAATGGC GAATTAAGGT TGnGATTTT CCCC GGGTAA 400

(2) INFORMATION FOR SEQ ID NO: 4275:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4275:

35 AACGTCGTTA ATTGAATAAC GCTTATGTTA TAAGAGCACT CATACCAAAC CATAATCATC 60
 TATAGATATA ACAATTCACG ATATAAGGGC TGTGTTTGGC ATAGCCTTTA GATATACACT 120
 TAATTCCTAT TAAAATAGTA GGGATTAAAA GGGGGCTTGT CATGGATTAA AATTCAACAA 180
 40 TTACAACATC ACTTTGGATC ACATAAAGTA ATTCATAACT TTAATTTGGA CATTAGCAAG 240
 GGAGAAATAG TCACTTTCAT AGGGGAAAAG TGGTTGCGGA AAGTCTACTT TACTCAATAT 300
 TATCGGTGGA TTTnTTCCAT CCATCGnCTG GTCGTGTCCA n 341

(2) INFORMATION FOR SEQ ID NO: 4276:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 368 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TAGTGATATA CGACATCACA GCATAATATT GCTTTAGAAA GTCGTGCCGA ACTGGAAC TT 60
 ACAAGTCTAG TTCGAACACA CACTGATGTG AGTGGTTTTT TTTATTTTAA ACATGAACAA 120
 5 TCAGATAAGT TACTAGCATT AGCAAATATT ATTAAATCAA AGGGCTTCGA TTCATAAAAT 180
 TTAACAAT GATTAAAT AGACGTGTAA ATTGTTAAAT TCTAAACGG AAATAACCAC 240
 CATTCCATTA AACCAC TTTT TTGTTTCATCA CTATATTTCA CACnGCTTCA TTAATAAACG 300
 10 GAATGCTTCA nCCGCTTCAA CTTCAACTGG CTTCAACTTC nGCCTACTTC ATCATACCAA 360
 ACGGTCCG 368

15 (2) INFORMATION FOR SEQ ID NO: 4277:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4277:

ATGGAAGTAC GTGACGTTCA CTACTCTCAC TATGGCCGTA TGTGTCCAAT TGAAACACCT 60
 GAGGGACCAA ACATTGGATT GATTAAC TCA TTATCAAGTT ATGCACGTGT AAATGAATTC 120
 GGCTTTATTG AACACCATA TCGTAAAGTT GATTTAGATA CACATGCTAT CACTGATCAA 180
 30 ATTGACTATT TAACAGCTGA CGAAGAAGAT AGCTATGTTG TAGCACAAGC AAACCTCTAAA 240
 TTAGATGAnA ATGGTCGTTT CATGGGATGA TGAAGTTGTA TGTCGTTTCC GTGGTAACAA 300
 35 TACAGTnATG GCTAAAGn 318

(2) INFORMATION FOR SEQ ID NO: 4278:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4278:

CACTTGTA CT TTCTGATGTT GAGCCAGACT CTGATGTA CT TACCGATGTA GATAAACTTG 60
 CAATGGTCGA CATGCGGTTT GAAGTTGATG TACTTAGCGA ATCACTTAAT GATGCTGATG 120
 50 TGCTTTGTGA ATCGGATTCG CTCGTGCTTG TACTTGTTGA GTTTGAGGCA CTTTGGCTTG 180
 CTGAGTTTGA GTCTACTCCG CTTTGATTCA TTGAGGCACT TAGTGACAAT GATGTACTCG 240

55

TACTTATGCT CATTGGATGT TGAATCGGAT TTACTTTTCAC TTGAATGATG TTGAGTCGGA 360
 TTCACTTTCA CTTGTAGAAC CACTTAATGA TGTGGGATGT 400

5 (2) INFORMATION FOR SEQ ID NO: 4279:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4279:

TTTGTACTTC GATTTAAAAG ATATTAGACA TAAATCTAA AAnCAGCAGT AAGATGATTT 60
 ATGATTAAAA ACTATCTTAC TGCTGTTTAC TTTTATAAT ACTTCTGAAT GTCTTCACTT 120
 20 ATACTTCTAG TCACAGATTT AAATAATCAA AAGTGCACAT TATTAAAATA TCAATTTTAC 180
 ACTCAATGCG GCTCATCGCA TTCATTTCTT GTCTAGCAAC GTTCTACTCT AGCGGAAGTA 240
 AGTTAGCTAC CATCCTCGCT AAGAACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC 300
 25 CTCTCCTTCG GCTCTCGCTT ACTC 324

(2) INFORMATION FOR SEQ ID NO: 4280:

- (i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4280:

CTCACTAGTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60
 40 GTGGATTGTC CTTTGGCATG TGnTTAGGAG AGCGTTCTAA GGGCGTTGAA GCATGATCGT 120
 AAGGACATGT GGAGCGCTTA GAAGTGAGAA TGCCGGTGTG AGTAGCGAAA GACGGGTGAG 180
 AATCCCGTCC ACCGATTGAC TAAGGTTTCC TGnGGAAGGC TCGTCCGCTC TGGGTTAGTC 240
 45 GnGTCCTAAG CTGAGGCCGA CAGTAGGGCG ATGGGATAAC AGGTTGATAT TCCTGTACCA 300
 CCTATAATCG TTTAATCGAT GGGGGG 326

50 (2) INFORMATION FOR SEQ ID NO: 4281:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 370 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4281:

5 TCGAACATGA GCGATTATTT CTTATGAATT CAAGCTTATT TAAAACTCTT TATTCACCTCG 60
 GTTTTGCTTG GTAAAATCTA TATTTTACTT ACTTATCTAG TTTTCAATGT ACAAATAATG 120
 GTGGGCCTAA GTGGACTCGA ACCACCGACC TCACGCTTAT CAGGCGTGCG CTCTAACCAG 180
 10 CTGAGCTATA GGCCCATTTT TTTGAATGTT AAATAAACAT TCAAACTGG AATACAATAT 240
 GTCACGTTAT TCCGCATCTT CTGAAGAAGA TGTTCGGAAT ATATCCTTAG AAAGGnAGGT 300
 15 GATCCAGCCG CACCTTCCGA TACGGGCTGA CCTTGTTGAC GACTTGCACC CCAAGCATT 360
 GTGCCCCAnCn 370

(2) INFORMATION FOR SEQ ID NO: 4282:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4282:

GAGAGATGAC ACGGnACTGA ATTGGTTTGA CACCACGTGA TGAATGTGAT CGTCGGCCTT 60
 30 CTTACAGATT GnaATACTTT TACATCAAGA ACGATACCGC CAGCGCCGTG AGGTACACGT 120
 AATGAAGTAT CTCTAACTTC ACGTGCTTTT TCACCAAAGA TTGCATGTAA CAATCTTTCT 180
 35 TCGGCAGTTA ACTCAGTTAC ACCTTTAGGC GTTACTTTAC CAACTAAAAT ATCTCCATCT 240
 TTTACTTCTG CACCAATATA AACGATACCA CGATCGTCTA AGTTCTTAAG TGCACTTTCA 300
 GAAACATTAG GnatATCTCT TGTGATTTCC TCAGGGCCTA ACTTAGTATC ACGTGCCTCT 360
 40 GAATCCATAC TCCTTCAATA TGAATAGAAG TATACACGGn 400

(2) INFORMATION FOR SEQ ID NO: 4283:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4283:

AATTCTACAG GCAATGCGAG TTGGGGTGTG GGCCCCAACA AAGAGAAATT GGATTCCCAA 60

55

TCTGTCCAC TCCCGATTAT CTCGTGCAA TATTTTTTTC AAAGCGATT AAATCATTAT 180
 CATGTCCAAT CATGATTAAA ATATCACCTA TTTCTAAATT AATATTTGGA TTTGGTGAAA 240
 5 TGATGGACTC TTTGCCTCGT TTAATTGCCA TAATGTTAAT nCCATATTGT GCTCTTATAT 300
 CTnAATCCAT GATAGACTGn CCCG 324

(2) INFORMATION FOR SEQ ID NO: 4284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4284:

20 AAATCGTAAC GAGTGAAC TTCTTATTTAG GTGGCGAAGT AACTTACTAG CACCTGACGA 60
 AACGGTTTTA GATCGTATTC AATTGAAAAG GCCGGTATTG AATGAATCAC ACTTAGCAGC 120
 GATTGATCAG GAACATTTTA AATTAACCTA TTTATCAACG GTATATGAAG GGGATTGGC 180
 25 AAGATGCGTT ATAAGCATTG GGCCGTAGAA GCAGTGAAAT GCTGTnAAAC AAGGGCGCTC 240
 AAATTCTAGT GTTAGATGAT AGTGGATTAG TTGGATAGCA ATGGCTTTGC AATGCCGATG 300
 TTTACTCGCA ATGAAGTGCA TGTGCCATGC AATTGACTTC TTTAAAGCCA GATTACGTG 360
 30 ATGTCTAACA AGTTTTnTnC GCTAAAATCn GGGTGGAGAC 400

(2) INFORMATION FOR SEQ ID NO: 4285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 560 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4285:

45 CATTTCCTT TGTGTTTACT TTTTATTTTG ACGTTT TAGA CATAAAAAA GAGACTCAGC 60
 GTCTCAACTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTGGCTA CCATCGTCGC 120
 TAAAGACCTT TCTTGACTTG TGACAATCGC TTGCATCTTT CCTCAnCATC GGnTnTAGCT 180
 50 TACTCATTTA GCTCTACTAA ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT 240
 TTTCACTTCG CCAAGCCATT TTTCTTTGTG TTTACTTTTT ATTTTGACGT TTTAGGCATA 300
 AAAAAAGAG ACCTTGnCGG TCTCAATGCG GGCTCATCGC ATCCATTTTT TGCCTGGCAA 360

TGACAATCGC TTGCTTCTTT CCTCTCCTTC GGCTCTCGCT TACTCATTTA GCTCTACTAA 480
 ACTCGTTGCG CTCTTTTCTC GTTTCGTCAG ATTCAAACGT TTTCACTTCG CCAAGCCATT 540
 5 TTTCTTTGTG TTTACTTTTT 560

(2) INFORMATION FOR SEQ ID NO: 4286:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4286:

GTAACACTCG GnATAACCTA CCTATAAGAC TGGGATAACT TCGGGAAACC GTAGCTAATA 60
 20 CCGGATAATA TTTTGAACCG CATGGTTAAA AGTGAAAGA CGGTCTTGCT GTCACCTATA 120
 GATGGATCCG CGCTGCATTA GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA 180
 TAGCCGACCT GAGAnGGTGA TCGGCCACAC TGGAAGTGA ACACGGTCCA GACTCCTACG 240
 25 GGAGGCAGCA GTAGGGAATC TTCCGCAATG GGCGAACTG GACGGAGCAA CGCCGCGTGA 300
 TgnATGGAAG GTCTTCGGAT CGTAAACTC TGTTATT 337

(2) INFORMATION FOR SEQ ID NO: 4287:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4287:

CAATCGTGCT CAnTGCGCAT CGTnACTCAT CTGTATGTGT TCCAGCATAT ACAATTTTGC 60
 CATCTTTAAT GACAACTGTA CCATTTTTCa CAACATTTAA TTCATCTAAT TCCTTACCCT 120
 TCAAAGGTTT ATCTGTTGAT CTCGGTAAAA TTAATTCCTGG CTATATGATT AATTATTAAA 180
 45 TCATCATTAC TTATCACCTG CTTTATCAAT CATGGAATAT GAATACCTTT TTCTTTAGCT 240
 GTTTGAATAG CGATGTCATA GCCAGCATCA ACATGTCGGG CAACACCCAT ACCTGGGTCA 300
 50 GTCGTCAATA CAGTTCCAA TCTTCTTTCA GCACGCTCTG AATCCATCTG G 351

(2) INFORMATION FOR SEQ ID NO: 4288:

(i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 316 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4288:

	CTATTCAC	CGGCTCTTCT	GGGCGTTAAC	CCTAAAGAGC	ACCCCTTCTC	CCGAAGTTAC	60
10	GGGGTCATTT	TGCCGAGTTC	CTTAACGAGA	GTTGCTCGC	TCACCTTAGA	ATTCTCATCT	120
	TGACTACCTG	TGTCGGTTTG	CGGTACGGGC	ACCTATTTTC	TATCTAGAGG	CTTTTCTCGG	180
	CAGTGTGAAA	TCAACGACTC	GAAGACACAA	TGTCTTCTCC	CCATCACAGC	TCAGCCTTAA	240
15	CGAGTACCGG	ATTTGCCTAA	TACTCAGCCT	TACTGCTTAG	GACGTGCAAT	CCAATCGCAC	300
	GGTTTnGCCT	ATCCTA					316

(2) INFORMATION FOR SEQ ID NO: 4289:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4289:

30	TnTTTATGT	CTAAAACGTC	AAAATAAAAG	CAAACACAAA	GAAAGATGGC	TTGGCGAAGT	60
	GAAAACGnTT	GAATCTGACG	AAACGAGAAA	TGTAAAGTAT	AATAAAAAGC	AGTCATAAGA	120
	TGATTTCAAT	TAGAAATCAA	TTTATGACTG	TTTTTCTTAC	TATGTGTTAA	ATTAACAATG	180
35	AATATAACAT	CTTATTTTCA	TTAATATAAA	TATTGGAAGG	ATCGAnATGA	TTTACACGTT	240
	GTTTGAGTTG	TATTAAATCA	TCATGATCTT	TAAGTTGAAT	ACCAATAATG	ACAGTACCTG	300
40	TATTTTGAGA	GATTTTTTTAA	GT				322

(2) INFORMATION FOR SEQ ID NO: 4290:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 338 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4290:

	TCATTTAGCT	CTACTAAACT	CGTTGCGCTC	TTTTCTCGTT	TCGTCAGATT	CAAACGTTTT	60
	CACTTCGCCA	AGCCATTTTT	CTTTGTGTTT	ACTTTTTATT	TTGACGTTTT	AGGCATAAAA	120

55

CTCTAGCGGA AnTAATTGGC TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC 240
 GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCnACT AAACTCGTTG 300
 5 CGCTCTTnTC TCGTTTCGTC AGATTTCAAA CGTTTTCa 338

(2) INFORMATION FOR SEQ ID NO: 4291:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4291:

AATTGGTTTA CACCAGGTGA TAATGTATCG TCGCCTTCTT CACGATTGAA TACTTTTACA 60
 20 TCAAGAACGA TACCGCCAGC GCCGTGAGGT ACACGTAATG AAGTATCTCT AACTTCACGT 120
 GCTTTTTTCA CAAAGATTGC ATGTAACAAT CTTTCTTCGG CAGTTAACTC AGTTACACCT 180
 TTAAGGCGTT ACTTTACCAA CTAAAATATC TCCATCTTTT ACTTCTGCAC CAATATAAAC 240
 25 GATACCACGA TCGTCTAAAG TTCTTGAAGT GCACTTTnCA GAAACATTGA GGAATGATC 300
 TCTTGTGATT TCTTCCAGGT CCTAACTTGA GTGATCACGT GGCTTCTGGA TTGCAGACGC 360
 TTGCAAGATG GAATGAGAAG TGAAnACACGT GCATCCTTGC 400

30

(2) INFORMATION FOR SEQ ID NO: 4292:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4292:

AAACGTTTTC ACTTCGCCAA GCCATTTTTT TTTGTGTTTA CTTTTTATTT TGACGTTTTA 60
 GGCATAAAAA AAAGAGACCT TGCGGTCTCA AATGCGGCTC ATCGCATCCA TTTTTTGCCT 120
 45 GGCAACGTTT TACTCTAGCG GAACGTAATT GGGCTACCAT CGTCGCTAAA GACCTTTCTT 180
 GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC 240
 TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTC ACTTCGCCAA 300
 50 GCCATTTTTT TTTGTGTnna CTTTnT 326

(2) INFORMATION FOR SEQ ID NO: 4293:

55

(A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4293:

10 GGGGACAATT CCCTGGGGGT TCAAGTCCTC TCGGGCCGGC ATCAAAATTC TTAATTTAAA 60
 TAAGCGGGTG TAGTTTAATG GCAAAACCTC AGCCTTCCAA GCTGATGTTG TGGGTTCGAT 120
 TCCCATCACC CGCTCCATAG ATAATTTTAA TGAACATTGA AAAGTGAATG ACAATATGTC 180
 15 AACGTTAATT CCAAAAACGT AACTATAAGT TACAAACATT ATTTAGTATT TATGAGCnAA 240
 TCAACATCA TAATTTTAT GGAGAGTTTG ATCCTGGCTC AGGATGAACG CTGGCGGCGT 300
 GCCTAATACA TGCCAGTCGA GCGAACGGAC GAGAAGCCTG CCTCnGnGAT GTTAGC 356

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(2) INFORMATION FOR SEQ ID NO: 4294:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4294:

30 TTATCACCCA TGTCTGACT CCCAAGTTAA ATTAATTGGC ATTCGGAGTT TGTCTGAATT 60
 CGGTAACCCG AGAGGnCCCC TCGTCCAAAC AGTGCTCTAC CTCCAATAAT CATCACTTGA 120
 35 GGCAGCCCTA AAGCTATTTC GGAGAGAACC AGCTATTTCC AGGTTTCGATT GGAATTTCTC 180
 CGCTACCCTC AGTTCATCCG CTCACITTTT AACGTAATCG GTTCGGTCCT CCATTCAAGT 240
 TTACCTGAAC TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT 300
 40 AAACGCCCTA TTCA 314

(2) INFORMATION FOR SEQ ID NO: 4295:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4295:

AAGTGAAAGA ACTCGGCGTG ACACCTATTG CACGATTCGT TGGTTTTAAG GCAGTAGGCG 60

55

GCAATCTATC TGTTGAAGAC ATTGATTGA TCGAATTGAA CGAAGCATT T GCTTCTCAAA 180
 CGATTGCATC TATTAAAGAA GTAGGTCTAG ATATATCACG TACGAATGTG AATGGTGGCG 240
 CTATTGCTTT AGGTCATCCA TTAGGTGCTA CAGGCGCCAA TGTTAACCCG CGCGTTTACC 300
 TAATGAAATG GGGTAAACCG nCCCGATAGn CCGTAnCGCA AGGGT 345

(2) INFORMATION FOR SEQ ID NO: 4296:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4296:

TAAATTGATT TCTAATTGAA ATCATCTTAT GACTGCTTTT TATTATACTT TACATTTCTC 60
 GTTCGTCAG ATTCAAACGT TTTCACCTCG CCAAGCCATC TTTCTTTGTG TTGCTTTTA 120
 TTTTGACGTT TTAGACATAA AAAAAGAGAC CTTGCGGTCT CAATGCGGCT CATCGCATCC 180
 ACTTTTGGCC TGGCAACGTT CTA CTCTAGC GGAAnTAATT CnACTACCA TCGACGCTAA 240
 GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGGCT ATAGTCACCA 300
 GACATATGAA TGTnAATTGA TACATTGCAA AACTAGGATA GTGAAGTAA AGTGATTTTG 360
 C 361

(2) INFORMATION FOR SEQ ID NO: 4297:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4297:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAAC TTTTCACTT CGCCAAGCCA 60
 TTTTCTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG 120
 TCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 180
 AAAGACCTTT CTTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 240
 ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TTTTCGTCAGA TTCAAACGTT 300
 TTCCTTCGC CAAGCCATTT TnCTTTGTGT nTACTnT 337

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4298:

10 GTATTCCTCC ATTATTATAG GTAAATCGCT ATTAATTATA AAATTAAATG GCGGTCTCGA 60
 CGGGAATCCT GCGTGACAGn CAGGCGTGT ACCGCTACAC TACGAGACCA TTAGTAAAC 120
 15 GGAGGAAGAG GGATTGGAAC CCCC GCAGC CGTTAAGCCC CTGTCGGTTT TCAAGACCGA 180
 TCCCTTCAGC CGGACTTGGG TATTCCTnCA AAATTATATG GACCTnGCAG GACTCGAACC 240
 TCGGACCGAA CGTTATGAGC CTTAGCTCTA ACCAACTGAG CTAAAGGTCC TAAATATAAT 300
 20 TTTTACAAC TATAAAATAG TGG 323

(2) INFORMATION FOR SEQ ID NO: 4299:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4299:

CTACATGCGT TGAATTAGG ATCGGTACTT TATATGAAGA CGTGCTGCTT CCATTAAATG 60
 AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT AAAATTGCCT 120
 35 ATAAATTTTT AGCACATAAA ATAAGAGGnG CCAACCATTG TTAGACTATA ACAACGGTTG 180
 GCTCTTTAAT TGTA AAAAAGA AAACCATACG CTATGnTGTT ACAAnGAAAA AGGTTCTACC 240
 40 ATTGTCACAA AAAATGCATC TCTACGTGCT AGAATAAATA TTGGTCAGCC AACCAAATA 300
 ATCAACACGA GGAGATGCTA TTT 323

(2) INFORMATION FOR SEQ ID NO: 4300:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 385 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4300:

TGAATCCAGA TAAAATTGGA ATGATTAACG CGAATCACTT TTACTACCAA TGTTCCAAAG 120
 CTGCTCTGCA AACGCATTGT ACTCTGAGCT TTTTGATTAA AATGAATTG CTCCAAATAA 180
 5 AAATACAATT GCCATTAAAA TACCACCAGA TATTACAAGT GGCAACATGT TAGAAACACC 240
 GTTnCATTTGA AGTGTtTGAT AGAATGCTTT ACCTGGGGCT TGAATTTTTC TTGGACTGTG 300
 CATTTGAGTT ACCTTTTCTT TGGACCATCA CGGGGCAACA AAAGGTTTGA CGACTTGTGA 360
 10 GCTGAATGGC TtGnTGAAT GAATT 385

(2) INFORMATION FOR SEQ ID NO: 4301:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 348 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4301:

TCCTGTACCA CCTATAATCG TTTTAATCGA TGGGGGGACG CATAGGAATA GGCGACGTGA 60
 25 CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 120
 GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC ACACTGCCGA 180
 GAAAAGCCTC TAGATAGAAA ATAGGTGCCC GTACCGCAAA CCGACACAGG TAGTCAAGAT 240
 30 GAGAATTCTA AAGTGAACGA ACGAACTCTC GTTAAGGGAC TCGGCAAAAT GAnCCCGTAA 300
 CTTGCGGGGAA AAGGGTnCTC TTTAnGGTTA ACGCCCCAAA AAACCGCT 348

(2) INFORMATION FOR SEQ ID NO: 4302:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 385 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4302:

45 AATGGAACGT GCTTCTGTAT TGGCCCAAGT AGATATTCAT CGTGCAGCAA CACATAATAA 60
 AGGTGTTATG AATGGCATAAC ATGCTGTTGT TTTAGCAACA GGGAAATGAT ACGCGTGGTG 120
 CAGAAGCAAG TCGCATGCA TnACGCGAGT CGTGACGGGA CAGTATCGTG GTATTGCTAC 180
 50 ATGGCGTTAC GATCAAGATC GTTCAACGAT TGATTGGTAC AATTGCAAGT GCCTATGGAC 240
 ATTGGGCAAT CGTTGGCGGT GGTACAAAAG TATTACCAAT TGCTAAAGCT TCCATTAGGn 300

55

TTTTGAGCGG CAAAACTTT GnCAG

385

(2) INFORMATION FOR SEQ ID NO: 4303:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4303:

AGTGCGACGA TTGGTATTTT ACAAGAATTT TATCAACAAG ATTTAATTAG CTTAAACGCA	60
GCAATCCCTG TGTTACTAGG CGATAACATT GGTACCACGA TTACAGCTAT CTTAGCTAGT	120
TTAGCCGGCT CAATCGCTGC AAAACGTGCG GCGCTTGAC ACGTCATCTT TAACTTAATC	180
GGGGTAATTA TCTTCACAAT TTTCTTGCCA GTTGTGATT C ATTTGATTAG TTTGTTACAA	240
GATTTATGGG CACTTAAAC CAGCGATGAC GATTGCAGTA TCACATGGnA TCCTTCAACA	300
TAACCAATAC CTTGGATTCC ATTTACCAAT TTGTAGCCnG GTTTAGCATn GGATTGGTTA	360
CCAAGCCTTG TCCC	374

(2) INFORMATION FOR SEQ ID NO: 4304:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4304:

AAAACAGGAT ACTTCGATAA GTTAATGATT TCTGTTGTGA ATCGCGCACC ACGTTTCTTA	60
ATTTTACCGA CTATTATATT AATTGGTATT TTAGGTAGTA CAGCCGGCGA TGCTGCGACA	120
ATTTCTTGCC GCCGCTTGCA GCAATGCTTT TTATTAAAT TGGCTATCAC CCTATCGCTG	180
GACTAACGAT GGCATATGCT TCCGCTGTTG GAGGATTTGC AGCAAATATA GTTGTGTTGTA	240
TGCAAGATGC TTTGGTCTAT TCATTTACAG AACCGGCAAC ACGTATCGTT TCAGATTCTA	300
TTAAAACAAA CGTT	314

(2) INFORMATION FOR SEQ ID NO: 4305:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4305:

5 CGTTGCAGAA TGTGTTGAAA TCATCAGAAA TATGCTTAGG CAAGCTAATA TCATTGTCAG 60
 CCATTAATTT ACGGTTACCA ACCAATATAT GGTGATGATC AATCGTTGCT TCAATACCAT 120
 GGCCAGGTAC TGCTTTAAAT GTTGTTGTCT CAGTTAATAT TAATTGCTTT TCTTTTGCAT 180
 10 AATTGACAAT GGCTTCTGCC AATGGGTGTT CAGAATCTTT TTCAGCAGTA GCAAGTAGTT 240
 GTAGCGTTTG ATTGTCACCA TGATAATCTG TCACGACTGG GACGACCATT TGTAATGGnA 300
 nCCGTCCTTA TCTAAAACGA TGGGTATCAA TTTGATGnGG GCGG 344

(2) INFORMATION FOR SEQ ID NO: 4306:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 378 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4306:

25 AGTTTCCCTG AAAATTAATC AAGGACTTAA CATTGCGAGT CAAGGTATTG ATCAAGCTAA 60
 TGGACAGTTA AATGATGCCA AAGCTTCGTC ACACAAGTTA GAAGTAGAGT CCGTGATTAT 120
 30 CAAGATGCAA TTCGACGCGC GCAAGATTTA AATCGAAGAA ACCAGCAACA GATTCCTCAA 180
 AATAGCGCGG CGAACAACGA AACATCAAAT AGTGCACCTG CAGCTGGTAA TGGTGTAGCA 240
 35 TCAACGCCAC CAAGTGCACC AAGTGGCGAT ACTGCACCAA ATAATAATGT TACGCAAAAT 300
 ACCGCACCAG ATGAGTGAAT AATGCGCCTG TATCGACTAC ACCACAAATG ACAnnCCGGG 360
 GAAAnAGATGG TCAAATTT 378

(2) INFORMATION FOR SEQ ID NO: 4307:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4307:

50 GGACTTGGGT ATTCTCCAA AATTATATGG ACCTTGCAAG ACTCGAACCT GCGACCGAAC 60
 GGTATGAGC CGTTAGCTCT AACCAACTGA GCTAAAGGTC CTAnATATAA TTTTACAACT 120

CTAGCCAGCT GAGCTACACC GCCTTATATA GTTTGTAAAT AATATGGTGG AGACTAGCGG 240
 GATCGAACCG CTGGACCTCC TGC GTGGCAA AGCAGnCGCT CTCCCAGCTG nGCTAAGCCC 300
 5 CCATAATAAT TACAGTAT 318

(2) INFORMATION FOR SEQ ID NO: 4308:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4308:

TGTACGTTTA ATACCTATGA TATATGCTGC AAGTCTCATA TCTATTTTTTC GGTTTTGAGA 60
 20 CAATTCGTAA ATCGTATCAA ATGCCGCTTC TAATTTTTTCA CGTAGCTTTT CATTAAC TTC
 TTCTTCAGAC CAATAATAAC CTTGATTATT TTGTACCCAT TCGAAGTAAG AAACCGTTAC 180
 ACCACCAGCA CTTGCTAATA CGTCTGGAAC TAATAATATA CCACGTTTCAG TTAAAATACG 240
 25 TGTGTCTTCT GGTGTTGTAG GTCCATTAGC AGCTTCAACA ACGATACTAG CTTTAATATC 300
 ATGTGCATTG TCCTCnGTAA TTGGGTTGAA TAGCGnGGGA CTAAATGCAC ATCnAATCAA 360
 CAATCCTATT GGATGTCCCA AnAATTGTAC GACCAACACC 400

30

(2) INFORMATION FOR SEQ ID NO: 4309:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4309:

CAAATAAACC AGAGCTAGTT GCAATTGCTG AACCACATCC TAATAGACCG AAAAAGAGAA 60
 GTAGACGTGC GGCACCGGCA GATCCTAATG CAACTCCAGC AGATCCAGCG GCTGCAGCGG 120
 45 GTAGGAAACG GTGGTGCACC AGTTGCAATT ACAGCGCCAT ATACGCCAAC AACTGATCCT 180
 AATGCCAATA ATGCAGGACA AAATGCACCT AACGAATnGT TGTTCAATTG ATGACAATGG 240
 50 TATTAGACCA AGTACCAACC GTTCTGTGCC AChTnAAACG TTGTTAATAA CTTGCCGGGG 300
 TTCACACTAA TCAATGGTGG CAAAGT 326

50

(2) INFORMATION FOR SEQ ID NO: 4310:

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(A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4310:

10 TCAAAGCGCC AATAACATCT TCTACTGAAG TTTCTTTAGA TTTAGCATTG AGTGATAATG 60
 TTATTGTTGC TTTTCTTCC ATTGGAATAC TTTGATGAAT CGTTAATACA GATAGTTCTA 120
 ACTTTGATAT AACATCTAGT ACACGTGCCA ACATACCAAC AATATCAGTT ACATATAAAA 180
 15 TTAATGTAAA TTCTCGATGG TCAAGCATTT TATCGGCTAC TGGAAATATC GTTTCTCTAT 240
 ATnTATAAnA AGCACTTCTA GATAGATCAA ACTGTTTAAC GGCATCATAA ATGGnCAATG 300
 TCGGATCACT TTT 313

20

(2) INFORMATION FOR SEQ ID NO: 4311:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4311:

GGTTCGAATC CAGCTAGCCC AGCCATTAGA GCCATTAGCT CAGTTGGTAG AGCATCTGAC 60
 TTTTAATCAG AGGGTCAGAG GTTCGAATCC TCTATGGCTC ACTACTTGCA CTTTCCATTT 120
 35 TTGGAAGTG CTTTTTTTTA GGTTCTCCAC CAAATGTGGT GGGTATATAA TTAAAGAAC 180
 TATTTTTAAA ATACAACCTT TAGAGCTTTT ATTATTAGGC GGCCAGTCCA TTATTGGGGC 240
 TGGTTGTCTT CnTTTTTTCT CCTTTGTACA AGCTGAAAAT CATCATTATA CGTGCTTAAA 300
 40 GTGGTGAATT CTGAACCAAA GAATCACTTG ATAATTTATC TATATAATCC TcNATAGACC 360
 ATATAATGCT GGAATAATGG ATCTACAnCC TGAGTTCCAn 400

45

(2) INFORMATION FOR SEQ ID NO: 4312:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4312:

ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 120
 AGGCATCCAC CGTGCGCCCT TAATAACTTA ATCTATGTTT CCACCATTTT TATAAGTCAA 180
 5 ACGCTCACAT ACGGCTTCGT TTTCATTATT TTAAATGCTC ATTTACATAA GTAAACTCTG 240
 CTTTAAAATA ATTAATCAT TGTCTGCnAA ACGTTTTCnT TTATAAAAAG ATTAAACGCG 300
 TTATTAA_nCT GTGGAGTG 318

(2) INFORMATION FOR SEQ ID NO: 4313:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4313:

ACGGTGATCA CTCACCGCAG ATTTTAAGTC CTGTGCGTCT GCCAGTTCCG CCACCCCGGC 60
 ACTATAAAAA TGGAGCAGAA GACGGGATTC GAACCCGCGA CCCCACCTT GGCAAGGTG 120
 25 TATTCTACCG CTGAACTACT TCTGCATATG CGGGTGAAnG GAGTCGAACC CCCACGCCGT 180
 AAGGCATAGA TCCTAAGTCT AGTGCCTCTG CCAATTCCGC CACACCCGCA AATGGTGAGC 240
 CATAGAGGAT TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCn 300
 30 AATGGnTCTT CCATGG 316

(2) INFORMATION FOR SEQ ID NO: 4314:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 356 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4314:

AGGAAAAGTC GTTGTGATAC ATCAACCAGC TGAAGAAGTA CCACCAGGTG GTGCTAAAC 60
 45 AATGATTGAA AATGGTGTAT TAGACGGTGT TGATCATGTA TTAGGTGTAC ACGTCATGAG 120
 CACAATGAAA ACAGGTAAAA GTGTATTACC AGACCTGGTT ATGTTCAAAC AGGACGCGCA 180
 50 TnCTTCAAAT TGAAAGTCAA GGTAAGTGG TCATGGTTCA TCACCACATA TGGCCAATGA 240
 TGCCATTGTT GCAGGTAGCT ACTTCGTCAC AGCGTTACAA ACAGTGTATC TAGACGACTA 300
 GGCCATTGTA ACCGGTGGTT TCACATCGGT CATTTnCCGT AAAAGnCCAT TCCATG 356

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 380 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4315:

10 TATCAGCATT TGTAAGTGT ATTGTTTATA ACTTCTGTGT GAAGCGCAAT ATTACAATTA 60
 AAATGCCGAA AGAAGTACCG CCGAATATTT CACAAGTATT TAAGGACTTA ATTCCATTTT 120
 15 CAGCGGTAAT CATCATTCTT TATGCATTAG ATTTAGTCAT CGCAACAGCT TTAAATCAAA 180
 TGTAGCGGAA GGNATTTTAA AATTATTCGA ACCATTATTT ACAGCAGCAG ATGGGATGGA 240
 TTGGTGTAC AATTATCCTT GGNGGCCTTT GCATATTCnG GGTGTAGGG AATCAGGTCC 300
 20 GTCAATGTAG AGCCAGCAAT TGCAGCCATT ACATATGCGA TATCGGAGCG GACTTCAAGT 360
 TGCCTCAGCG GAGGACACGC 380

(2) INFORMATION FOR SEQ ID NO: 4316:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4316:

35 GCTCTAGGAT GACTGATTGA ATGTCCATGA ATGAACAACC CCTTTGTTTA ATATCGAGTT 60
 TGGCAAATTT ACGTTTATCA GCGTTTCTAT GATCAGTACT TCTACGGGTA GCGTTTCTAT 120
 GTAATTTACA TCATCTTAAC ATATAAATAC TTCGCTATTT AATTGAAAAC ATATCCTATT 180
 40 ATTCTTTGTC CGTTCTGACG TTTAATATCT AGCCTTAGGC ATTTCACTTG TTAATGAATT 240
 TAACTTTCTT CCACTAACCG TCCCTAAACC CAATCCCGCA ACAGTTTTTA ACTTTTTCGT 300
 TGTGTCTCTG ACATCTCATT AAGAAAGTTT ATTCTGCTTA AACTTATAA TCCACACCCT 360
 45 GAGCAAACGn TnCTTATGAC AGAGTATTAA AATAAGCCGn 400

(2) INFORMATION FOR SEQ ID NO: 4317:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4317:

5 CTTTATTGAT AATGGTATGA GAATATTTGT TCGAGATGGA TGAAGGTAAT GAGTGAGAAA 60
 CTGGATTTTT AAAGTATGAG ACAATATTTT AAAAAGTTCA ATTATTAACT TATAAGCAAA 120
 TAATTGCTAT AAAAAGTTT GGACGTGTAC AATTGCAATA TGAAGATTTT AAATTAATTG 180
 TAAAGTATCG TGGAGTGGGT AACGTGTCAG AACATGTATA TAATCTTGTG AAAAAGCATC 240
 10 ATTCTGTTAG AAAATTTAAG AATAAACCTT TAAGTGAAGA CGTTGTTAGG AAATTGGTAG 300
 GAGCTGGGCA AAGCGCTTCG ACGTCAAGTT TCCTGCCAGC ATACTCCATT ATTGGTTCGG 360
 15 CGGTGGGAGG TTAAnGGAAT TTACGGGGAG GTTCTGGGCA 400

(2) INFORMATION FOR SEQ ID NO: 4318:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4318:

25 TAACTACGTC TCCTGTTTCT GGATTCTTAA TTCCTGGTTT ACCTGGAACT TCCTCTTTCT 60
 CTCCTGTTGG TAACTTCGGA TCAAATTCGT CTCGATGACC TGGTGTTATC GTTCTGGTC 120
 30 CGTATTCTGT TAATTCATTA ATCGGATCTn TTGTGATTTC TTCTTTTCGAT TCACCTGTAC 180
 TAATAATTTT TCCAGTTAAT GGATTTTTTA GTGTTGGCGT CGTTATTGTC TTCTCACCTn 240
 35 TTTGTCCTTC TCTGTAACT TTTCTGTCC CGGTGCTAAA TnCGGATTAA ATTACGGTCT 300
 TTCTTGAAGG AATCTCTTC 319

(2) INFORMATION FOR SEQ ID NO: 4319:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 368 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4319:

50 AGGTGCATTG AGAGAATTTG TAAATGACGT ATTAGGACCT CAAGACGATA TTAATAAATT 60
 TGAATACTTA AAAAAATCTT CTCAAATAC AGGTACTGTC AATTATGGT ATTCAACTTA 120
 AAGATCATGA TGATTTAATA CAACTCAAAC AACGTGtnAA ATCATTTCGA TCCTTCCAAT 180

ACAGTCATAA ATTGATTTCT AATTGAAATC ATCTTATGAC TGCTTTTTAT TATACTTTAC 300
 ATTTGCTCGT TTCGTCAGAT TGCAAACGTT TTCACTTCGC CAAGCCCATC TTTCnTTGGn 360
 5 GTTTGCCT 368

(2) INFORMATION FOR SEQ ID NO: 4320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4320:

TAAGTTAGCT ACCATCCTCG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60
 20 TCCTCTCCTT CGGCTCTCGC TTAATCATT AGCTCTACTA AACTCGTTGC GCTCTTTTCT 120
 CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT GTTACTTTTT 180
 TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT CTCAACTTGC CTGGCAACGT 240
 25 TCTACTCTAG CGGAAnTAAA GTTGGnCTAC CATCGTCGCT AAAGACCTTT CTTGACTTGT 300
 GACAATCGCT TGCTTCTTTT CCTCTCCTnC GGCTCTCGGT TAACTCA 347

(2) INFORMATION FOR SEQ ID NO: 4321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4321:

GGGCAAGTTA CAGTGGTGCA TGTTTGTCGT CACTCGTGTC GTGAGATGTT GGGTTAAGTC 60
 CChCAACGAG CGGCAACCCT TAAGCTTAGT TGCCATCATT AAGTTGGGCA CTCTAAGTTG 120
 ACTGCCGGTG ACAAACCGTA GGAAGGTGGG GATGACGTCA AATCATCATG CCCCTTATGA 180
 45 TTTGGcTACA CACGTGCTAC AATGGACAAT ACAAAGGGCA GCGAAACCGC GAGTCaAGCA 240
 AATCCCATAA AGTTGTTCTC AGTTCGGATT GTAGTCTGCA ACTCGaCTaC ATGaAGCTGG 300
 50 aATCGCTaGT aATCgTGGTC CAGCATGCTA CGGT 334

(2) INFORMATION FOR SEQ ID NO: 4322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 330 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4322:

CTGTTAAACG ACTACAGGAA GTATTTACAA TCAAATAAG CAAAAGTATT CAGATGCCTC	60
AGATAAAGCT TGGGCGCATT CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA	120
CGATATAAAA GTGCAAAGGG TTGGCTAATA GATATGGCTA ATAAATCGCG CTCGAAATGG	180
GATAATATTT CTAGTACAGC ATGGTCGAAT GCAAAATCCG TTTGGAAAGG AGCATCGAAA	240
TGGTTTAGTA nCTCATTACA AnTCTTTAAA GGGTTGGACT GGGGATATGT ATTCAGAGCC	300
CACGATCGTT TTGATGCATT TCAGTCGGC	330

20

(2) INFORMATION FOR SEQ ID NO: 4323:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4323:

CAATGATGCC ATGAGCAGTG CCTCCTTTAA TAGCATTTTA GCACTGTTTT GTCGTATTTT	60
TAAATATAAA TTTGGAATGA ATAATAAAGT AGTGATTAAA TTAAGTTGTG TGATAGGAAA	120
CTTGGACATC AATCAAAGTA ATAGGCACTA CAACGCTTAT TGGCGGGGCC CCAACAAAGA	180
AGCTGACGAA AAGTCACTTG CAATAATGTG CAAGTCnGGG ATGGGCCCCA ACATAGAGAA	240
ATTGGGTCCG nAATTTCTAC AGACAATGCC AGTTGGCGGG GCCCCACAT AGAGAATTTT	300
GAAAAGGAAT TCTACCAGCA ATGCCAGTTG GGGGAnG	337

40

(2) INFORMATION FOR SEQ ID NO: 4324:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4324:

TTACTTACTA TCTAGTTTGT AATGTATAAA TTACATTCAT ATGTCTGGTG ACTATAGCAA	60
GGAGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG TCGATGGTAG	120

55

GCATTGAGAC CGCAAGnTCT TTTTTTTATG TCTAAAACGT CAAAATAAAA AGCAAACACA 240
 AAGAAAAATG GCTTGGCGAA GTGAAAACGT TTGAATCTGC CGAACGAGAA AGAGCGnACC 300
 5 GAGTTTAGTA GAnTAAATGA GTAAGCGAGA 330

(2) INFORMATION FOR SEQ ID NO: 4325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4325:

TTCATCCGCT CACTTTTCAA CGTAATCGGT TCGGTCCTCC ATTCAGTGTT ACCTGAACTT 60
 20 CAACCTGACC AAGGGTAGAT CACCTGGTTT CnGGTCTACG ACAAATACTA AACGCCCTAT 120
 TCAGACTCGC TTTCGCTACG GCTCCACATT TACTGCTTAA CCTTGACATC AAATCGTAAC 180
 TCGCCGGTTC ATTCTACAAA AGGCACGCCA TCACCCATTA ACGGGCTCTG ACTACTTGTA 240
 25 AGCACACGGT TTCAGGTTTCG ATTTCACTCC CCTTCCGGGG TGGCTTTTCA nCTTTCCCTC 300
 ACGGnACTGG TTCAC 315

(2) INFORMATION FOR SEQ ID NO: 4326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4326:

TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTTGCGGT TAnATGCGGC TCATCGCATC 60
 CACTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGAACTAC CATCGACGCT 120
 AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC TATAGTCACC 180
 45 AGACATATGA ATGTAAATTA TACATTCAAA ACTAGATAGT AAGTAAAAGT GTTTTGCTTC 240
 GCAAAACCAT TTATTTTGAT TAAGTCTTCG ATCGnTTAGT ATTCGTCAAC TCCACATGTC 300
 ACCATGCTT 309

(2) INFORMATION FOR SEQ ID NO: 4327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4327:

AAAGCTTATA AACGCTCATC TGACATTGTA GAATTCATGC TTTCAAAAGA CGATATACTA 60
CGACACTCCT ACGAACTTGT CCAAGGATTA CGAAAAGACC TAAGGTTATG TAATTnGCCT 120
AAATTTATTA ATCGTTTAAA TTCAGTTAGT AAAAAGTCTG TGAGTAAGGG TGTATGGAAA 180
GTGGTTAAAT ATTATAGAAA ACATCAAAGG ATGTTAAGAA ATACAATTTA TTACCCAGCA 240
TTTAATAATG GTGCTATAGA AGGAATTAAT AATAAGATnA AATTAATCAA GTGAATTTCT 300
TTTGGTTnCA G 311

(2) INFORMATION FOR SEQ ID NO: 4328:

20

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 340 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4328:

TAGCTTCTGC GAGCTAGCGG AATCGAAGCC CCAGTAAACG GCGGCCGTAA CTATAACGGT 60
CCTAAGGTAG CGAAATTCCT TGTCGGGTAA GTTCCGACCC GCACGAAAGG CGTAACGATT 120
TGGGCACTGT CTCAACGAGA GACTCGGTGA AATCATAGTA CCTGTGAAGA TGCAGGTTAC 180
CCGCGACAGG ACGGAAAGAC CCCGTGGAGC TTTACTGTAG CCTGATATTG AAATTCGGCA 240
CAGCTTGTAAG AGGATAGTAG GAGCTTTGAA ACGTGAGCGC TACTTACGTG GAGGCGCTGG 300
TGGGATACTA CCCTAGCTGT TTTGGTnTCT nACCCGACCA 340

40

(2) INFORMATION FOR SEQ ID NO: 4329:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4329:

50

AATCCATAGC GAAATGTATA CCATCACCCA TCGTCCTTC TAAAGGTAAA TCTCTACCTT 60
TTTGTGCACC AGTACATAAT ATAATGGCAT CATACTCAGA TTCTAACGTT GCTTTATCAA 120

55

TACGACGTCG AACCACATCT TTATCAAGTT TCATATTCGG AATACCATAC ATTAATAAAC 240
 CGCCTGATTG TCTAGCACGT TCATAAATAG TTAAGTTCTT 300
 5 CAGCAGCAGT AATCCTGnTG GACCG 325

(2) INFORMATION FOR SEQ ID NO: 4330:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4330:

CACTTCACCA CAGCCGCCAT GGCAGGnGCA GTAGGAATCG AACCCACACC AAAGGTTTTG 60
 20 GAGACCTCTA TTCTACCGTT GAACTATGCC CCTATTAAAA ATAATAAATG GAGGGGGGCA 120
 GATTGGAAGT GCCGAACCCG AAGAGCGGAT TTACAGTCCG CCGCGTTTTAA CCACTTCGCT 180
 ACCCCTCCAT AAATGGTGCG GCGGnGnAGG ACTTGAAACC CCCAACCTAC TGATTACAAG 240
 25 TCAGTTGCTC TGACCAATTG AGCTAAGGCC GGCTAAGAAA TGGTTCCAGG ACAGAGTCGA 300
 AACTGCCGAC ACATGGGAGC TTTCAAT 327

(2) INFORMATION FOR SEQ ID NO: 4331:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4331:

GCATCATTTT CAGCTTCCCA CTTCACATT TGGAAAATTT CTCCAGTAAC AATGAAAGAC 60
 CATATACTTT TTCCTACAAG AGCAGGACCC GGTAACAATA CAGGTTGGTA ATGCCCAATA 120
 ATAATGACCA TTTCCCAAAT GCCTAAGAAA ATAATAAATG TGATAATAGG TAATATAAAT 180
 45 TTGTTATTTG TGGGACGTGT CATGAACGCG ATGCCTCCTT ATACAATGAC GGTTCACAA 240
 AGTCATCATA TGCAGGTGGA TTAAACAAAT GATGTTGTTT TACCAATGTC GTAATTTCTT 300
 50 GGATAGCCGG ATGGnTTAAA TTGTTAAAAT CACCATAGGG TGTCCnGCC GTGGACTGTG 360
 GTTAAAAACG TCACGGACTT TGTTTAAAAn GGTGCGTCAT 400

(2) INFORMATION FOR SEQ ID NO: 4332:

- (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4332:

10 CTGGTATGCA GATTACCAC CTGCCTCTCC ACAAnTnnGG GGAGAGCAAA CAGATGTGCC 60
 TGAATCAAGT GACTGGTATA ACGCATCATA CATTATTATG TGGGGCTCTA ATGTACCTTT 120
 AACACGTA CTCCGATGCAC ATTTTATGAC TGAAGTCCGC TATAAAGGTA CAAAAGTCAT 180
 15 TTCAGTAGCA CCAGATTACG CAGAAAATGT GAAATTTGCA GATAACTGGC TAGCACCGAA 240
 TCCTGGTTCA GATGCTGCAA TTGCACAAGC AATGACGGCA TGTATTTTTA CAAGGAACAT 300
 TATGTTAAAT CCAACCTGAA TGAACGGTTT TTATTAAATT ACGGTTAAAA CCATTATTAC 360
 20 CAGGAT 366

(2) INFORMATION FOR SEQ ID NO: 4333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4333:

TATTATTCA TTGAGCAGAA AGAAAATTAT GGCACCAAAC TTAAATATTT TTTCAATGT 60
 35 CATTCTTTTG AnGGGAGTGG GACAGAAATG ATATTTTCGC AAAATTTATT TCGTCGTCCC 120
 ACCCCAACCTT GCATTGTCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCATC 180
 CCCAACTTGG CACATTATTG TGAAGCTGAC TTTCGTGAC TTGCTGTGTT GGGGCCCTCA 240
 40 CCCCAACTCG CATTGCCTGT AGAATTTCTT TTCGAAATTC TCTGTGTTGG GGCCCTGGA 300
 CTGAGAATTG GAAAAAGCT TGTGACAAG CGCnATTTTC GTTCCATGCA ACTGACTGCC 360
 45 AAGAGAAcTn CGTGAGAGCn ATGAAGAAGA TTGGATTTGA 400

(2) INFORMATION FOR SEQ ID NO: 4334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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CGCCCTTAAT AACTTAATCT ATGTTTCCAT CCTACAGGAA ACGCGTTATT AATCTTGTGA 60
 GTGTTCTTTC GAACnTATGC GATTATTTCT TATGAATTCA AGCTTATTTA AAACCTCTTTA 120
 5 TTCACTCGGT TTTGCTTGGT AAAATCTATA TnTTACTTAC TTATCTAGTT TTCAATGTAC 180
 AATTTCTTTT TAGTCAAGCG CTCGCATAAG CAATATCACT TTAACCAAAA AATATTTGAA 240
 10 TGTAAATAA ACATTCAAAA CTGAATACAA TATGTCACAT TATTCCGCCA TCTTCTGnAA 300
 GAAGATGTT 309

(2) INFORMATION FOR SEQ ID NO: 4335:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4335:

nAGGACTTTT CTCGGTCAGT GTGAAAATCA ACGCACTCGT AnACACAATG TCTTCTCCCC 60
 25 ATCACAGCTC AGCCTTAACG AGTACCGGTA TTTGCCTAAT ACTCAGCCTT ACTGCTTAGA 120
 CGTGCAATCC AATCGCACGC TTCGCCTATC CTA CTGCGTC CCCCCATCGA TTAAACGAT 180
 TATAGGTGGT ACAGGAATAT CAACCTGTTA TCCATCGCCT ACGCCTGTG GnCTCAGCTT 240
 30 AGGACCCGAC TAACCCAGAG CGGACGAGCC TTCCTCTGGA AACCTTAGTC AATCGGTGGA 300
 CGGGATTCTC ACCCGTCTTT CGCTACTCA 329

35 (2) INFORMATION FOR SEQ ID NO: 4336:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4336:

CAAAGTGACA GGTGGTG CAT GGTGTGTC AGCTCGTGTC GTGAGATGTT GGGTTAAGTC 60
 CCGCAACGAG CGCAACCCTT AAGCTTAGTT GCCATCATTA AGTTGGGCAC TCTAAGTTGA 120
 50 CTGCCGGTGA CAAACCGnnn GAAGGTGGGG ATGACGTCAA ATCATCATGC CCCTTATGCA 180
 TTTGGGCTAC ACACGTGCTA CAATGGGACA ATACAAAGGG CAGCGAAACC GTGAGTGCAA 240
 GCAAATCCCA TTAAAGTTGT TCTCAGTTCG GATTGTAGTC TGCAACTCGG ACTACATGAA 300

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(2) INFORMATION FOR SEQ ID NO: 4337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4337:

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CCAGCACC GG GGCAGGCGTC ACCCTCATAC ATCACCTTAC GGTTTAGCAG AGACCTGTGT      60
TTTTGATAAA CAGTCGCTTG GGCCTATTCA CTGCGGCTCT TCTGGGCGTT AACCCCTAAAG      120
AGCACCCCTT CTCCCGAAGT TACGGGGTCA TTTTGCCGAG TTCCTTAACG AGAGTTCGCT      180
CGCTCACCTT AGAATTCTCA TCTTGACTAC CTGTGTCGGT TTGCGGTACG GGCACCTATT      240
TCTATCTAGA nGGCTTTCTC GGCAGTGTGA AATCAACGAC TCGAAGACAC AntGGCTnCT      300
CCCATCAGAG CTCAGCCTTA ACGA                                             324

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(2) INFORMATION FOR SEQ ID NO: 4338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 399 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4338:

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CGGACATCAA ACGGATGCTG CTCGATTGGC AAATGCATAT AACTAGTAAC ATGATCATCG      60
ACATCAAATT TAGATGATCA AATGTcCCCA ATcATTAATT TGATTcGGTT GTTTGCTCAA      120
TTGATTATAT GTTTTTCTTA GCACTTCATG CGGCACCATA TCTTTACCTA GTAGCCACAA      180
AGATAAGTCT AACAAAGTGGC AACCATAATC GATTAAACTA CCGCCACCTT GCAACGCTTT      240
ATTGGTAAAA ACACCCACAGC CAGGCACTTT ACGCCTACGC ATCGCTTGTA CACGTGCTAC      300
TAAAGGTTTA CCAACCACAC CTGATTCAAT TGCTTTTTTA GCAGTAATTG CCACATCTGT      360
GTGACGATAA TGATATGCGC CAGTAATAnt TTGTGnTTT                             399

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(2) INFORMATION FOR SEQ ID NO: 4339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4339:

5 TGAGGCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTTATTCA CTCGGTTTTG 60
 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGC 120
 CTAAGTGGAC TCGAACCACC GACCTCACGC nTATCAGGCG TCGGCTCTAA CCAGCTGAGC 180
 10 TATAGGCCCA TTTnTTTGAA TGTAAATAA ACATTCAAAA CTGGAATACA ATATGTGCAC 240
 GTTATCCGC ATCTTCTGAA GAAGATGTTn CCGAATATAT CCTTAGAAAG GAGGTGATCC 300
 AGCCGCACCT TCCGATACG GCT 323

15 (2) INFORMATION FOR SEQ ID NO: 4340:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4340:

GGCTAGCCCT AAAGCTATTT CGGAGAGAAC CAGCTATTC CAGGTTGAT TGGAATTTCT 60
 CCGTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTCCGTC CTCCATTCAG 120
 30 TGTACCTGA ACTTCAACCT GACCAAGGGT AGATCACCTG GTTTCGGGTC TACGACCAAA 180
 TACTAAACGC CCTATTCAGA CTCGCTTTCG CTACGGCTCC ACATTTACTG CTTAACCTTG 240
 CATCAAATCG TAACTCGCCG GTTCATTCTT ACAAAGGCA CGCCATCACC CATTACGGG 300
 35 CTCTGAACTA ACTTGGTAAA GCnCCGGTTT nCnGGTCCAA TTTT 344

(2) INFORMATION FOR SEQ ID NO: 4341:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4341:

TGTACCACCT ATAATCGTTT TAATCGATGG GGGGACGCAT AGnGATAGGC GAACGTGCGA 60
 50 TTGATTGCA CGTCTAAGCA GTAAGGCTGA GTATTAGGCA AATCCGGTAC TCGTTAAGGC 120
 TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA 180
 AAGCCTCTAG ATAGAAAATA GGTGCCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240

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TTCnGGGAAA AAGGGnTCCC CTTTAAGGGT TAACCGCCCC AAAAAACCCC C

351

(2) INFORMATION FOR SEQ ID NO: 4342:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4342:

15	AATAATGACT CCTACGGGAC TCGAACCCGn GTTACCGCCG TGAAAGGGCG TGTACTTAAC	60
	CGTATGACCA AGGAGCCATG GCTCACCAGG TAGGACTCGA ACCTACGACC GATCGGTAA	120
	CAGCCGATAG CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC	180
20	TCTAGCGGAA nTAAATTCGA ACTACCATCG ACGCTAAnGA GCTTAACTTC TGTGTTCCGC	240
	ATGGGAACAG GTGTGACCTC CTTGCTATAG TCACCAGACA TATGAATGTA ATTTATACAT	300
	TCAAAACTAG ATAGTAAGTA AAAGTGA	327

(2) INFORMATION FOR SEQ ID NO: 4343:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 360 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4343:

35	ACCGCTTGGG CTGACATTTT TGGCTTGTTA AGCAGCTTGC CTACTTTTTT GGCAATAGCA	60
	CCATACGTTG TTAGAGTCCC ATAAGGAACC TGTCTTAATT CATTCCAAAC AACTGTTGA	120
40	AAATGACTAC CTGTTGGCTT TAAAGGTATT GTGATTTTCA GATTGTCACC TTAAAAATAC	180
	GCGTCTAACC ACTGTGTCGC CTCTCTAAAT ATCGCTAAAG ACGTATTTTC TTCCCTAGTA	240
	CCATCACCTT GTTGATTTTC AAACAAAACA GCGGTCAGAC TTACCCCATC ACTCAAAAGT	300
45	TCCAAAnCGTC CTGACAGGCG AAnCAGAGTG AACGCTGAGA CTCCAGAAAA ATCCCCCTnT	360

(2) INFORMATION FOR SEQ ID NO: 4344:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4344:

5 ATTCGACAT CTTCTGAAGA AGATGTTnCC GAATATATCC TTAGAAAGGA GGTGATCCAG 60
 CCGCACCTTC CGATACGnCT ACCTTGTTAC GACTTCACCC CAATCATTTG TCCCACCTTC 120
 GACGGCTAGC TCCTAAAAGG TTA CTCCACC GGCTTCGGGT GTTACAAACT CTCGTGGTGT 180
 10 GACGGGCGGT GTGTACAAGA CCCGGGAACG TATTCACCGT AGCATGCTGA TCTACGATTA 240
 CTAGCGATT CAGCTTCATG TAGTCGAGTT GCAGACTACA ATCCGAACTG AGAACAACCTT 300
 TATGGGATTT GCT 313

(2) INFORMATION FOR SEQ ID NO: 4345:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4345:

25 ATTTTATCGT AAGATTTTTT CGCAATGAGA TTTGGATCGT TTTGTCCAC TACAATATCT 60
 AATAGTTTTA CTTTAAGTCC AGCATT CACA AAAAGTGCTG CCAGTTGAGC GCCCATTGTG 120
 CCTGCGCCAA GAACGGTTAC TTTATTAATT GTCATAGTGA TTCCTCCAAT TTAGTTGAGG 180
 30 ATAAGATAAC CATTAAGATA ATTGGAATAA CGTTGCTATT TTATAAAATT AATTAAGTAT 240
 CTTTGACAGT CATCTTAGCC TCTTATTTAA GGnAAAAGCn TTATGCTTAA nATAAGTCTT 300
 TTTTA 305

(2) INFORMATION FOR SEQ ID NO: 4346:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4346:

45 GTCAGTTATG GCAAGTGCAT CAACATTTTC AGACACAGCA AGTCTTACGG CATCTTCTAT 60
 TTTTAAGCTT GAATTTAACA AATCATAAGC CGTATGAATA TTAAATATG CCACCATGAT 120
 50 TGAATGGnCC CTTTCTATTA GTTAAGTTTG TCGTAAAGC TGTAAGCAAGT TGCTCAAATT 180
 CATCCCCAGC TGTCCACTGA AACTCCTGGA CGCATTCGGA TGAnCAACGC CAACCAAAAT 240

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AnTACCTTCA TCGACTGCAA ATACCCATAA TTTCCAGCCT TGATGTCAGC AATGTAATAA 360
 CCAACTGAGA TGCTCATTGG CTGATACGAT GntCCATACA 400

5 (2) INFORMATION FOR SEQ ID NO: 4347:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4347:

TCTGGGTTGA GTCGGGTCCT AAGCTGAGGC CGACACGTAG GCGATGGATA ACAGGTTGAT 60
 ATTCCTGTAC CACCTATAAT CGTTTAAATC GATGGGGGGA CGCATAGGGA TAGGCGAnGT 120
 20 GGCGATTGGA TTGCACGTCT AAGCAGTAAG GCTGAGTATT AGGCAAATCC GGTACTCGTT 180
 AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA GTCGTTGATT TCACACTGGC 240
 CGAGAAAAGC CTCTAGATAG AAATAnGTGC CCGTACCGCA ACCGACACAG GTAGTCCAAG 300
 25 ATGAGATTCh TAAGGTGGAG CGACGAATCT CCGTTAA 337

(2) INFORMATION FOR SEQ ID NO: 4348:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4348:

GTTAAGACAC CGCCCTTTCA CGGCGTAACA CGGGTTCGAG TCCCGTAGAG GTCACCATT 60
 40 TTTAGGTCTC GTAGTGTAGC GATTAACACG CCTGCCTGTC ACGCAGAGAT CGsGGGTTTCG 120
 ATTCCCGTCG AGACCGTACA AATGCCTATC CAAGAGGATA GnATTTTTTTT TCGGTTTAAT 180
 ATTATATTAA TAAAAGATAT ATGGACGAAT GATAATCATA TTGATTTATC TGTTTCGTCCA 240
 45 TTTTCTTTAA AATGTATGAA CCTCAAGTAA CTTAGTGGTT GGATATGAAA GATAAACGTh 300
 GACAATAAAA TCTTTATT 318

(2) INFORMATION FOR SEQ ID NO: 4349:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4349:

CTTTAAAGCA CGTATAATGA TGATTTTCAG CTTGTACAAA GGAGAAAAAA AGAAGACAAC 60
 5 CAAGCCCAAT AATGGACTGG CCGCCTAATA ATAAAAGCTC TAAAAGTTGT ATTTTAAAAA 120
 TAGTTCTTTA AATTATATAC CCACCACATT TGGTGnAGnA ACCTAAAAAA AnGCACTTCC 180
 CAAAATGGA AAGTGCAAGT AGTGAGCCAT AGAGGATTCTG AACCTCTGAC CCTCTGATTA 240
 10 AAAGTCAGAT GCTCTACCAA CTGAGCTAAA TGGCTCTAAA TGGCTGGGCT AGCTGGGATT 300
 CGAACCAACG AGTGACGGA 319

15 (2) INFORMATION FOR SEQ ID NO: 4350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4350:

25 ACTTCGCTAC CCCTCCAGCT TATTCATATA ATTTAATAAT CAAAATGGTG GAGAATGACG 60
 GGTTCGAACC GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC 120
 CAAAATAATG ACTCCTACGG GACTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 180
 30 AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACCGATCGGT 240
 TAACAGCCGA TAGCTCTACC ACTGnAGCTA CTGTGGATTG AATCATTATG CCTGGCAACG 300
 TTCTTACTAT AGCGGAAnGT CAAGTTCCGC ATnACCATAC GAAGCT 346

35 (2) INFORMATION FOR SEQ ID NO: 4351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4351:

ACGTCCTTCA TCGGCTTCTA GTGCCAAGGC ATCCACCGTG CGCCCTTAAT AACTTAATCT 60
 ATGTTTCCAC CATTTTTATA AGTnAAACGT TAACATGAAG TTACGTTCTT TTATAAAAAG 120
 50 ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ACTAGCGATT ATTTCTTATG 180

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ACTTACTTAT CTAGTTTTCA ATGTACAAAT AATGGTGGGA GACTAGCGGG ATCGAACCGC 300
TGACC 305

5 (2) INFORMATION FOR SEQ ID NO: 4352:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 302 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4352:

GTTCATCAAT TGCTAATTCC AGTCCGCCTA ACGGATCAAT TTCATCCGCA TGTATTTTCA 60
CTTTAAACC TGGCTTCTTT GGCTTTTGC ATATAATGTT GCGATTGTTT TATTGTAAAT 120
20 ACACCTGTTT CACAGAAAAT ATCCGCAAAG TCTGCATATT GTTTTACTTC CGGAAGTAAC 180
GCAATCATTT CTCTAAAAA TGCCTCATTT GAACTGCCT CTTTAGGTAC AGCATGAGGC 240
CCTAGGAAAG TATGTTTCAT GTCTAAATCA TATTCTCAG CTAAACGATT AGnCACTTTC 300
25 AA 302

(2) INFORMATION FOR SEQ ID NO: 4353:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 411 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4353:

TCTACCGCTG AACTACTTCT GCGGGTGAAG GGAGTCGAAC CCCCACGCCG TAnnTGAGGA 60
TCCTAAGTCT AGTGCCTCTG CCAATTCGC CACACCGCA AATGGTGAGC CATAGAGGAT 120
40 TCGAACCTCT GACCCTCTGA TTAAAAGTCA GATGCTCTAC CAACTGAGCT AAtGGCTCTT 180
CCATGGTGCC GGCCAGAGGA CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA 240
45 CCAATTGAGC TAGGCCGGCA ATATGTAAGA ATAAATGGTG GAGAATGACG GGTTCGAACC 300
GCCGACCCTC TGCTTGTAAG GCAGATGCTC TCCCAGCTGA GCTAATTCTC CnTTTTAAAA 360
CTGCTGGCnA CGGTCTAnTC TAAGGGGACG TAAGGTGAC TACCATCGAC G 411

50 (2) INFORMATION FOR SEQ ID NO: 4354:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 367 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4354:

	TGCTTAGATG CTTTCAGCAC TTATCCCGTC CACACATAGC TACCCAGCTA TGCCGTTGGa	60
10	CGACAACCTGG TACACCAGAG GTATGTCCAT CCCGGTCCTC TCGTACTAAG GACAGCTCCT	120
	CTCAAATTTC CTACGACCAC GACGGATAGG GACCGAACTG TCTCAGCAGC TTCTGAACCC	180
	AGCTCGCGTa CCGCTTTAAT GGGCGAACAG ACAAGCCCTT GGGGACCGAC TACAGCCCCA	240
15	GGATGCGATG AGCCGACATC GAGGTGCCAA ACCTnCCCGT CGATGTGAac TCTTGGGGGA	300
	GATAAGnCTG TTATCCCCGG GGTAACTTTT ATCCGTTGAG CGATGGGCCC TTACCATGCG	360
	GAAACCA	367

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(2) INFORMATION FOR SEQ ID NO: 4355:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4355:

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	GTATTTTAAA TCATAGTGGT TTATGCGTCT TTTTCAAATT CTATAAAAAA TCGGATGACG	60
	TGTAATCTGC CATAGATTAA CACATTCATC CGATTTATAA TAATAAGATA GACTAACATT	120
35	TATTGAGAGC GGGACGGAAA TGATAAAGAA CGACTAATGA TTGATTATGT AGCGATTCTT	180
	TATCATTAGT CACAGCTAAT GTGTACTTAA AAATATGAAT GCATGAGTTA CACTCAnATT	240
	AGAGGAAATA CTAATTTCTA AAGAAAAAGT ATTTCTTTAT GTTGGGGnCC ACCCCAACCTT	300
40	GnCATTTGTCT GTT	313

(2) INFORMATION FOR SEQ ID NO: 4356:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4356:

GGGCTGGGTT CAGAACGTCG AGGCAGTTCG yTCCCTATCC GTCGTGGGCG TAGGAAATTT	60
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TCGTGCCAnG CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AGATCCTGAA 180
 GCATGAAGCC CCCCTCAAGA TGAGATTTCC CAACTTCGGT TATAAGATCC CTCAAAGATG 240
 5 ATGAGGTTAA TAGGTTGAG GTGnGAAGCA TGGTGACAGT GgAGCTGAC GAATACTAAT 300
 CGATCGAGGA CTTAATCAAA ATAAATGTTT TGCGA 335

(2) INFORMATION FOR SEQ ID NO: 4357:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4357:

20 GCTCTAAAAG TTGTATTTTA AAAATAGTTC TTAAATTAT ATACCCACCA CATTGGTGn 60
 nGAACCTAAA AAAAAGCACT TCCCAAAAT GGAAAGTGCA AGTAGTGAGC CATAGAGGAT 120
 TCGAACCTCT GACCCTCTGA TTAAGTCA GATGCTCTAC CAACTGAGCT AATGGCTCTA 180
 25 ATGGCTGGGC TAGCTGGATT CGAACCAACG AGTGACGGAT nAAAGTCCGT TGCCTTACCG 240
 CTTGGCTATA GCCCAATATA TAGATGGTGG AGGGGGGCAG ATTTCGAACTG CCGAACCCGA 300
 AGAG 304

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(2) INFORMATION FOR SEQ ID NO: 4358:

35

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4358:

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ATAATGGTGA CGTTGATGAT GCATTAACAC AAGGTAAAGC AGCAATTGAT GCTATTCAAG 60
 TAGATGCTAC TGTTAAACCT AAAGCGAACC AAGCTATTGA AGTTAAAGCA GAAGATACGA 120
 AAGAATCTAT TGATCAAAGT GACCAGTTAA CTGCTGAAGA AAAAAGTGA GCATTAGCAA 180
 TGATTAAACA AATTACAGAT CAAGCTAAAC AAGGTATTAC TGATGCAACA ACAACTGCTG 240
 AAGTTGAAAA AGCGAAACTC AAGGACTTGA AGCATTGAT AACATTCAnn TCGACTCAnC 300
 AG 302

(2) INFORMATION FOR SEQ ID NO: 4359:

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(A) LENGTH: 350 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4359:

10 GGTGTTGGGAAA TCATTGCATG AGAGTGTGAA AGGGCATAAG GGGAGCTTGG ACTGCGAGAC 60
 CTACAAGTCG AGCAGGGTCG AAAGAGGACT TAGTGATCCG GTGGTTCCGC ATGGAAGGGC 120
 CATCGCTCAA CGGATAAAAG CTACCCCGGG GATAACAGGC TTATCTCCCC CAAGAGTTCA 180
 15 CATCGACGGG GAAGTTTGGC ACCTCGATGT CGGCTCATCG CATCCTGGGG CTGTAGTCGG 240
 TCCCAAGGGT TGGGCTGTTC GCCCATTAAA GCGGTACAnG GCTGGGTTCA GAACGTCGTh 300
 AGAAAGTTCG GTCCCTATCC GTCCTGGGGC GTAGGAAATT ThGAGAGGAG 350

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(2) INFORMATION FOR SEQ ID NO: 4360:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4360:

AGCTCCTAAA AGGTACTCC ACCGGCTTCG GGTGTTACAA ACTCTCGTGG TGTGACGGGC 60
 GGTGTGTACA AGACCCGGGA ACGTATTACG CGTAGCATGC TGATCTACGA TTACTAGCGA 120
 35 TTCCAGCTTC ATGTAGTCGA GTTGCAGACT CACAATCCGA ACTGAGAACA ACTTTATGGG 180
 ATTTGCTTGC ACCTCGnGGT TTCGCTGTCC CTTTGTATTG TCCATTGTCA GCACGTGTGT 240
 AGCCCAAATC ATAAGGGGCA TGATGATTTG GACGTTTCATC CCCAnCTTCC TCCGGnTTGT 300
 40 ACACCGGCAG TTCAACTTAG AGTGCCCAA 329

40

(2) INFORMATION FOR SEQ ID NO: 4361:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 424 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4361:

55 AGACATAAAA AAAGAGACCT CACGGTCTCA ACTTGCTTGG CAACGTTCTA CTCTAGCGGA 60

CThTCCTCTC CTTCGGCTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGGCTCTTT 180
 TCTCGTTTCG TCAGATTCAA ACGTTTTCAC ThCGnCAAGC CATTTTTCTT TGTGTTTACT 240
 5 TTTTATTTTG ACGTTTTAGG CATAAAAAAA wGAGAcCTTG CGGTCTCAAT GCGGCTCATC 300
 GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA CGTAAGTTGG GCTAACAACG 360
 10 TCGCCAAAGA CCTTTCTTGA CTTGTGACAA TCGGCTTGCT TCTTTCCTCT CCTTCGGCTC 420
 TCGC 424

(2) INFORMATION FOR SEQ ID NO: 4362:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4362:

25 CACAACAAGT ATCTAAGATA CTGGCCGAAG ATTGTCACAG ACGGTAGGGG AAGGGGGTCA 60
 CGTGTCAGAC CCAACATGTG GTTCCGGTTC ATnGTTGTTA CGTGTTGGTA AAGAAACGCA 120
 ATThAnTCGT TATTTCCGAC AAGAACGTAA CAATACTACA TACAACTTAG CACCATGAAT 180
 30 ATGTTATTAC ATGATGTGCG TTATGAGAAC TTCGAGATCC GTAATGATGA CACATTGGAA 240
 AATCCAGCCT TTTTAGGCAA TACATTGAT GCGGTTATTG CGAACCATAC AGTGCGAAAT 300
 TGGACAGCAG ATTCCA 316

35

(2) INFORMATION FOR SEQ ID NO: 4363:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4363:

GGGTACTAAG ATGTTTCAGT TCTCCGGGTG TGCCTTCTGA TATGCTATGT ATTCACATAT 60
 CGATAACATG ACATAACTCA TGCTGGGTTT CCCCATTCGG AAATCTCTGG ATCAAAGCTT 120
 50 ACTTACAGCT CCCCAAAGCA TATCGTCGTT AGTAACGTCC TTCATCGGCT TCTAGTGCCA 180
 AGGCATCCAC CGTGCGCCCT TGAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG 240
 55 TTGATTAATC TTGTGGAGTG TTCTTTGAA CATAGCGATT ATnTCTTATG GAATTCAGC 300

(2) INFORMATION FOR SEQ ID NO: 4364:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4364:

```

nTGCACTTAA GAACTTAGAC GATCGTGGTA TCGTTTATAT TGGTGCAGAA GTAAAAGATG      60
GAGATATTTT AGTTGGTAAA GTAACGCCTA AAGGTGTACT GCAGTTAACT GCCGAAGAnA      120
GATTGTCACA TGCAATCTTT GGGTGAAAAA GCACGTGAAG TTAGAGnATA CTTcATTACG      180
TGTACCTCAC GCGCTGGCG GGTATCGTTC TTGCATGTTA AAAGTATTCC AATCGTGCAA      240
GAAGGGCGAC GATACATTAT CCACCTGGTG TTAACCAAT TTAGTACGT GGTATATATC      300
GTTCCAAAAA CGT                                     313

```

(2) INFORMATION FOR SEQ ID NO: 4365:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4365:

```

AACCATTCGA TGCAATAGCG TCATTCTTGG ATATTAATCC CTAAATTGCC GTGATATCCC      60
GCGTCTATCT TGGCCTGTTT CAATCACTAA ATGCGTTTTA CTACTTACAC CACTACGGGC      120
TAGTTAATAG TCCGACATAG CCCTCTGGTA TGCTTACAGC TACATCTGTn TTAATCACTG      180
CCTTTTCTTG TGGCTCAAGT ACGACAGTTC AGCTGAGAAT ATGTCATAAC CTGCATCCGn      240
CTTATGATTT CGTTCGGGCA TTCTAGCATT TTCTGATAAT AGCCTTACTT GTAATGTGTn      300
AGTCATTTTC                                     310

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(2) INFORMATION FOR SEQ ID NO: 4366:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AGTGGTACTT CTGTTAATTG GTGAATTTGG ATACTGGTTA TATTCAGCTG CACCGCAAGC 60
 AACTTCTATT GATGGCCTAA CTGCCTTTTT ACCTCAAGCA ATGGGTATGG TAATTGTTGC 120
 5 AGTCATTTAT GGCTTTATGA ATATGAAAGC AGAGAATCCA TTCCGTAATA AAATTACGTG 180
 GTTACAAATT ATTTACAGGT TCTTCTTTGC ATTTGGTGCT TTAACATATC TTATTTTCAGC 240
 10 ACAACCTAAT ATGAATGGTT TAGCACTGGA TTTATCCTTC TCAACATCCG TGGTGCTGCT 300
 ACATTAAAGG TATTAATTCT TAAACCACAT AAACGTCAAA GAATGGTAAT ACAATCACGG 360
 CTAGTACCAT TTAGTAGCCG CTCCGTACCG nAATTATAAA 400

15 (2) INFORMATION FOR SEQ ID NO: 4367:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4367:

CACCTGGACG AAACGGTTTT AGATCGTATT CAATTGAAAA GGCCGGTATT GAATGAATCA 60
 CACTTAGCAG CGATTGATCA GGAACATTTT AAATTAACCT ATTTATCAAC GGTATATGAA 120
 30 GGGGATTTGG AAGATGCGTT AGAAGCATTG TGCCGAGAAG CAGTGAATGC TGTAACAAG 180
 GCGCTCAAAT TCTAGTGTTA GATGATAGTG GATTAGTTGA TAGCAATGGC TTGCAATGC 240
 CGATGTTACT CGnATAAGT CATGTGCATC AATTACTTAT TAAAGCAGAT TACGnATGnC 300
 35 TACAAATTTA ATCGCTAAAT CTGGTG 326

(2) INFORMATION FOR SEQ ID NO: 4368:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4368:
 ATTATAGCCG AAATGCCCAA AATAGATTTT GACGAATATT ACGAATGGTT GCTTTACTTG 60

50 CATAAATGGC TTTAGGAATA AGCATCAAGT CGCCACCAAG AATAGTAATA TCAGCTGCTT 120
 CAATGGCAAC TTCTGTACCT GTAnCAATGG CGATACCGAT ATCAGCTTTA ACTAATGCAG 180
 GTGCATCATT TACACCGTCA CCAAnCCATCG CAACCTTCTT ACCTTGTTGC TGTAGTTTCG 240

55

GTTTTGC

307

(2) INFORMATION FOR SEQ ID NO: 4369:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 396 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4369:

15	TTCTTTCTCT TCCTCCGGGT ACTAAGATGT TTCAGTTCAC CGGGTGTGCC TTCTGATATG	60
	CTATGTATTC ACATATCGAT AACATGACAT AACTCATGCT GGGTTTCCCC ATTCGGAAAT	120
	CTCTGGATCA AAGCTTACTT ACAGCTCCCC AAAGCATATC GTCGTTAGTA ACGTCCTTCA	180
20	TCGGCTTCTA GTGCCAAGgC ATCCACCGTG CGCCCTTAAT AACTTAATCT ATGTTTCCAT	240
	CCTACAGGAA ACGCGTTATT AATCTTGTGA GTGTTCTTTC GAACAYTAGC GATTATTTCT	300
25	TATGAATTCA AGCTTATTTA AAACCTCTTA TTCAATCGGT TTGCTTGGG TAAAATCCTA	360
	TATTTTACnT ACCnTATCGA GTTTTCAATG TAACAA	396

(2) INFORMATION FOR SEQ ID NO: 4370:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 315 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4370:

40	CAGTAAGATA ATTTTCAATT AGAAAATATC TTAGTGCTGT TCTCTATTTA TACAATACTT	60
	CGTATTGAAT GGCTTCGCTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT	120
	GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACA TGTAATTTTA CTTTACATA	180
45	CTTTTAAAAA ATAAGACACT TTGCCAACT TGCACATAAA TGTTTAATTC AATAATTGA	240
	ATTTTCTGTG TTGGGTCCCT TCGTATAATT TAATAAATAC CACTAAACTA AaTTArTGAA	300
	GTGCCTTATG TATAA	315

(2) INFORMATION FOR SEQ ID NO: 4371:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4371:

5 GTCGTCAAAT GTACCTTCAC CAAGTAGTGA TGTACATATT TACCGCCTTG TTCAACAGCA 60
 CGTGTCGGCG CACCTGTAAT CGCAATGACA GGTATGCGTT CAATATGAA CCTGCGATAC 120
 CGTTGACGGC ACTTAATTCG CCAACACCAA ATGTAGTAAC TAATGCAGCG AGTCCATTAA 180
 10 GACGGGCATA ACCGTCCGCT GCGTAACTTG CGTTTAATTC ATTTGTATTT CCTACCCAAT 240
 CTACAATGGG GTTGCTGATA ATATCGTCTA GAAAAGCGAG ATTAAATCA CCAGGGnCAC 300
 15 CAAAATTTTT ATCGACGGCn TG 322

(2) INFORMATION FOR SEQ ID NO: 4372:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4372:

25 CCTAAGTCTA GTGCGTCTGC CAATCCGCC ACACCCGCAA ATGGTGAGCC ATAGAGGATT 60
 CGAACCTCTG ACCCTCTGAT TAAAGTCAG ATGCTCTACC AACTGAGCnA ATGGCTCTTC 120
 30 CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA GTTTGCTCTA 180
 CCAATTGAGC TAGGCCGGCA ATATGTAAAG AATAAATGGT GGGAGAATGA CGGGTTCGnA 240
 35 ACGGCCGAAC CCTCTGCTTG TAAAGCAGAT GCTCTCCAGC TTGAGCTAAA TCTCCGATTT 300
 AAAACTGCTG GGCAAGTTCT ACTCTAG 327

(2) INFORMATION FOR SEQ ID NO: 4373:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4373:

50 CATTTTAATT TATTGTACAG AACGAAATGT GATGTTAGTA GATCATAGGG TTGATGATAA 60
 TATTAAAGCT GAAAACGTTA TATTTATTTG CCTTTTGTGT AAACATGGAC ATTGGCATGC 120
 AGTCATTTAT GACATTGCTC AAGACAAAAC TGCCGAACTC GAAATTGAAA ATATTATAGA 180

55

TCAATTTTTA AACCCCATCG ATTCCTAAAA AACAGCAGTA AGATGATTTT CAATTAGAAA 300
 ATATCTTGCT GCTGTTCTCT ATTTATACAA TACTTCGTAT TGAATGGCTC GCTTTCCCAG 360
 5 GGnGCCGCTC AGCCTGGGCC TCGACTGGCA ATGCTCCCTC 400

(2) INFORMATION FOR SEQ ID NO: 4374:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4374:

TAATGGATTT TTTAGTGTG GTGTCGTTAT TGTCTTCTCA CCTTTTGTG CTTCTCTTGT 60
 20 TACTTTTTCT GTCCCTGGTG CTAAATCAGG ATTAATTTA CGTTCCTTCT CGAATGGAAT 120
 CTCTCTTTT TCTACAATCG AGTCTCCTT TACAGGTCCA TATTTTGTTA CGCTATCGAC 180
 CGGTGGTCTA ACTACATCTC CTGTTTCTGG ATTCTTAATT CCTGGTTTAC CTGGGAACTT 240
 25 CCTCTTCTC TCCTGTTGGT AACTTCGGGA TCAAATTCGT CTCGATGGAC CTGGTGTGTA 300
 nCGTTTCTGG GTCCGnAAGT CTGTnGAATT GCAG 334

(2) INFORMATION FOR SEQ ID NO: 4375:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4375:

ATACATGCAA GTCGAGCGAA CGGACGAGAA GCTTGCTTnG TGAATGTTAG CGGCGGACGG 60
 GTGAGTAACA CTGGATAACC TACCTATAAG ACTGGGATAA CTTCGGGAAA CCGnAGCTAA 120
 TACCGGATAA TATTTTGAAC CGCATGGTnA AAGCTTGCAA AGACGGTCTT GCTGTCACTT 180
 45 ATAGATGGAT CCGCGCTGCA TTAGCTAGTT GGTAAGGTAA CGGCTTACCA AGGCAACGAT 240
 GCATAGCCGA CCTGAGAGGG TGATCGGCCA CACTGGAACCT GAGACACGGT CCAGACTCCT 300
 50 ACGGG 305

(2) INFORMATION FOR SEQ ID NO: 4376:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4376:

	GATAAAGTGA AAGAACTCGG ACGTGACACC TATTGCACGA TTCGTTGGTT TTAAGGCAGT	60
10	AGGCGTTGAC CCGAAAATTA TGGGTATTGG GCCTGGCATA TGCATTTCCT GAAGTATTGT	120
	CACTCAGCAA TCTATCTGTT GAAGACATTG ATTTGATCGA ATTGAACGAn CATTTGCTCT	180
	CAAACGATTG CATCTATTAA AGAAGTAGGT CTAGATATAT CACGTACGAA TGTGAATGnT	240
15	GGCGCTATTG CTTTAGGTCA TCCATTAGGT GCTACAGGCG CAATGTTAAC CGCGCGTTTA	300
	CTTAA	305

20

(2) INFORMATION FOR SEQ ID NO: 4377:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4377:

30	AATGTCTTCT ACCCCATCAC AGCTCAGCCT TGAACGAGTA CCGGGTTTGn CCTAATACTC	60
	AGACCTTGAC TGCTTAGACG TGACAATCCA ATACGACACG CTTCGCCTAT CCTACTGCGT	120
	CCCCCATCG ATTAAACGA TTATAGGTGG TACAGGAAAT ATCAACCTGT TATCCATCGC	180
35	CTACGCCTGT CGGCCTCAGC TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG	240
	GAAACCTTAG TCAATCGGTG GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT	300
40	TCTCACTTCT AAGCGCTCCA CATG	324

40

(2) INFORMATION FOR SEQ ID NO: 4378:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4378:

	CATCATGCTT AGAAAACGCT TAATTTAGGT TTTGACTTTT TAATCAGAGT ATATAAGCAA	60
	AACTTATCAT ACAGGTAAGG TGTAATAAGT ATTTTATTATT AATTGAGAAT AATTATCAAT	120

55

TGGCACCAAA CTTTAATATT TTTTCAATG TCATTCTTTT GATGGGAGTG GGACAGAAAT 240
 GATATTTTCG CAAAATTTAT TTCGTCGTCC CACCCCAACT TGCATTGTCT GTAGAAATTG 300
 5 GGAATCCCA ATTCCTCCTT GGTGGGGGCC CATCCCCACC TTGCACATAA TGGnAGCnGG 360
 ACCTTTCCGC CGCTCCGGGG TGGGGGCCTC nACCCCAATC 400

(2) INFORMATION FOR SEQ ID NO: 4379:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4379:

20 ATAAATATA TCACTTGAAA AATTTTCATGT AGAAAAGATG ATGGATAGGC TATAAAGTAA 60
 TTGTGACTGA GATGAACTTT TATGTCTTAG AACTACAAC ACTATATTGG CAGTAGTTGA 120
 CTGCGGGGCC CCAACATAGA GCAAATTGGA TTCCCAATTT CTACAGACAA TGCAAGTTGG 180
 25 GGTGGGGCCC AACATGAAAG AAATACTTTT TCTTTAGAAA TTAGTATTTT TTATGCATGA 240
 GTGTACTCAT GTTGCATTAA TTTTnAGTA CACATTAGCT GTGGACTAAT GATAAAGGnn 300
 TCGCTACATA ATCCATCCAT TAGGTCGTTC CTTGATTCAT TCCCT 345
 30

(2) INFORMATION FOR SEQ ID NO: 4380:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4380:

CTAAAGCTGn CATATGCGGC TGCCGATGA AGCCAACCCT GCTGCTGTTG GTACAAAATT 60
 GTCGCTTTCA ATTTCTGCAT ACCAATCGAT GCCAGCTCTA TTTCTGACAA TATCCATATA 120
 45 TTTTGAAATT TTCTCTAATT CTTTGCCACT AACCTTTTCA CCATTCAACC AAAATTGATC 180
 CTGTGTTAAC TGGTCGTTAA AAGTGACTTT CGTTTCAGTG TAAAATTTTT CTAATGTAAC 240
 AGATATGCTA TTATTCATGG AAGATTAGTG CTTTCATCTT TTTACCCCAA TATTTTATAA 300
 50 GTGCAATATC GTAGTCAGG CTTGCCACTT TAACACGCAT AACTCCTAAA TCTCAACCAG 360
 ATn 363

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4381:

ACCTGAATGA CTCAAACCTTG ACTTTnCGAC AATTGACTGT nCATTTTGCA TAGTTGTATG 60
 nCTCCATnCGA GTAATTATTA GATTGTTCG CTTACGTCTA TTGAATCATA CAGCTTTATT 120
 ATAGTTAGCG TATTTCGACC TTTGCACATT AAACCATGTT TAATAATCAT TGAATCATT 180
 TTAAGTAAAT TAAGGAATCT ATAATGTTCG TTAAATAAAA CTGATCCCGT TGTGGCTTCA 240
 CACCCGATAG ATAGGGATTT ACAGATAAAT TCAGGTCTCT TCCACGTCCA TATTGGGAC 300
 CCATCGAAAA TCGGGTTCTC AAATCATCGA ACATAACAAA AGAAGCTAAG CAACAGTAGG 360
 GCCGTTGTCA CTTAACTTCT GTTTTCCGA TGACAGCTTC 400

(2) INFORMATION FOR SEQ ID NO: 4382:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4382:

GnACTACAAA GCAATGGGGT TTGCCAGTTT CTTTATTTAC TGACGAATAC TGGCAATGAC 60
 ATCAGATACA TGTGGCAnCA CCAATCCATT TCTTTTCACC ATTGATAACC CAAGTATCGC 120
 CTTGGGTTGC AGGGACTGTT TCAAGACCTC CCGCAACGTC CGAACCGTGT TCTGGTTCAG 180
 TTAAAGCAAA GCATGTTACG CnTTCATGTG AACTGTAATT TAGGTACATA TTTCGCAATT 240
 TGTTCTTTGC TACCTCCGAA ATAGAAAGTG TTATGCCCTA AACCTTGGTG AACACCGAGT 300
 AGGG 304

(2) INFORMATION FOR SEQ ID NO: 4383:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GTGCATTATT TTGGAGAATT AGCTCAGCTG GGAGAGCATC TGCCTTACAA GCAGAGGGTC 60
 GGGCGTTCGA ACCCGTCATT CTCCACCATT TTGATTATTA AATTATATGA ATAAGCTGGA 120
 5 GGGGTAGCGA ATGGCTAAAC GCGGCGGACT GTAAATCCGC TCCTTCGGGT TCGGCAGTTC 180
 GAATCTGCCC CCCTCCACCA TCTATATATT GGGCTATAnC CAAGCGGTAA GGCAACGGAC 240
 10 TTTGACTCCG TCACTCGTTG GTTCGAATCC AnCTAGCCCA GCCATTAGAG nCATTAACTC 300
 AGTTGGTA 308

(2) INFORMATION FOR SEQ ID NO: 4384:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4384:

AATTTTGGCC AAAACACCCA TCCGCTGTAA CTTCAGAGTG TCATTGGCAT TTATTACACT 60
 25 ATCTCCAACCT CCTAGTGGAA CAACCACATC TCGTCCTTGG GGTGCATGGA ATGTTCCGTC 120
 AGCCCTGTGA ATTATTTCTT GAACTCCACC ACCTGGGGCG TTTCCAGAAC CTCTATCATT 180
 30 TAATACAGCA AATGTCGGTT GCGTTAATGC TCCTGAATTA TCGGKAGCTA CACCCCTTTC 240
 TGCTAAAGTA CCAGTAGACA ATGTAGGTAT TGGCTTGATG AGATTtTAT CAGTAATGGC 300
 TTTAGAnAT 309

35 (2) INFORMATION FOR SEQ ID NO: 4385:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4385:

45 AAAGGTGAAA AGCACCCCGG AAGGnAGGTG AAATAGAACC TGAAACCGTG TGCTTACAAG 60
 TAGTCAGAGC CCGTTAATGG GTGATGGCGT GCCTTTTGTA GAATGAACCG GCGAGTTACG 120
 50 ATTTGATGCA AGGTTAAGCA GTAAATGTGG AGCCGTAGCA nAACAGGTCT GAATAGGGCG 180
 TTTAGTATTT GGTCGTAGCC GAnAACCAGG TGATCTACCC TTGGTCAGGT TGAATTCACT 240
 AACACTGAAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA ACTGAAGGTA 300

55

(2) INFORMATION FOR SEQ ID NO: 4386:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4386:

TAGAATCTTC ATCAATATGA TCTAACCAAT ATTGATAAAA CCTTGATGTG TTTCGTGTCA	60
ATGACATACC ATATCGACTA GGTACCTTTT TAGAATGTTG ATTAATCAnG GCAAATATCA	120
TGGCAAGGTC ATCTTCAAAA TGATTGATT CAAGTGAAG GCATATGACG TCTCATCACT	180
ATACCCTTTT TCCCATTCTG CAAATCCACC ATAAATACTA CGCGACGCGG AACCCGGACC	240
CATTCGCGGC AATCTCGGTh AATCCTTATC TGGACAGCTG GCATGTCTAG CGGCTGGATT	300
TACAAGCTGG CTGGCTAAAG CTGGCATATG CGCTTGCCGG TTGAAGCCCA ACCTGGCTGG	360
CTGGTGGGGn ACAAATTGGT CGCTTTTCAA TTTCnGGCAT	400

(2) INFORMATION FOR SEQ ID NO: 4387:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4387:

TCAATTTATG GGGCATTATG ACTTTATATA CCTAAAATAC TATTAAGAAG TCCTGAAAAA	60
TTACATTAG CAGTTGGATT GTTCAACTTT ATTAATGATA AGTATGCAAA TAATTTACA	120
GTGTTTGCAG CAGGGGCAAT TATGATTGCA GTACCTATAG CAATCGTATT CTTGTTCTTG	180
CAACGCTATT TAGTATCAGG TTTAACAACA GGTGCGACAA AAGGTTAGTT TGAAATTCnC	240
GnGTGGGGCA GAATTGATAA AGAACCACnA ATGACGATAA AGATTAAAAG GAGGACGTTA	300
TGGATGACGA	310

(2) INFORMATION FOR SEQ ID NO: 4388:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 310 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4388:

AACATCATGC TGATGTTGTT GAATATGAAG AAGATACAAA CCCAGGTGGT GGTGAGGTTA 60
 5 CTA CTAGTGC TAACCTAGTT GAATTTGACG AGATTCTACA AAAGGTATTG TAACTGGTGC 120
 TGTTAGCGAT nCATACAACA ATTGAAGATA CGAAAGAATA TACGACTGAA GTAATCTGAT 180
 10 TGA ACTAGTA GATGAACTAC CTGAGGAACA TGGTCAAGCG CAAGGACCCA TTCGAGGAAA 240
 TTACTGGAAA ACATCATCAT ATTTCTCATC nGGTTTAGGn ACTGAAATGG TCACGGTAAT 300
 TTTGGCGTGG 310

(2) INFORMATION FOR SEQ ID NO: 4389:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 302 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4389:

25 TTTACCATAT CATCCACTAT TTATTAAACC TAATAAGAT GAATTAGAAG TGATGTTTAA 60
 TACAACAGTG AACTCAGACA CAGATGTTAT TAAATATGGT CGTTTGTTAG TTGATAAAGG 120
 TCGCAATCT GTTATTGTCT CGCTTGGCnG TGGATGGTGC TATTTATATT GATAAnGAAA 180
 30 TCAGTATTAA AGCAGTTAAT CCACAAGGGA AAGTGTTAA TACAGTTGGC TCTGGTGATA 240
 GTACAGTTGC AGGCATGGTG GCTGGGAATT GCTTCAGGTT TAACGnTTGA AAAGGCATTC 300
 35 CA 302

(2) INFORMATION FOR SEQ ID NO: 4390:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4390:

AAAGAGTGCG TAATAGCTCA CTAGTCGAGT GACTGCGC CGAAAATGTA CCGGGGCTAA 60
 50 ACATATTACC GAAGCTGTGG ATTGTCCTTT GGACAATGGT AGGAGAGCGT TCTAAGGGCG 120
 TTGAAGCATG ATCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG 180
 CGAAAGACGG GTGAGAATCC CGTCCACCGA TTGACTAAGG TTTCCAGAGG AAGGCTCGTC 240

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TnCTTACCA CCTATAATCG nTTAATCGTG GGG

333

(2) INFORMATION FOR SEQ ID NO: 4391:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 306 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4391:

AGTGCGTTTG TGCACAnACT TGACTIONAAC TTAGTGCCAT TGCAGCACCA GCAACCCATG	60
GCGCAATAAG CCCAATGCAG CTATAGGGAT ACCGnCAATA TTATAGCCGA ATGCCCCAAA	120
TAGATTTTGA CGAATATTAC GAATGGTTGC TTTACTTGCA TAAATGGCTT TAGGAATAAG	180
CATCAAGTCG CCACCAAGAA TAGTAATATC AGCTGCTTCA ATGGCAACTT CTGTACCTGT	240
ACCAATGGCG ATACCGATAT CAGCTTTAAC TAATGCAGGT GCATCATTTA CACCGTCACC	300
AACCAT	306

(2) INFORMATION FOR SEQ ID NO: 4392:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 355 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4392:

TACGGTATGC ATATCTTTTA AAACCTATTC TTTTGTTATT AGGACATATA AATTCATCAT	60
TAAGTTCGTC ATATTTCCAA TTITAAGTGT TGAAATGTC ACTTTTAAAC TTTCTAGTTT	120
TATCTTTAAT AAACATGCCA TACGTAATAA GTGGCGTTT ATTAAATCA TCTATAATAG	180
CCATATAGTT TTGCTCACTA CCATAACCTG CATCAGCTAC AATATACTCC GGTAAATAAC	240
CGAAGGGATT TTGAATCATT GTTAAAAATG GAATTAAAGT TCTAGTATCT GTTGGGTTTT	300
GAATAGGGTC ATGGGATAAA CCAAATGnGG AATTTGCCnC AATTnGTAAA TGGAA	355

(2) INFORMATION FOR SEQ ID NO: 4393:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 364 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4393:

5 CATTCCGTAA TAAAATTACG TGGTTACAAA TTATTTTCAGG TTTCTTCTTT GCATTGCGTG 60
 CTTTAACATA TCTTATTTCA GCACAACCTA ATATGAATGG TTTAGCAACT GGATTTATTC 120
 TTTCTCAAAC ATCCGTTGTG CTTGCTACAT TAACTGGTAT TTATTTCTTA AAACAACATA 180
 10 AAACGTCAAA AGAAATGGTT ATTACAATCA TCGGCTTAGT ACTCATTTTA GTAGCCGCTT 240
 CTGTTACAGT ATTTATAAAA TAAGGAGTGT AGATGTCATG AAAAAATCAG CGGTTTAAAT 300
 GGAACCTATT CCAAAGCCAT CGCGACCAAT GGGTCATTTG GATTAnTAAC GATAATGGCG 360
 15 nnGG 364

(2) INFORMATION FOR SEQ ID NO: 4394:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4394:

GATTAAACG ATTATAGGTG GTACAGGAAT ATCAACCTGT TATCCATCGC CTACGCCTGT 60
 30 CGGCCTCAGC TTAGGACCCG ACTAACCCAG GAnCGGACGA GCCTTCCTCT GGAAACCTTA 120
 GTCAATCGGT GGACGGGATT CTCACCCGTC TTTGCTACT CACACCGGCA TTCTCACTTC 180
 TAAGCGCTCC ACATGTCCTT ACGATCATGC TTCAACGCC TTAGAAGCT CTCCTAnCAT 240
 35 TGTGCCAAAG GACATGCCAC AGCTTCGGTG AATATGTTTA GCCCCGGTAC ATTTTCGGCG 300
 CATGTnCACT CGACT 315

(2) INFORMATION FOR SEQ ID NO: 4395:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 322 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4395:

50 AGCCCCAAA TGGGTATTGA AATTGAATGG TGGGnCTGA AnTGGACTCG AACCACCGAC 60
 CTCACGCTTA TCAGGCGTGC GCTCTAACCA GCTGAGCTAT AGGCCCATTA ATTTGAATGA 120
 ACAACATTC AAAACTGAAT ACAATATGTC ACGTTATTCC GCATCTTCTG AAGAAGATGT 180

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TACGACTTCA CCCCAATCAT TTGTCCCACC TTCGACGGCT AGCTCCTAAA AGGTTACTCC 300
 ACCGGCTTCG GGTGTTACAA AC 322

5 (2) INFORMATION FOR SEQ ID NO: 4396:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4396:

TGGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC 60
 AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 120
 20 GTTTTAGACA TAAAAAAGA nACCTCACGG TCCAACTTG CCTGGCAACG TTCTACTCTA 180
 GCGGAAnTGA ATTGGCTACC ATCGnCGCTA AAGACCTTTC TTGACTTGTG ACAATCGCTT 240
 GCTTCTTTCC TCTCCTTCGG CTCTCGCTTA CTCATTAGC TCTACTAAAC TCGTTGCGCT 300
 25 CTT 303

(2) INFORMATION FOR SEQ ID NO: 4397:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 377 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4397:

TAAGAATATA AATGATTTTG AAAGCATTTG AAAGCTACAA CATTCTATA AAATTTTTCa 60
 40 ATAACAATTG CGCCACTAAA ACTCAAAATT TCCACCACCA ACATCCAAAT TATCAACATC 120
 GCAACATAAC CAAATGTTAT AATAAATCTA TTACACAAAG AGATAAATTA CTTATGCAAA 180
 GGCGGAGGAA TCACATGTCT ATTACTGAAA AACACGTCA GCAACAAGCT GAATTACATA 240
 45 AAAAATTATG GTCGATTGCG AATGATTTAA GAGGGACATG GATGCGAGTG AATTCCGTAA 300
 TTACATTTTA GGCTTGATTT TCCTATCGCn TCCTTATCTG GAAAAAnCCG ACCAGGATnT 360
 GCAGATGCCT GGCCAGG 377

50 (2) INFORMATION FOR SEQ ID NO: 4398:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4398:

	TGCAATAACA GTATCTATGC CTACTTGTTT TGCAATGGCT TGAGCAGTGT TTTTATTATC	60
10	GCCAGTTAAC ATGGGCAACT TCAATGCCCA TATCATGGCA ATTGTTTTAT AGCATCTTTG	120
	GGCATGATnT TTGACAGTAT CTGCCACTGC GATGATACCA GTTAATGAAT AATTAACAGC	180
	AATGAGCATA nCAGTTTTAC CATCTCGTTC ATAATGTGTT AAATCATCAG AAATATGCTT	240
15	AAGCAACTAA TATCATTGTC AACCATTAAAT TTACCGTTAC CAACCAATAT ATGGTGATGA	300
	TnATCCTTC CTC	313

(2) INFORMATION FOR SEQ ID NO: 4399:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4399:

30	TGGCTATGAT CATCCAAAAT ATGGTGAATC AATGCTGCA GCCATTATAC TTCGCGAAGA	60
	TGAACCTCAT TACGCTGAAA TTTTAAATCA ACATATGCGA AGTCGTTTAG CAGGTTATAA	120
	AGTCCCAAGA ATGTATGTAC CAGTGACACA TATGCCGTTA AACAGTACGC AGAAACCAGA	180
35	TAAACTTTCG ATTCGACAAA TGATGAATGA CAAAGTCTCG CAAACACTTT AAAGGTGATA	240
	AAAATTTTTG ACATTTAGTG TAAGCGTTTA CAAATAAAGC GTGTTGTTTT TGAATTAAAT	300
	GCATTTTACA TTAGTATTCA TATTATnTTT AGGAGGAATT TATATGACAT TTGAAAAGA	360
40	ACGGGCTTAA AACATTATTC CTGAGATGTA CTAGTATGCT	400

(2) INFORMATION FOR SEQ ID NO: 4400:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 409 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4400:

	CTCATTTAGC TCTACTAAAC TCGTTGCGCT CTTTTCTCGT TTCGTCAGAT TCAAACGTTT	60
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AAAAGAGACC TCgtCTCAAC TTGCCTGGCA ACGTTCTACT CTAGCGGAAC GTAAGTTGGC 180
 TACCATCGTC GCTAAAGACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 240
 5 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACGCTTG CGCTCTTTTC TCGTTTCGTC 300
 ArATTCAAAC GtTTTCacTT CGGCCAAGGC ATTTTCTTT GTGGTTACTT TTTAATTG 360
 10 ACGGTTTTAG GCATAAAAAA AAAGGGGACC CTGCGGGCTC nAAAGGGG 409

(2) INFORMATION FOR SEQ ID NO: 4401:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 311 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4401:

TCATGTAGAC TTTCAAGAAT CGACACATGA AAATTCAAAA CATCATGCTG ATGTTGTTGA 60
 ATATGAAGAA GATACAAACC CAGGTGGTGG TCAGGTTACT ACTGAGTCTA ACCTAGTTGA 120
 25 ATTTGACGAA GATTCTACAA AAGGTATTGT AACTGGTGCT GTTAGCGATC ATACAACAAT 180
 TGAAGATACG AAAGAATATA CGACTGACAT nnATCTGATT GAACTAGTAG ATGAACTACC 240
 TGGAAGAACA TGGTCCAAGC GCAAGGnCCA ATCCGAGGAA ATTGACTGGA AAACAATCCA 300
 30 TCCATATTTT C 311

(2) INFORMATION FOR SEQ ID NO: 4402:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4402:

TTAACGGATT ATTTGGCAAT TCGGTTAGTT GTCGAACAAT TGCTAGTTGG TGATGAGTTT 60
 45 AAGTCAGTCG CTAAAGATTG TGAAAGTAGA TCGGAAAATT GGTTTAAGCA AACTGTTGCA 120
 TCATGGTGTT ACTACAGTGA TATGCCTAGC GATGTATTAC TACAACATGG ACGTCAATGT 180
 AAATThCAAA CGTTTATTCA TTTTGGCAGC AACTATGGAA TAAAAATGTA TTTAAAAATT 240
 50 TATGGCTAAT TGCCTGGGGA AATGACATAC GAATCTCAGG TTAAACAGA AAATTAAAGC 300
 AGGTCCATGT nAAGTGTGGG CGGGnCGCAT 330

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4403:

10 TGNTCACACA TAATTTGCGG CCATATGTTG TTGGCACTGG CCGTTTTGAT TATCTGGCAC 60
 TTTGGGCCCA TATGTTGnCA AAATACGCGC CAATTGCTTC TTTATAAGTT GTTATTTTTT 120
 15 TACTTTTTCC ATCGATAAGC CATACCTCTG GATGATACAT ATGATGCCCC ATCGCAGACC 180
 AATAGCGAAA TTCACCCGTT AAAGTTTCGA GCTCTGATAA TTGTATAGAC CATTGATGAT 240
 TTTGAGGTGG TACTTGATAT AAATTTCTT CTCTAAAATA TTCATTTAAA ATGCGTTCGA 300
 20 TAGCCGCATA CGCTGCCATG TTGTATTAAT CnTTAATTTG 340

(2) INFORMATION FOR SEQ ID NO: 4404:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4404:

30 TTAACATATA TTTTGGGACC TTAGCTGGTG GTCTGGGCTG TTTCCCTnnA CGAACACGGA 60
 CTTATCACC CATGTTCTGA CTCCCAAGTT AAATTAATTG GCATTGCGAG TTTGTCTGAA 120
 35 TTCGGTAACC CGAGAGGGGC CCCTCGTGCC AAACAGTGCT CTACCTCAA TAATCATCAC 180
 TTGAGGCTAG CCCTGAAAGC TATTTGCGGA GAGAACCAGC TGATTTCAG GTTCGATTGG 240
 40 AATTTCTCCG CTACCCTCAG TTCATCCGCT CACTTTTCCA ACGTnAATCG GTTCGGTGCC 300
 TGCCATT 307

(2) INFORMATION FOR SEQ ID NO: 4405:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4405:

AnACTTGAGT GCAGAAGAGG AAAGTGAAT TCCATGTGTA GCGGTGAAAT GCGCAGAGAT 120
 ATGGAGGAAC ACCAGTGGGC GAAGGCGACT TTCTGGTCTG TAACTGACGC TGATGTGCGA 180
 5 AACGTGnGGG ATCAAACAGG ATTAGATACC CTGGTAGTCC ACGCCGTAAA CGATGAGTGC 240
 TAAGTGTTAG GGGGTTTCCG CCCCTTGAGT GCTGnCAGCT AAACGCATTA AGCACTCCGC 300
 CTGGGGGAGT GACGGACCGC AAG 323

(2) INFORMATION FOR SEQ ID NO: 4406:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4406:

AATTATGGGA TGCAATGGGA TACGAACGTG TTAAACACG TATGGAAGAC GAACTTGGAG 60
 ACTTACCACA ATGGATTAGT GATTTAGATG GTGGCTTTTA TAAACAAGAT GAGACCATTG 120
 25 AATATGCAAC ACCTATTTCT CACTTCGTAA AAGATGAACT TTGGGATAAA GGTGATGCCA 180
 AACTTTCCGT AACTCATGAT GATCAACTGT TACTGAAATT ACAAAGTAAA AATAATGTCA 240
 TTACCGATGA ATTCAACGGT GCGTTAGTTG ATGCGATTGA TTTACTGGGA AATGACCCTT 300
 30 ACnChAGnAT GGGTA 315

(2) INFORMATION FOR SEQ ID NO: 4407:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4407:

CACCACCTCC CTACCTACTC GCGCCCATC ATAAATAGG TGGACAGGAA TATCAACCTG 60
 45 TTATCCATCG CCTACCCTGT CGCTCAGCT TAGGACCGCA CTAACCCAGA GCGGACGAGC 120
 CTTCTCTGG AAACCTTAnT CAATCGGTGG ACGGGATTCT CACCGTCTT TCGCTACTCA 180
 CACCGGCATT CTCACTTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT 240
 50 AGAACGCTCT CCTACCATTG TCCAAAGGAA TChCACAGCT TCGGTAATAT GTTTAGCCCC 300
 GGTACATTTT CGGCGCATGT CACTCGACTA nTG 333

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 393 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4408:

ATTTAATGAA GTGCTTGTTA ATGAACCAAG CGTAAAGAT ACTGTTGAAA TTTTAAAAGG	60
TATTCGCGAA AAATTCTGAAG AACACCATCA AGTAAAATTA CCAGATGACG TATTAAAAGC	120
ATGTGTTGAC TTATCAATTC AATATATTCC ACAACGATTA TTACCAGATA AAGCAATCGA	180
TGTGTTAGAT ATTACAGCAG CACATTTATC TCGCGAAAGT CCCAGCTGTC GATAAAGGTT	240
GAAACTGAAA AACGGATTTC TGGATTTnGA AAATGATAAA CGTAAAGCAG TAAGTGCTTG	300
AAGGGATTTT AAAAAAGCTG ACGGACCATT CCAAAATTGG AATCCAAATC nnTTACCAGG	360
TTAAATTTGG GAAAATGGTT AATTGGTGGG ACC	393

(2) INFORMATION FOR SEQ ID NO: 4409:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 319 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4409:

GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT CATTTAGCTC	60
TACTAAACTC GTTGCCTCTT TTTCTCGTTT CGTCAGATTC AAACGTTTTTC ACTTCGCCAA	120
GCCATTTTTTC TTTGTGTTTA CTTTTTATTT TGACGTTTTTA GGCATAAAAA AAAGAGACCT	180
TGCGGTCTCA ATGCGGCTCA TCGCATCCAT TTTTGCCTG GCAACGTTCT ACTCTAGCGG	240
AAGTnAATTG GGCTACCATC GTCGCTAAAG ACCTTTCTTG ACTTGTGGAC AATCGCTTGG	300
CnTCTnTCCT CTCCTTCGG	319

(2) INFORMATION FOR SEQ ID NO: 4410:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

AATTAAACAT TTCATTTTAA TCAATGAGAC TAAnATACGC CTAAC TTCGT TAACTTTTAA 60
 AATGTATTAA AATTCTAAAG TTTCTTTTGC TTTTTCnATG ATGTCATTTT TGTTTGGTAA 120
 5 CCAAACATTT TCAGCTTGAG TGAATGGATA AATTGTATCT GCCTGCCTGA ACTCTTCCAA 180
 TAGGTGCTTC TAATGAAAGG ATTGCACGTC ACTTAATTCA GCTAACAACT GCTGCACCAA 240
 CACCAGCTTG CnGTTGTGCT TCTTGACTAC AAAGTACGA CCAGTTTTTC AACTGAGCAC 300
 10 AATTGTGCAC ATCGATTGGT GACAG 325

(2) INFORMATION FOR SEQ ID NO: 4411:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4411:

GAGTTGGACA ATGCCGAAGC GTGAGCAAAG TTTTACCAT GCATGGTTGC ATTTAGCGCA 60
 25 ACATGACCAT AGTTTTACTA AAGCACAGCG CCAAGTGATT AAAGGCTTAC CCAATGATCC 120
 TGAAATGACG ATAGAGTCAG TATTAECTCA TTTTCAATA GATCAGGAAG ACTAnCAAGC 180
 TTATGTTGAA GGACATCTTT TGGCGTTACC GGGTTnGGCA nGTATGTTGT ATTACCGTTC 240
 30 ACCACAGCAT CACTTTGAAC CACCTTTGTT AACGGGTAA TTGGCCATTC GGGTAAGTTG 300
 TCCGACCATT GCCAAGTGGG TGATGAGTTn AGGCCAGTCC GCAAAAGATT GGGAAAGTAG 360
 TCCGAAAAT GGGTTAAGCC AACCTGTTGC CATCCAGGGG 400

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(2) INFORMATION FOR SEQ ID NO: 4412:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 369 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4412:

45 GATATATGGC AGCTCAAAGG AATGGGTTTC AGTTGAAGTG AAATTATCAC AGTCACTAGA 60
 CCCGAGCACA TTATTTATC TCACTGACAA TGAGGCAGGA GATCGCTTTT ATATGCGTTT 120
 50 GAATGATAAT CGAACGTCAT ATTTGGCTA CAAAGCAATT CAATTATTCA AAAATAATTC 180
 TAAAAATAAA CAATCTATTT TAAAAGACTG GGGAAAATTA AACATAACCA TCACCATTTA 240

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CCATAAATCA GATGATGAAT GGCGnGAGTT TGGCCTAAAn CATTGGAAT ACCCGGAGTT 360
TTAATTCCA 369

5 (2) INFORMATION FOR SEQ ID NO: 4413:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4413:

15 TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 60
 TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACCTCGTTG CGCTCTTTTC TCGTTTCGTC 120
 20 AGATTCAAAC GTTTTCACCT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TTATTTTGAC 180
 GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG TTCnACTCTA 240
 GCGGAAGTAA GTGGGCTACC ATCGTCGCTA AAGACCTTTC TTGGACTTGT GGACAAncGC 300
 25 TTGCGTCCTT ncCTC 315

(2) INFORMATION FOR SEQ ID NO: 4414:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4414:

GACCATCTCC TAAGGCTAAA TACTCTCTAG TGACCGATAG TGAACCACTA CCGTGAGGAA 60
 AGGTGAAAAG CACCCCGGAA GGAGGTGAAA TAGAACCTGC AAACCGTGTG CTTACAAGTA 120
 40 GTCAGAGCCC GTTAATGGGT GATGGCGTGC CTTTGTAGA ATGAACCGGC GAGTTACGAT 180
 TTGATGCAAG GTTAAGCAGT AAATGTGGAG CCGTAGCAGA ACAGGGTCTG GAATAGGGCG 240
 TTTAGTATTT GGTCGTAnCC GnAAACCAGG TGATCTACCC TTGGTCCAGT TGAAGTTCAG 300
 45 GTTnACACT 309

(2) INFORMATION FOR SEQ ID NO: 4415:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4415:

5 TTTATTATAC TTTACATTTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT CGCCAAGCCA 60
 TCTTTCTTTG TGTTTGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTTGCGGT 120
 CTCAAATGCG GTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAAnTA 180
 10 AGTTCGGACT ACCATCGACG CTAAGGAGCT TAACTTCTGT GTTCGGCATG GGAACAGGTG 240
 TGACCTCCTT GGCTATAGTC ACCAGnACAT ATGAATGTGA AATTTATACA TTCAAAACTn 300

(2) INFORMATION FOR SEQ ID NO: 4416:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4416:

25 AGAAAAATAA GCGAACTGnA ATAAATAAAG ATTCAATTAA CGCATCAGTA TTAGGATTCA 60
 CTCTAAAACG ATTAATAGTT TTATAAGAAG GTGTTTGATC TTGAGCTAAC CACATCATTC 120
 GAATACTGTC ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT TGAGTATATG 180
 30 CATATAAGAT GATTTTTAAC ATCATCTTTG GATGATAGGA TGTTCGCGCA CGATGATGTC 240
 TGAATTCATC GAATTTGCTA TCAGGTATCG TTTCAACAAT TTCATT 286

(2) INFORMATION FOR SEQ ID NO: 4417:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4417:

45 TTTGATAAAA ATGGGCCATC GTCACGAGCT TCAACAATTC GTTTCGCAAC GTTTTCGCCA 60
 AGCCCAGCCT GATATATTAC ATGAGGAGCG GTGCAATGT TGTTAGAAAT TAAAGATTTA 120
 GTGTATAAAG CGAGCGATAG AATCATACTA GATCATATCA GTCTAAAAGT AGATAAAGGC 180
 50 GAGAGTATTG CCATTATAGG TCCATCAGGT AGTGGTAAAA GTACATTTC AAGCAAATA 240
 TGTAATTTGT TTAGTCCAAC TAGTGGAGAA CTTTATTTTA AAGGTAAACC CTATAATGAT 300

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GTTTGGTGGA ACGnATTGGA nGATAACCAT GGATAATTCC

400

(2) INFORMATION FOR SEQ ID NO: 4418:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4418:

15 GTATTTACAA TCAAACTAAG CAAAAGTATT CAGATGCCTC AGATAAAGCT TGGGCGCATT 60
 CAAAATCTAT TTGGAGAGGC ACATCAAAAT GGTTTAGCAA CGCATATAAA AGTGCAAAGG 120
 GTTGGCTAAT AGATATGGCT AATAAATCGC GCTCGAAATG GGATAATATT TCTAGTACAG 180
 20 CATGGTCGAA TGCAAAATCC GTTTGGnAAA GGAnCATCGA AATGGTTTAG TAACTCATAC 240
 AAATCTTTAA AAGGTTGGAC TGGGGATATG TATTCAAGAG CCCACG 286

(2) INFORMATION FOR SEQ ID NO: 4419:

25

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4419:

35 CTCACCTTCTA AGCGCTCCAC ATGTCCTTAC GATCATGCTT CAACGCCCTT AGAACGCTCT 60
 CCTACCATTG TCCAAAGGnA TGChCACAGC TTCGGTAATA TGTTTAGCCC CGGTACATTT 120
 TCGGCGCATG TCACTCGACT AGTGAGCTAT TACGCACTCT TTAAATGATG GCTGCTTCTA 180
 40 AGCCAACATC CTAGTTGTCT GGGCAACGCC ACATCCTTnT CCACTTAACA TATATTTTGG 240
 GACCTTAGCT GGGTGGTCTG GGCTGTTTCC CTTTCGAACA CGGACCTTGA TCACCCCATG 300

(2) INFORMATION FOR SEQ ID NO: 4420:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4420:

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GGTGAGCGGA GCGAACTCnC GTTAAGGAAC TCGGCAAAAT GACCCCGTAA CTTCGGGAGA 120
 AGGGGTGCTC TTAGGTTAA CGCCAGAAG AGCCGCAGTG AATAGGCCCA AGCGACTGTT 180
 5 TATCAAAAAC ACAGGTCTCT GCTAAACCGT AAGTGATGTA TAGGGGCTGA CGCCTGCCCCG 240
 GTGCTGGAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAAcT ACGAATCGAA GCCCCAGTAA 300
 ACGGcGGCCG TAACTATAAC GGTCTAGACG ATCTGC 336
 10

(2) INFORMATION FOR SEQ ID NO: 4421:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 297 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4421:

GGnCACCTC GTGCCAAACA GTGCTCTACC TCCAATAATC ATCACTTGAG GCTAGCCCTA 60
 AAGCTATTTT GGAGAGAACC AGCTATCTCC AGGTTTCGATT GGAATTTCTC CGCTACCCTC 120
 25 AGTTCATCCG CTCACCTTTT AACGTAATCG GTTCGGTCCT CCATTTCAGTG TTACCTGAAC 180
 TTCAACCTGA CCAAGGTAGA TCACCTGGTT TCGGGTCTAC GACAAATACT AAACGCCCTA 240
 TTCAGACTCG CTTTCGCTAC GGCTCCACAT TTA CTGCTTA ACCTTGCA TC AAATCGT 297
 30

(2) INFORMATION FOR SEQ ID NO: 4422:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4422:

GTACATCGTC TAATAATAAG TTGACGATAT CTTGCAATGC ATCTTTATCT AAATGTAAGA 60
 ATTCAACGAT GCCGTTGAAG CGGTTAAGGA ATTCAAGGCG GAAGAATTTT TTCATTTTCGT 120
 45 GCATAATATC TTTTCTTCA GCGTCATTGC CATTGCCAAA GCCAGCATTT GATGTACAAA 180
 TAATAATTGT ATTTTAAAG TTGATGACAT TACCTTGACC ATCAGTCAAA TTACCATCAT 240
 50 CCATTACTTG TAATAACAAT GTTAAAATTG TGGATTGCTT TTCGATTCAn CAATAGAATG 300
 ACTGAGAnGG GATACGGCGA CTTTTCAGTA AACGGATTGA ATGGCATCAT AnCCACATAC 360
 CAGCGTGGAC CATCATTTTG GAACAGCGTG GGCACATATC 400
 55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4423:

AAGTTGAGTC GCATAGCTAG TATGAAACGT GGTGTGCGCA TGGGAACTAT CAAGCTTTGA 60
 AGATGTGGTA CTACATGCGT TGAATTAGGG ATCGGTACTT TATATGAAGA CGTGCTGCTT 120
 CCATTAAATG AGTGATGCGA TTTTGGCATG AAGGTCACCT TAAATGTACA TTGTTGTAAT 180
 AAAATTGCCT ATAAATTTTT AGCACATAAA ATAAGAnGnG CCAACCATTG TTAGACTATA 240
 ACAACGGTTG GCTCTTTAAT TGTAAAAAGA AAACCATACG CTATGGTAGT T 291

(2) INFORMATION FOR SEQ ID NO: 4424:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4424:

AACTGCCACC ACCTGGGGnG GTTTCAGAA CCTCTATGCA TTTCAATCAC AGnCAAATGT 60
 GCGGTTGACG TTCAATGACT ACCTGCAATT CATCGGTCAG CTCACACCCT TTACCTGnCT 120
 AAAGTACCAG TAGACAATGT AGGTATTGGA CTTGCATGAG CATTTTTATn CAGTAATGGG 180
 CTTTAGATAT TTTATTAATA CCGGCCAATC ATGCTATTCA AACCGCCAAT AGCTTTATTA 240
 GCAACATTTT TACCTAAATC AGCCGCAGCT CTTCCCATGT CTTACCAAT ATCTCTAATC 300
 CAATCATATG TTTTGCATA GCCATTTTCT AAAACCATTA AATACTGATT TAGCGTTAGA 360
 CCATGCCGAA CTTGAAATTG CATCAAAACG ATCGTGGGCT 400

(2) INFORMATION FOR SEQ ID NO: 4425:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 340 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4425:

AGATGATAAA AGCAACAGGT GGTtTTGCGA AAAGTGAAGT ATGGCGTCAA ATGATGTCAG 120
 ATATATTtGA CACAGAGTtA GTGGTtCCTG AAAGTtATGA AAGTtCATGC TTAGGTGCCT 180
 5 GCGTGCTCGG ACTTAAAGCT GTAGGTGACA TTGAAGATTT TTCAATCGTT TCATCGATGG 240
 TCGGTGCCAC AAACAATCAT ACGCCGATTG AAGAAAATGC ACTGTTACCA AGAnTCGAAT 300
 10 CCATtTtTAT CATTAAAGCGT CTTAnCAGAG ATATGACAAT 340

(2) INFORMATION FOR SEQ ID NO: 4426:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4426:

CTGAAGATGA TAAAGATGCA GATGGTGGCG AGTtGCACGT AACAAATTACG GATCATGATG 60
 ATtTCACACT TGATAACGGA TACTTCGAnG AATTATCATC AGACAGCGAT TCAGACTCAG 120
 25 ATAGTGACTC AGACAGCGAC TCAGACTCAG ACAGCGACTC AGACTCAGAC AGTGATTtCAG 180
 ATTCAGACAG CGACTCAGAT TCAGATAGCG ACTCAGATtC GGACAGCGAT TCAGACTCAG 240
 30 ATAGCGACTC AGATTtCAGAT AGCGATTtCAG ACTCAGACAG CGACTCAGAT TC 292

(2) INFORMATION FOR SEQ ID NO: 4427:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 307 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4427:

AACAGTGCTC TACCTCCAAT AATCATCACT TGAGGCTAGC CCTAAAGCTA TTTCGGAGAG 60
 AACCAGCTAT TTCCAGGTtC GATTGGAATT TCTCCGCTAC CCTCAGTTCA TCCGCTCACT 120
 45 TTtCAACGTA ATCGGTtCGG TCCTCCATtC AGTGTtACCT GAACTtCAAC CTGACCAGGG 180
 TAGATCACCT GGTtTTCGGGT CTACGACAAA TACTAAACGG CCCTATTtCAG ACTCGGCTTT 240
 50 CGCTACGGTT CCCACATtTA CTGGCTAAAC CTTGCATCAA AATCGGTAAC TCAnCGGGTC 300
 ATTCTAn 307

(2) INFORMATION FOR SEQ ID NO: 4428:

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(A) LENGTH: 354 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4428:

10 GACCATACAT CGTCATCGTT TGCACCGTCA AATACTGGTG ATGCAACGTG AATACCAAGA 60
 TTTTtagcag CCATACCTAA GTGTAGCTCT AATACTTGTC CGATGTTTCAT ACGAGATGGT 120
 ACACCAAGAG GATTTAACAT GGATATCGAT CGGGACGTCC ATCTGGTGAA GTGAAGGCAT 180
 15 ATCTTCTTCA GGAACAATC TTGAGGAAAT GGACACCTTT GTTGACCATG TCGGACCACA 240
 CATGCTTATG CACCAACATG GAATTTTACG TTTTGGAAa GATGATTATT ACACGTnACT 300
 AATTGGTTTA CACCAGGTGG AnaATGTTAT CGTCGGCCTT GCTTCACGAT TGGA 354

20

(2) INFORMATION FOR SEQ ID NO: 4429:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4429:

30 GTGnACTATC nGCTTGTCTA TGATAATATT ATTCTTTGTA CTTGTTTAAA AGATATTAGA 60
 CTAAAACTAA AAACAGCAGT AAGATGATTT ATGATTAAAA CTATCTTACT GCTGTTCACT 120
 35 TTTTATAATA CTTCTGAATG TCTCACTTAT ACTTCTAGTC ACAGATTTAA ATAATCAAAA 180
 GTGCACATTA TTAAATATC AATTTACAC TCAATGCGGC TCATCGCATT CATTTCTTGT 240
 CTAGCAACGT TCTACTCTAG CGGAACGTAA GTAGCTACCA TCTCGCTAAG GAACTTTCTT 300
 40 GACCTGGTGA CAACCGCTGC GnCTnTCTCT CTTGGGCTCT CGCTTACTCC ATTTAGCTCC 360
 ACTAAACTCG TGCGGCCCTT CCCGTTGCGC AGATCCAACG 400

45

(2) INFORMATION FOR SEQ ID NO: 4430:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4430:

55

ACCATTACACA CCTTGACAGC CACATAACAT AACTAAGTTT AAGATnGGGG GATAAATCGT 120
 ATCTGAGTTA AACCAATGGT TAATACCCGC ACCCATGATA ATCATTGAAC GCCCTTCAGT 180
 5 ATCGATAGCG TTTTGCGCAA ATTCTTTCGC TACTTGAATG ACAACACTTT GTTTTACGCC 240
 TGAAATGGCT TCTTGCCAAG CAGGTGTATA TTTTGATTCT GCATCGTCGT AA 292

(2) INFORMATION FOR SEQ ID NO: 4431:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 284 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4431:

20 TGAGCCGnAC ATCGAGGTGC CAAACCTCCC CGTTCGATGT GAACTCTTGG GGGAGATAAG 60
 CCTGTTATCC CCGGGGTAGC TTTTATCCGT TGAGCGATGG CCCTTCCATG CGGAACCACC 120
 GGATCACTAA GTCCGTCTTT CGACCCTGCT CGACTTGTAG GTCTCGCATC AAGCTCCCTT 180
 25 ATGCCTTTAC ACTCTATGAA TGATTTCCAA CCATTCTGAG GGAACCTTGA GCGCCTCCGT 240
 TACCTTTTATG GAGGCGACCG CCCAGTCAAA CTGCCCCGCT GACA 284

(2) INFORMATION FOR SEQ ID NO: 4432:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 312 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4432:

40 TATCATTGTG GTACGATAAG GCATATGTTG TACCTATGnA TGGTGGAAGA GCCTTCAGTT 60
 GTCGCTGCAG CTAGTTATGG TGCAAAGCTA GTGAATCAGA CTGGCGGATT TAAAACGGTA 120
 TCTTCTGAAC GTATTATGAT AGGTCAAATC GTCTTTGATG GCGTTGACGn TACTGGAAAA 180
 45 TTATCAGCAG ACATTAAAGC TTTAGAAAAG CAAATTCATA AAATTGCGGn TGAGGCATAT 240
 CCTTCTATTA AGCGCGTGTG GTGGTTACCA CGTATAGCGA TTGATACATT CCTGGCCACC 300
 50 AGTTCTATCT TT 312

(2) INFORMATION FOR SEQ ID NO: 4433:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 288 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4433:

	CGGTACTCGT TAAGGCTGAG CTGTGATGGG GAGAAGACAT TGAGTCTTCG AGTCGTTGAT	60
10	TTCACACTGC CGAGAAAAGC CTCTAGATAG AAAATAGGTG CCCGTACCGC AAACCGACAC	120
	AGGTAGTCAA GATGAGAATT CTAAGGTGAG CGAGCGAACT CTCGTTAAnG AACTCGGCAA	180
	AATGACCCCG TAAC TTCGGG AnAAAGGGTG CTC TTTAAGG TTAACGCCCA GAAGAGCCGC	240
15	AGTGAATAAG CCCAAGCGAC TGT TTTATCC AAAACACAGG TCTCTGCT	288

(2) INFORMATION FOR SEQ ID NO: 4434:

(i) SEQUENCE CHARACTERISTICS:

20	(A) LENGTH: 336 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4434:

	GGACCGAACC GACTTACGTT GAAAAGTGAG CGGATGAACT GAGGGTAGCG GAGAAATTC	60
30	AATCGAACCT GGAGATAGCT GGTTCCTCTCn nAAATAGCTT TAGGGCTAGC CTCAAGTGAT	120
	GATTATTGGA GGTAGAGCAC TGTTTGGACG AGGGGCCCCCT CTCGGGTTAC CAATTTTCA	180
	CAAACTCCGA ATGCCAATTA AATTTAACTT GGAATTCAG AACATGGGTG ATnAAGTCCG	240
35	TGTTTCGAAA GGAAACAGCC CAGACCACCA GCCAAGTCCC AAAATATATG TTTAATGGGA	300
	AAAGGTGTGG CCTTTGCCCA GGACAACCAA GAAGTT	336

(2) INFORMATION FOR SEQ ID NO: 4435:

40

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 304 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4435:

50	ATTGACGCCG CATTTTTACG GAATGGGAAT AAAGCGACAC AAACCGTCAC GTCnGTGTTG	60
	GTGTCATGAC AAGGTAATGC GAGTGATCTG ATGTATGGCT TATCATGGCA ATCTGTTATG	120
	GnCTGACTGA TCGGACGATG TATCATTCGC CAATTCGTTT ACTTGTCGTT ATTCAAGCAC	180

55

AATCATTGGC TGC GTTTTAA TGAGCGTAAT GAGGAAGGGG CGTTTAAAAA GTTGGATTTA 300

ACGA 304

5 (2) INFORMATION FOR SEQ ID NO: 4436:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4436:

AATATACTCC GGTAATAAC CGAAGAGTTT TGAATCATTG TTAAAAATGG AATTAnAGTT 60
 CTAGTATCTG TTGGGTTTTG AAATAGGTCA TAGGATAAAA CAAATnGAGA ATTTGTCGCT 120
 20 ATTTGTAAAT TGTATCCTGG CTTAAGTTGG CCATTTTTCA TATGGTCTTC CTTCAATCTC 180
 ATAAAAGTTG CATCATGGAT CAGTTTTAGA AAAGCTATTT CTATCTTTAA GAATCGATTT 240
 TTGTTCTTCA TATTTATTTT TTCCTTCGGA ATAATCATCA AATTTATnTT TGGAACCTCT 300
 25 TAATC 305

(2) INFORMATION FOR SEQ ID NO: 4437:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 359 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4437:

ATCGTTTAAA TCAGTTAGTA AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAAATA 60
 40 TTATAGAAAA CATCAAAGGA TGTTAAGAAA TACAATTTAT TACCCAGCAT TTAATAATGG 120
 TGCTATAGAA GGAATTAATA ATAAGATAAA ATTAATCAAG TGAATTTCTT TTGGTTACAG 180
 AAATTTCAAC AACTTTAAAG CACGTATAAT GATGATTTTC AGCTTGTACA AGGGGGAnAA 240
 45 AAGGAnGnCA ACCAAGCCCA ATAATGGACT GGCCGCCTAA TATTAAAAAC TCTAAAGGTT 300
 GTATTTTAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA CCCGTTAAC 359

(2) INFORMATION FOR SEQ ID NO: 4438:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4438:

5 ACTTACAGTT ATTTTAACTT GGnCAGAATC CATCATCCAT AAGTTCGAAA TGTTGTAAAA 60
 CATAAACCTT GnaAACGGCA ACATTTTTGG GTCCTTCTCC ATCATTTTAT TTAAAAGCGC 120
 ATTATGATCA ATATCATGCC CAATTAACCTT TCCAGCAATT TCCATAGTAT GTTCTGAGGT 180
 10 ATTGTTAAAA AGGAATCGCC CAGTATCACC GACGATACCA AGATATAAAA CGCTCGCGAT 240
 ATCTTTATTA ACAATTGCTT CATCATTAAT ATGTGAGATT AAATCG 286

(2) INFORMATION FOR SEQ ID NO: 4439:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 394 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4439:

TCGCTTGACT TCTTTCCTCT CCTTCGGCTC TCGCTTACTC ATTTAnCTCT ACTAAACTCG 60
 25 TTGCGCTCTT TTCTCGTTTC GTCAGATTCA AACGTTTTCA CTTGCGCAAG CCATTTTTCT 120
 TTGTGTTTAC TTTTATTTT GACGTTTTAG ACATAAAAAA AAGAGACCTT GCGGTCTCAA 180
 TGCGGCTCAT CGCATCCATT TTTGCGCTGG CAACGTTCTA CTCTAGCGGA ACGTAAGTTG 240
 30 GCTACCATCG ACGCTAAGAA CCTtTCTTGA CTTGTGACAA aTCGCTTGCT TCTTTCCTCn 300
 TCTTCGGTCT CGCTTACTCA TTTAGCTCTA CTAAACTCGT TCGGCTCTTT TCTCGTTTCG 360
 35 TCAGATTCAA CAGTTTTTCAT TCGCCAAGCC ATTT 394

(2) INFORMATION FOR SEQ ID NO: 4440:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 295 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4440:

TAATAGGTTT GAGGTGGAAG CATGGTGACA TTGGCAGCTG ACGAATACTA ATCGATCGAA 60
 GACTTAATCA AAATAAATGT TTTGCGACAA TGCAACTTTT ACTTACTATC TAGTTTTGAA 120
 50 TGTATAAATT ACATTCATAT GTCTGGTGAC TATAGCAAGG AGGTCACACC TGTCCCCATG 180

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TAGAACGTTG CCAGGCAAAA AATGGATGCG ATGACCGCAT TGAGACCGCA GcNtn

295

(2) INFORMATION FOR SEQ ID NO: 4441:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 345 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4441:

15

TTTCATAAAA AGATTTCAAA CGCGTTCATC AAnCCTCGTC GCAGGTCTTT CGAACACTAG	60
CGATTATTTT tTATGAATTC AAGCTTATTT AAAACTCTTT ATTCaCTCGG TTTTGCTTGG	120
TAAAATCTAT ATTTTACTTA CTTATCTAGT TTTCAATGTA CAATTTCTTT TTAGTCAAGC	180
GCTCGCATAC TGCTTTATTT TCATAAGCAA TATCACTTTA ACCAAAAAAT ATTTGAATGT	240
TAAATAAACA TTCAAACTG AATACAATAT GTCACGTTAT TCCgCATCTT CTGAAGAAGA	300
TGTTCCGAAT ATATCCTTAG AAAGGAGGTG ATCCnGCCGn ACCTT	345

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(2) INFORMATION FOR SEQ ID NO: 4442:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4442:

AATCATTGTC AAAACTACGT TCTGGTAAAC AAGGACAACC CGTTTGAACC ATTGGCCCAC	60
ACCATTTGAT AGGCAGnCAT GTGCGCAATG GACATCCACA TAGTTGCGTA ATGTTTCATA	120
CGTCATTGCT CAAATCATTC ATGACTAGCG CAACATGATT ACCTTGTCGT GnGCACCTTC	180
ATTAAAGnAA CTTATGATAG ATTTATTTCC CGGGACATTA AGCATTGCA TCGTTAACAT	240
GCGTATTGCA CCCAATTTAG AAGTTCCTCC GTGCCGTTTG GTATATCACA AATTTGTAGT	300
GTATCTTGGA TGC	313

45

(2) INFORMATION FOR SEQ ID NO: 4443:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 336 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4443:

AGCATGGTGT TTCTCAGATT GTCGGATGTA TAAATGTGTA TGTTATGTTT TAATTTTTTCC 60
 5 CAGTCTTTAA AAATAGATTG TTTATTTTTA GAATTATTTT TGAATAATTG AATTGCTTTG 120
 TAGCCAAAAT ATGACGTTTC ATTATCATTC AAACGCATAT AAAGCGTATC TnCTGCCTCA 180
 TTGTCAGTGA GATGAAATAA TGTGCTCGGG GTCTAGTGAC TGTGGATAAT TTCACTTCAA 240
 10 CTGAAACCCC ATTCCTTTTG AGCTGCCCAT ATATCTCTTT GGACAATATC GGTCCCTCTA 300
 ATACGnCCG TAGnCCATTC CATTTCAATT CTTTTC 336

(2) INFORMATION FOR SEQ ID NO: 4444:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4444:

25 CAGACTGGGA TATTTATAAA ACGTTGGCAA AAGCATTTTC AGAAATGGCA AAAGACTATT 60
 TACCTGGAAC GTTTAAAGAT GTTGTGACAA CTCCACTTAG TCATGATACA AAGCAAGAAA 120
 TTTCAACACC ATACGGCGTA GTGAAAGATT GGTCGAAGGG TGAAATTGAA GCGGTACCTG 180
 30 GACGTACAAT GCCTAACTTT GCAATTGTAG AACGCGACTA CACTAAAATT TACGACAAAT 240
 ATGTCACGCT TGGGCTGTGA CTTGAAAAAA GGGGAAATTT GGAGCACCTG GGGGTAAGTT 300
 TCCGTGTCCA GTTGAACCAT TATGGAGGAn TTnAAAAAGT ATGTTAAGGG ACCTGGGAGT 360
 35 TGAATACCCA ATGGATnGAT TCCCGTGAAG AGCCGAATCC 400

(2) INFORMATION FOR SEQ ID NO: 4445:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 339 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4445:

50 TACGCCCACG ACGGATAGGG ACCGAACTGT CTCACGACGT TCTGAACCCA GCTCGCGTAC 60
 CGCTTGTAAT GGGCGAACAG CnATCGCCTT GGGACCGACT ACAGCCCCAG GATGCGATGA 120
 GCCGACATCG AGGTGCCAAA CCTCCCCGTC GATGTGAACT CTTGGGGGAG ATAAGCCTGT 180

55

CACTAAGTCC GTGCTTTTCGA CCCTGACTAC GGACTTGThA GGTCTGCGGC ATTCAAGCTT 300
 CCCTTGATGG CCTTTGACAC TGCTTATGGA ATGnATTG 339

5 (2) INFORMATION FOR SEQ ID NO: 4446:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4446:

CAATTTTAAG TGTTGAAAAT GTCACTTTTA AACTTTCTAG TTTTATCTTT AATAAACATG 60
 CCATnCGTAA TAAGTGGCGT TTTATTAAAA TCATCTATAA TAGCCATATA GTTTTGCTCA 120
 20 CTACCATAAC CTGCATCAGC TACAATATAC TCCGGTAAAT AACCGAAGGA TnTTTGAAT 180
 CATTGTATAA AATGGAATTG AAAGTTCTAG TATCTGTTGG GTTTTGAAAT AGGTCATAGG 240
 ATAAAACAGG GTGAGAATTT GTCGCTATTT GTAAATTGTA TCCTGGCTTA AGTTGGCCAT 300
 25 TTTTnCATAG GTCTTCCT 318

(2) INFORMATION FOR SEQ ID NO: 4447:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4447:

TTTTGAAATT CTCTATGTTG GGGCCCCGAC TATAATTGAA AAATGCTTGT TACAAGTGCA 60
 40 TTTTATTTC A GTCAACTACT AACAAATATAA CATTGTGGAG CCCAGAnCTT TGATTAATGT 120
 ATATGAAAAT CAAAGTAATG CTTATGTATG ATTATTTCAA ATATTTTACA TACATGAACT 180
 TTTCCAATGT ACGATACTAT TATTATAAAG CGCTCGCTAA GATTTTACGA TGATTAGAGG 240
 45 GTAAAAAATG AACGATCAAT GGTnTAACCA TTAAATTGG 279

(2) INFORMATION FOR SEQ ID NO: 4448:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 302 base pairs
 50 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4448:

5 GACACCGGCA TTCTCACTTT CTAAGCGCTC CACATGTCCT TACGATCATG CTTCAACGCC 60
 CTTAGAACGC TCTCCTACCA TTGTCCAAAG GACAATCCAC AGCTTCGGTA ATATGTTTAG 120
 CCCCAGGTACA TTTTCGGCGC AGTGTCACTC GACTAGTGAG CTATTACGCA CTCTTTAAAT 180
 GATGGCTGCT TCTAAGCCAA CATCCTAGTT GTCTGGGGCA ACGnCACATC CTTTTCCTACT 240
 10 TAACATATAT TTTGGGACCT TTAGCTGGTG GTCTnGGGCT GTTTTCTGnA TTGAACACGG 300
 GA 302

(2) INFORMATION FOR SEQ ID NO: 4449:

15

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 359 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4449:

25 CGTTGGTATA TAGAGGGCAA CCGTCACCTG ATAAAATGTG GACACAGTTT TTACAAGAGG 60
 TTAAGGAAAT GAGTTTGGAG GCATACGAGC ATCAAGAATA CCCATTGAA TGTTTAGTAA 120
 ATGACTTAGA TCAATCACAT GATGCCTCAC GGAATCCATT ATTTGATGTC ATGTTAGTAC 180
 30 TACAAAACAA TGAACGAAA TCATGCTCAT TTTGGGCATA GTAAATTAA CACACATTCA 240
 ACCCAAATC AGTGACGGGC GGAAATTTGG ATTTnTCCTT TTCCATCATT GGAAGAAGGA 300
 TCGCGGATGA CCTAATAnCA ATCCAATTAT CGGGGTATAA ATACCGGATT TTATAACCA 359

(2) INFORMATION FOR SEQ ID NO: 4450:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4450:

45 GATGACAAAA TTTGCTTGAA AACCGAAATG GATGGTCATC ATTGACTGnA TCAAGGTACA 60
 TCATTCTTTG GTGCTTATGC ATTTAGACAT TATACAAAA CAATACTTTT ATAGGGCAAC 120
 50 CTTATGGGGT TCTATCGGCT ATACATTACC TGCAACATTA GGTTCACAAT TAGCAGACAA 180
 AGATCGTCGn TAACTTATTA TTAATTGGTG ATGGCTCATT GCCAACTAAC TGTTCAGCT 240

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GCTATACGGT AGAACGACTT ATTCCC

326

(2) INFORMATION FOR SEQ ID NO: 4451:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 381 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4451:

15 GAAAACATCA AAGGATGTTA AGAAATACAA TTTATTACCC AGCATTTAAT AATGGTGCTA 60
 TAGAAGGAAT TAATAATAAG ATAAATTAA TCAAGTGAAT TTCTTTTGGT TACAGAAATT 120
 TCAACAACCTT TAAAGCACGT ATAATGATGA TTTTCAGCTT GTACAAAGGA GAAAAAAGA 180
 20 AGACAACCAA GCCCAATAAT GGAATGGCCG CCTAATAATA AAAACTCTAA AAGTTGTATT 240
 TTAAAAATAG GTCTTTAAAT TATATACCCC CCCCATTTGG GTGGAGAACC GGTAAACCAT 300
 GCCTAGGTGC CTAACCTCCn ATAATGGnAC CCTCCTTAC CATTTGGGCC ATGGGGCCAA 360
 25 TAAAGCGGGG GGCAATTGGG G 381

(2) INFORMATION FOR SEQ ID NO: 4452:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4452:

TTAATAACTT AATCTATGTT TCCATCCTAC AGGAAACGCG TTATTAATCT TGTGAGTGTT 60
 40 CTTTCGAACA CTAGCGATTA TTTCTTATGA ATTCAAGCTT ATTTAAACT CTTTATTCAC 120
 TCGGTTTTGC TTGGTAAAT CTATATTTTA CTTACTTATC TAGTTTTCAA TGTACAATTT 180
 CTTTTTAGTC AAGCGCTCGC ATAAGCAATA TCACTTTAAC CAAAAAATAT TTGAATGTTA 240
 45 AATAAACATT CAAACTGAA TACAATATGT CACATn 276

(2) INFORMATION FOR SEQ ID NO: 4453:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 341 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4453:

5 GGCGAAACCG CGTAGCGTTT TTAAAGTCTG ATGTGAAAGC CCACGGTCAA CCGGGAGGGT 60
 CATTGGAAAC TGGAAACTT GAGTGCAGAA GAGGAAAGTG GAATTCCATG TGTAGCGGTG 120
 AAATGCGCAG AGATATGGAG GAACACCACT GAGCGAAGCG ACTTTCTGGT CTGTAAGTGA 180
 CGCTGATGTG CGAAACGTGG GGGATCAAAC AGGATTAGAT ACCCTGGTGA GTCCACGCCG 240
 10 TAAACGATGA nTGCTAAATG TTAGGGGGTT TCCGCCCTT AGTGGCTGCC AGCTAnACGC 300
 ATTGAAGCAC TGCCGCCTGG GGAGTGACGA CCGCAAnTTG A 341

(2) INFORMATION FOR SEQ ID NO: 4454:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 281 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4454:

25 ACnCTCCCCA AAGTCATATC GTCGTTAGTA ACGTCCTTCA TCGGCTTCTA GTGnCCAAGG 60
 CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA CCATTTTAT AAGTCAAACG 120
 CTCACATACG GCTTCGTTTT CATTATTTTA AATGCTCATT TACATAAGTA AACTCTGCTT 180
 30 TAAATAATT TAACTCATTG TCTGCTAAAC GTTTTCTTTT ATAAAAAGAT TTAAACGCGT 240
 TATTAATCTT GTGAGTGTTT TTTGGAACAC TAGCGATTAT G 281

(2) INFORMATION FOR SEQ ID NO: 4455:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 279 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4455:

45 ATGTCTTCAC TTATACTTCT AGTCACAGAT TTAAATAATC AAAAGTGCAC ATTATTAAAA 60
 TATCAATTTT AACTCAATG CGGCTCATCG CATTCAATTC TTGTCTAGCA ACGTTCTACT 120
 50 CTAGCGGAAC GTAAGTTAGC TACCATCTC GCTAAGAACC TTTCTTGACT TGTGACAATC 180
 GCTTGnTCT TTCCTCTCCT TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACTCGTTG 240
 CGCTCTTTTC TCGTTTCGTC AGATTCAAAC GTTTTCnGT 279

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4456:

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ATTTTGACGT TTTAGGCATA AAAAAAAGAG ACCTTGCGGT CTCAATGCGG CTCATCGCAT 60
 CCATTTTTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA AGTTGGCTAC CATCGTCGCT 120
 AAAGACCTTT CTGACTTGT GACAATCGCT TGCTTCTTTC CTCTCCTTCG GCTCTCGCTT 180
 ACTCATTTAG CTCTACTAAA CTCGTTGCGC TCTTTTCTCG TnTCGTCAGA TTCAAACGTT 240
 nTCACTTCGC CAAGCCATTT TTCTTGTTT TACTT 275

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(2) INFORMATION FOR SEQ ID NO: 4457:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4457:

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ATCCGATTCA CAAAGCACAT CATCATATAC AAGTCAGTCA ACAAGCCAAA GTGAATCCAC 60
 ATCGACATCA ACGTCACTAA GCGATTCAAC AAGTATATCT AAAAGTACGA GTCAATCAGG 120
 TTCGGTAAGC ACATCAGCGT CATTAAAGTG TTCAGAGAGT GAATCTGATT CACAAAGTAT 180
 CTCAACAAGT GCAAGTGAGT CAACATCAGA AAGTGCGTCA ACATCACTCA GTGACTCAAC 240
 AAGTACAAGT AACTCAGGAT CAGCAAGTAC GTCAACATCG CTCAGTAACT CAGCAAGCGC 300
 AnTGGAAATCC GATTGTGCGT CAACATCTTT AAGTGGATTG AACATCTGCG TChATGCCAA 360
 AGnnGTGAAT CCGATTCACA AAGCACATCA GCATCCTTAA 400

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(2) INFORMATION FOR SEQ ID NO: 4458:

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4458:

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AGTCGCTGTC TGAATCTGAA TCACTGTCTG AATCCGAATC GCTATCTGAT TCTGAGTCGC 120
 TATCTGAACC TGAGTCGCTG TCTGAGCCTG AGTCACTGTC TGAATCCGAA TCCGGATCCG 180
 5 GGTCTGGGGn TGGTTCCGGT TCTGGGTCTG GGACTTGGTT CTGGATCTGG CGTTGGTTCT 240
 GGGTCTGGGG TCTGGACTGG TTCTGGGGTC AAACGGCGGC CCTGGAGTGG GGTCTTTCGG 300
 AATnAACGGC GGAATCACCA TCAAGCAACT TnCAACAACC ATAACGAAAA A 351
 10

(2) INFORMATION FOR SEQ ID NO: 4459:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 271 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4459:

ATCCTGCAGT TGATCAGTAT GGTGATATTA ATTTAGTTAA TACGAACGCG TCATCTACAA 60
 GTGAAATCAT TTACGATTTA ATCTCACATT TTAATGATGA AGCAATTGTT AATAAAGATA 120
 25 TCGCGAGCGT TTTATATCTT GGTATCGTCG GTGATACTGG GCGATTCCCTT TTTnACAATA 180
 CCTCAGAACA TACTATGGAA ATTGCTGGAA AGTTAATTGG GCATGATATT GATCATAATG 240
 CGCTTTTAAA TAAAATGATG GAGAAGGnCC C 271
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(2) INFORMATION FOR SEQ ID NO: 4460:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 283 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4460:

ACTGTGGATT AATATTATGC CTGGCAACGT TCTACTCTAG CGGAACGTAA GTTCGACTAC 60
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 120
 45 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAGATAGT AAGTAAAAGT 180
 GATTTTGCTT CGCAnAACAT TTATTTTGAT TAAGTCTTCG ATCGATTAGT ATTCGTCAGC 240
 GCCACATGTC ACCATGCTTC CACCTCGAAC CTATnAACCT CAG 283
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(2) INFORMATION FOR SEQ ID NO: 4461:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 274 base pairs
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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4461:

CTTCTACAAG TCCTGAATAT ACTTATGAAT CTCTTCTTTC GTGTATGCAA ACTGACGTTG 60
TAATTTAAAT AACGTCTCAT CTTTCCATTG CGAATCTTGA TATTGTATAT TTTCAAAATC 120
AAAGTCAACT TTATGGTTAT CAATCCACGC TTTATATGGT AATTCTCCAG CAATCGCACC 180
TTTTAAATCA TTATTTTCAA TGACTTTATT CTGTTAAAT CAACAA_nCAT AACTTTCC_nG 240
GATTCAATTG ACCTTTAAAA GCAACATTAC TTCC 274

(2) INFORMATION FOR SEQ ID NO: 4462:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 271 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4462:

GGCTGCTAAA AATCTTGGTA TTCACGTTGC ATCACCAGTA TTTGACGGTG CAAACGATGA 60
CGATGTATGG TCAACAATTG AAGAAGCTGG TATGGCTCGT GATGGTAAAA CTGTACTTTA 120
TGATGGACGT ACAGGTGAAC CATTGATAA CCGTATTTC A GTAGGTGTAA TGTACATGTT 180
GAAACTTGCG CACATGGTTG ATGATAAATT ACATGCGCGT TCAACAGGAC CATATTCACT 240
TG_nTACACAA CAACCACTTG GCGGT_nAAGC G 271

(2) INFORMATION FOR SEQ ID NO: 4463:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 300 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4463:

GCGGCTCATC GCATTCATTT CTTGTCTAGC AACGTTCTAC TCTAGCGGAA CGTAATTAGC 60
TACCATCCTC GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT 120
TCGGCTCTCG CTTACTCATT TAGCTCTACT AAACGTTG CGCTCTTTTC TCGTTTCGTC 180
AGATTCAAAC GTTTTCACTT CGCCAAGCCA TTTTCTTTG TGTTTACTTT TT_nTTTGAC 240

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(2) INFORMATION FOR SEQ ID NO: 4464:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4464:

TACCGAATCG AAGCCCCAGT AAACGGCGGC CGTAACTATA ACGGTCCTAA GGTAGCGAAA 60
 TTCCTTGTCG GGTAAGTTCC GACCCGCACG AAAGGCGTAA CGATTGGGC ACTGTCTCAA 120
 CGAGAGACTC GGTGAAATCA TAGTACCTGT GAAGATGCAG GTTACCCGCG GACAGGACGG 180
 GAAAGACCCC GTGGGAGCTT TTA CTGGTTA GCCTGGATAT TGGAAATTCG GGCACACTTG 240
 GTTACAGGAT AGGTAAGGAG CCTTTTGGAA ACGTTGAGCG CTACTTTAnG TTGGGAGGCG 300
 CTGGTnGGGA TACTTACCCT AACTGTGTTT GGCTTTCTn AACCGGCACC ACTTATCCTG 360
 G 361

(2) INFORMATION FOR SEQ ID NO: 4465:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 292 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4465:

CTGTATGTAC ACCACCAATC GGTTTAGGTT TAGCAACGTT TGTTCAAAAG TATAAATTCA 60
 ATCATTCCGA AAGAGAAATG GGTAAGGCTT CCTTCACTAT GGGACTATTT GGTATTACTG 120
 AAGGTGCTAT TCCTTTCGCA GCCCAAGATC CATTGCGCAT TATACCTGCA AACATCATTG 180
 GTGCAATGAT TGCATCAGTC ATTGCAGCCA TTGGTGGTGT CGGCGATAGA GTCGCACATG 240
 GnGGTCCCAA TCGTGGCTGT ATTAGGTGGG TTTTGT TTTTnTTTT TT 292

(2) INFORMATION FOR SEQ ID NO: 4466:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GCAAACAAAA CAGTATTAGT AGATTATGAA AAATATGGTA AGTTTTATAA CTTATCTATT 60
 AAAGGTACAA TTGACCAAAT CGATAAAACA AATAATACGT ATCGTCAGAC AATTTATGTC 120
 5 AATCCAAGTG GAGATAACGT TATTGCGCCG GTTTTAACAG GTAATTTAAA ACCAAATACG 180
 GATAGTAATG CATTAAAGA TCAGCAAAAT ACAAGTATTA AAGTATATAA AAGTAGATAA 240
 TGCCnCTGAT TTATCTGAAA GTTACTTTGT GGAATCCCGG AAACCTTGAG GGTGGCCCCCT 300
 10 AATAnTGG 308

(2) INFORMATION FOR SEQ ID NO: 4467:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 271 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4467:

AAGCAGGCGC TCTCCAGCT GAGCTAAGCC CCCATAATAA TTACAGTATA TCGGGAAGAC 60
 25 AGGATTCGAA CCTGnGACCC CTTGGTCCCA AACCAAGTGC TCTACCAAGC TGAGCTACTT 120
 CCCGTATAAT TAAngCGCCC GATAGGAGTC GAACCCATAA CCTCTTGATC CGTAGTCAAA 180
 CGTCTATCC AATTGAGCTA CGGGCGCATA TGTTTTTATT GAAAATAGTG CCGAGGACCG 240
 30 GAATCGAACC GGTACGTGAT CACTCACCGC A 271

(2) INFORMATION FOR SEQ ID NO: 4468:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 306 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4468:

TGTGTTAGGT ATTACATCAT CACATTTATC TGCGTCAAAG TCCAGCTGTC GATAAAGTTG 60
 45 TAAACTGTAA AAACGCAATT TCTGAATTAG AAAATGATAA ACGTAAAGCA GTAAGTGCTG 120
 AAGAnTATAA AAAAGCTGAC GACATTCAAA ATGAAATCAA ATCATTACAA GATAAATTAG 180
 50 AAAATAGTAA TGGTGAACAT ACTGCTGTTG CTACAGTTCA TGATATTTCA GATACTATTC 240
 AACGATTAAC TGGTATTCCA GTTCTCAAA TnGATGATAA CgnTATTGAA CGTTTAAAAA 300
 ATATTT 306

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 329 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4469:

10 GGTTTATTAA CAGCATTCTT ATCAGCATTT GTAAGTGTTA TTGTTTATAA CTTCGTGTG 60
 AAGCGCAATA TTACAATTAA AATGCCGAAA GAAGTACCGC CGAATATTTT ACAAGTATTT 120
 15 AAGGACTTAA TTCCATTTTC AGCGGTAATC ATCATTCTTT ATGCATTAGA TTTAGTCATT 180
 CGCAACAGCT TTAAATCAAA TGTCGCGAA GGTATTTTAA AATTATTCGA ACCATTATTT 240
 ACAGCAGCAG ATGGATGGGT TGGTGGTCAC CATTAAACnT TGGGnGCnTT TGCATTAATC 300
 20 CTGGGTTTGT AGGGTAATCC ATGGGTCCG 329

(2) INFORMATION FOR SEQ ID NO: 4470:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4470:

AACTGGGTGA TAAGGTCCTG TTCGAAAGGA AACAGCCCAG ACCACCAGCT AAGGTCCCAA 60
 AATATATGTT AAGTGGAAAA GGATGTGGCG TTGCCAGAC AACTAGGATG TTGGCTTAGA 120
 35 AGCAGCCATC ATTTAAAGAG TGCCTAATAG CTCCTAGTC GAGTGACACT GCGCCGAAAA 180
 TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTGGACAAT GGTAGGAGAG 240
 40 CTTCTAAGGA CTTGAAGCTG ATCGTAAGAC TGTGGAGCGn TAGAATGAGA TGCCGTGTGA 300
 TAGnAAAGAC GGTGAGATCC CTCCACCGTT GACTAAGTTC CAGAGGAAGC TCTCCGTCGG 360
 GTTATCCGGT CCTAAGnGAG GCCGACAGCT AGGCATGGnT 400

(2) INFORMATION FOR SEQ ID NO: 4471:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

TCATTTTtag AAATATTATC TTTTCACAA ATCATTtGAT ATAAAGTGCG ATCATTtGCC 60
 GCGAGTGCTG CCATTGACAC TAGCTGTTGC GTATCATTtT TGGCTAGCAC TTCGGGATAC 120
 5 TTTCTTAGCT GAACAGTTAG ATGACCTAAT TGATCTTTGA AAATATCATT ATCTTGACCC 180
 ATATATGACC ACCAAGCTGT TTCATCACAA ACCATGACAT ACTTAGCTAG TGCTTCATCT 240
 TTTTCTATAA GCTGACGTAA TAATTGTCTG CTTGTCTCC GTTTTnCATG TACCGCGAGG 300
 10 CGTAAnCTTA AAGGGCCCAA GGnCG 325

(2) INFORMATION FOR SEQ ID NO: 4472:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4472:

CCCGTCTTTC GCTACTCACA CCGGCATTCT CACTTCTAAG CGCTCCACAT GTCCTTACGA 60
 25 TCATGCTTCA ACGCCCTTAG AACGCTCTCC TACCATTGTC CAAAGGACAA TCCACAGCTT 120
 CGGTAATATG TTTAGCCCGG TACATTTTCG GGGGCAGTGT CACTCGACTA GTGAGCTATT 180
 ACGCACTCTT TAAATGATGG GCTGCTTCTA AGnCAACATC CTAGTTGGTC TGGGGCAACG 240
 30 CCACATCCTT TTTCCACTTT AACAnATATT TTGGGA 276

(2) INFORMATION FOR SEQ ID NO: 4473:

(i) SEQUENCE CHARACTERISTICS:
 35 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4473:

AATTTnCCAA AAAATTCAAA TGGCTCATTt ACCAAAAGGT AAACCTCCGC CTTTAAnTTT 60
 45 CTTaATGCAT kGTCTAACAA cCGCTTTCTT TAAAaAATA GATTGTCAAG CGCTCGCATA 120
 AGCAATATCA CTTTAACCAA AAAATATTTG AATGTtAAAT AAACATTCAA AACTGAATAC 180
 50 AATATGTCAC GTTATTCCGC ATCTTCTGAA GAAGATGTTT CGAATATATC CTTAGAAAGG 240
 AGGTGATCCA GCCGCACCTT CCGATACGGC TACCTtGTTA CGACTTCACC CCAATnCATt 300
 TGTCACACCT TCGACGGGCT AGCTCCGAAA AGG 333

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4474:

10 TATAAAATAG CAACGTTATT CCAATTATCT TAATGGTTAT CTTATCCTCA ACTAAATTGG 60
 AGGAATCACT ATGACAATTA ATAAAGTAAC CGTTCTTGGC GCAGGCACAA TGGGCGCTCA 120
 15 ACTGGCAGCA CTTTTTGTGA ATGCTGGACT TAAAGTAAnA CTATTAGATA TTGTAGTGGA 180
 CAAAAACGAT CChAATCTCA TTGCGAAAAA ATCTTACGGT TAAATTACAG GTAAGAAACG 240
 GCCGCTACTA TTCGnCTTAA ATCTAGCGGT CATTTACCAT ATGGTATTTT GATGTGCTTG 300
 20 GTAAATGTGT GCTGTTTGAT ATCGA 325

(2) INFORMATION FOR SEQ ID NO: 4475:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4475:

TAAGTCCGGC AACATTTGCT TGTTTTGGTT ATGGTTGGCA CATTGATGTC GGCATTCATA 60
 35 CAATACATCT AGTATTATCT GGTATTTTTG ATCGTTATCC AAAGTTAAAT AATGATTATT 120
 GGACATTGGG GTGAGTTTAT CCCATTCTTC TTAGAAACGT ATGGATGAAG CTTATTCGCT 180
 GACATTTnAC CACCCTGTAA GCTATACTTT AAAAATAATT TTTAATCACA CCGAGTGGCA 240
 40 TGTTAACGAG CCACAGTTTG ATTTAGTCAA GAAGnAGAGG TATTGTAGAn TCTTATGCGC 300
 TGATATCC 308

(2) INFORMATION FOR SEQ ID NO: 4476:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 280 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4476:

CCTACCTATC CTGTACAAGC TGTGCCGAAT TnCAATATCA GGCTACAGTA AAGCTCCACG 120
 GGGTCTTTCC GTTCCTGTGC CGGGTAACCT GCATCTTCAC AGGTACTATG ATTTCCACCGA 180
 5 GTCTCTCGTT GAGACAGTGC CCAAATCGTT ACGCCTTTTCG TCGGGGTCGG AACTTACnCG 240
 ACAAGGAATT TCGCTACCTT TAGGACCGTT ATAGTTACGG 280

10 (2) INFORMATION FOR SEQ ID NO: 4477:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 279 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4477:

20 GCTAAGAACC TTTCTTGACT TGTGACAATC GCTTGCTTCT TTCCTCTCCT TCGGCTCTCG 60
 CTTACTCATT TAGCTCTACT AAACTCGTTG CGCTCTTTTC TCGTTTCGTC AGATTCAAAC 120
 25 GTTTTCACTT CGCCAAGCCA TTTTCTTTTG TGTTTACTTT TTATTTTGAC GTTTTAGACA 180
 TAAAAAAGA GACCTCACGG nCTCAACTTG CCTGGCAACG TTCTACTCTA GCGGAACGTA 240
 ATTGGGCTAC CATCGnCGCT AAAGACCTTT CTTGACTTG 279

30 (2) INFORMATION FOR SEQ ID NO: 4478:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4478:

40 GAGGATCCCG GAATGTTGAA CCCATCACTG ATTCTGGTTC ATAATTATCC ATCATCCATA 60
 ACGTTAAATC TAAAGCGTGT GTACCGATAT CGATTAATGG TCCTCCACCT TGAGCTTCTT 120
 45 CGTCTAGAAA GACACCCCAT GTTGGnACTG CTCGACGACG AATGGCATGT GCCTTTCCGA 180
 AGTAAATGTC TCCTAAGTCG CCACGTTGCG CTGCTTGATG TAAAAATTGA CTATCTGCTC 240
 GGAhACGATT TTGATAACCT ATTGTTAATT TT 272

50 (2) INFORMATION FOR SEQ ID NO: 4479:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 265 base pairs
 - (B) TYPE: nucleic acid
 - 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4479:

5 GAAATTGGGA ATCCAATTTT nCTTTGTTGG GGCCCATCCC CAACTTGCAC ATTATTGTAA 60
 GCTGACTTTT CGTCnCTTAC TGTGTTGGGG CCCTCACCCC AACTCGCATT GCCTGGTAGA 120
 ATTTCTTTTC GAAATTCTCT GTGTTGGGGC CCCTGACTAG AATTGAAAAA AGCTTGTTAC 180
 AAGCGCATT TCGTTCAGTC AACTACTGCC AATATACTT CGTAGAGCAT AGAATATTGA 240
 10 TTTATGTCCC AGCCTGAGTT AATTT 265

(2) INFORMATION FOR SEQ ID NO: 4480:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 343 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4480:

25 ACATAGAAAT GCCACTTTTA CAAACAAATG AATATTCGTC TTTTACATC ATTACGCATA 60
 ATAAAAGAAG CTAAGCAACA TGTAACCGT TGTCATTAA CTTCTTGTTT TTCCGATGAC 120
 AGCTTCTATT TAGAGAATGT CATGATTATT TTATATTCAC TTCAATGTTA TCAATATTAG 180
 TGCCATCTAT GACGTCTGCC ATACGATGCT CTGGCAGTTT TTTGGTGGTA ATTCAAACGT 240
 30 ATATTCCCAC CGTTTTTCATT TAATAACGTT GTCCnGGACC CATGTACCGT AAGATATGTT 300
 TTCATAGTGG TTCCAATTAA ACCAnTCTTC AGGAACCTCh TAG 343

35 (2) INFORMATION FOR SEQ ID NO: 4481:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 288 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4481:

45 ACTGCGGCAA TAGCAGCAGC ACCACAAACG GCCTGTGTCC GGACACCTAG GTAATAATGC 60
 GCATGTTTTT GTCACCATGC CAACAGTTTG TTGACAAAGA GCATCATTAC AATACTGGAA 120
 50 AATAACGACA CCTACATCGA TGGCTAATAG TTTACTACCT TGACCGATAA TATCGAATAT 180
 ATTGAGTTTA AGTCCATATA GGATGATTGC AAATCTTAAT AAATATTTAG ATGAAAACGT 240

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(2) INFORMATION FOR SEQ ID NO: 4482:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4482:

GAGGCATCCC CGGGCCTTCC TTCCCAACAG TCGCTTCAAA GTTTGGTGGT AAACCTGnTA 60
 CATCAAATTA TCGGTGCTAC TGtnAGGTAC GTGTAATCTT CGCTATTTTA TTAGCCGTAT 120
 CACATCAAGT GGCTTCCCTA CTGGAACCAA TTTGCTATTC GCCTTATTAT CAGGTGCAGG 180
 ATGGGGATTG GGACAAATCA TTACATTTAA AGCGTTCGAA TTAGTCGGCT CATCTCGTGG 240
 CCATGCCAGT CACAACAGCA TTCCAATTAT TAGGCGCATC TTTATGGGG 289

(2) INFORMATION FOR SEQ ID NO: 4483:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4483:

AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC ATCGCATTCA 60
 TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT CCTCGCTAAG 120
 AACCTTTCTT GACTTGTGAC AATCGCTTGC TTCTTTCCTC TCCTTCGGCT CTCGCTTACT 180
 CATTTAGCTC TACTAAACTC GTTGCGCTCT TTTCTCGTTT CGTCAGATTC AAACGTTnC 240
 ACTTCGCCAA GnCATTTTTTC TTTG 264

(2) INFORMATION FOR SEQ ID NO: 4484:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4484:

CTGTACCACC TATAATCGTT TTAATCGATT GGGGGACGCA TAGGATAGGC GAnGTGGCGA 60

TGAGCTGTGA TGGGGAGAAG ACATTGTGTC TTCGAGTCGT TGATTTTACA CTGCCGAGAA 180
 nAAGCCTCTA GATAGAAAAA GGTGCCCCGTA CCGCAAACCG ACACAGGTAG TCAAGATGAG 240
 5 AATTCTAAGG TGAGCGAGCG A 261

(2) INFORMATION FOR SEQ ID NO: 4485:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4485:

ATGCAGCTAT TATTTTTGAC AGATTCCATA TCGTTCAACA TTAAATAGA GAACTTAATA 60
 20 AGTATCGTGT ACAAGTTATG AATGAATACC GTAATAAAAA AGGACCTGAT TATACAATTT 120
 TTAAGAATAA CTGGAAAGTC CTATTGATGG ATACTAGTAA AACCATATTT AGTAAATACA 180
 25 GATGGAnTAA ATCTTTTAAG GCTTATAAAC GCTCATCTGA CATTGTAGAn GTCATGCTTT 240
 CAAAAGACGA TATACTACGA C 261

(2) INFORMATION FOR SEQ ID NO: 4486:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4486:

AGCAACATGA TGCACTTCTC GTGTCTCACC AGATTTAGCG ACTAAACTTG TAGACATACG 60
 40 TAAATCTGCT TTAATAAGTA ATnATGCAC ATGACTTATT GCGAGTAACA TCGGCATTGC 120
 AAAGCCATTG CTATCAACTA ATCCACTATC ATCTAACACT AGAnTTTGAG CGCCTTGCTT 180
 45 TACAGCATTC ACTGCTTCTC GGCCTAATGC TTCTAACGCA TCTTCAAAT CCCCTTCATA 240
 TACCGTTGAT AAATAAGTTA 260

(2) INFORMATION FOR SEQ ID NO: 4487:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 316 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4487:

5 ATGAGGTGCA TAGGGATAAA ACAGnnAGCA GCAATTTGTC GCTATTTGTA AATTGTATCC 60
 TGGCTTAAGT TGGCCATTTT TCATATGGTC TTCCTTCATT CTCATAAAAG TTGCATCATG 120
 ATCAGTTTTA GAAAAGCTAT TTCTATCTTT AAGAATCGAT TTTGTTCTT CATATTTATT 180
 10 TTTCTTTTCG GAATAATCAT CAAATTTATT TTTGAACTTC TTAATCTTAG TTCTTTTTTA 240
 CGGGTCTGTT TTCCAATTTG AGTACTATCC TCGTTCCCCA ATAGAATGAA TTAAACCTT 300
 CCGATTTTCCT TTAAnC 316

15 (2) INFORMATION FOR SEQ ID NO: 4488:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 307 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4488:

CACTTTTACT GCTAAAACGT CAATTGTTGA TGAGTCGTGT TTTATCTCAA GATGTGTTAC 60
 TCAAAAAGTT ATAGAAGAAG CTAATAAGT TAAACAGAG ATTGATACTG CCAGAAGATA 120
 30 ACTGTATCTC TCCATCTACT GTAAGTCCGT ATTAGAATA AAGCGGCTAA TTCATTACGA 180
 ATTAAACCTT TTAATTGTTT GCCAGACACA TCGCTATGGA TGAATTTAAA GCGTnAAAAT 240
 GTACTGGATC ATGAGTTTCAT TTTTATAGnT ATGTACnCAT GTGTATAGTA TTTAGAAATA 300
 35 GACTCAA 307

(2) INFORMATION FOR SEQ ID NO: 4489:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 344 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4489:

TTGGCAAATG TCATATAACT AGTAACATGA TCATCGACAT CAAATTTAGT ATGATCAAAT 60
 50 GTTCCCCAAT CATTAATTTG ATTCGGTTGT TTGCTCAATT GATTATATGT TTTTCCTAGC 120
 ACTTCATGCG GCACCATATC TTTACCTAGT AGCCCCACAA AGATAAGTCT AACAAGTGGC 180
 ACCATAATCG ATAAACTACC GCCACCTGCA CGCTTATGGT AAAACACCCA GCCAGCACTT 240
 55

TAGCAGTATG CCACnCCGGn GACGATATGG TAGCGACGTA AnAA

344

(2) INFORMATION FOR SEQ ID NO: 4490:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 313 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4490:

CCCAACCGGC ACATTGTTGT AAGCTGACTA TATGTCACCT CnTGTGTTGG GGCCCTGTC 60
 TTCGACTGGC ACTGCTCCCT CAGGAGTCTC GCCATTAATA CTACGTATTA ACATGTAATT 120
 TTACTTTTAA ATACTTTTAAA AAAATAAGAC ACTTTGGTCC AACTTAAGCC AGGGATACAA 180
 TTTACAAATA GCGACAAATT CTCAATTTGT nTTATCCTAT GGACCTATTT CAAAACCCAA 240
 CAGGTACTnA GTAACTTTGA ATTCCATTTT TTAACAATGG ATTGCAAAAT GACCTTACGG 300
 TTCATTTGAC CGG 313

(2) INFORMATION FOR SEQ ID NO: 4491:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 291 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4491:

AGGTCTGACT CTAGAGGATC CCCGATGAGT TTAAAGAAAA ATATCAAACA CCTGAATTAT 60
 ATTTTAAAGC TTGGCAAGGT TTTTACCACG AGGTTACACAA TGAGCCAGAA CGTGATGAAG 120
 TAATGCGTTA TATTCTGACT TTCTTAAATA ACAGCGTCAA TACAATGGGC TTTATTGTTG 180
 AAGATGACGA AATTGTAGAA ATTTAATATT CTAAAAAGGT TGGGACATAA ATCCCTAAAA 240
 AACAGCAGTA AGATAATTTT CCATTAGAAA ATATCTTACT GCTGTGChCh A 291

(2) INFORMATION FOR SEQ ID NO: 4492:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5 GCCGTCTCAG CCTTGGTCTT CGACTGGCAC TGCTCCCTCA GGAGTCTCGC CATTAACTACT 60
 ACGTATTAAC ATGTAATTTT ACTTTGAAAT ACTTAAAAAA ATAAACACT TTGCCCAACT 120
 10 TACACTACCA ATAGAACTG CTGTTAGAAT TCCTCAAAAT GATATTTTCGC GATATGTTAA 180
 TGAAATTGTT AAAAAGATAG CTGATAGCGA GATTGATGG AATTCAGACA TCATCGTGGG 240
 CGCAACATCC TATCATCTAA AAATGATGTT AAAAATCACC TGCATATTGC ATATACTGCA 300
 15 ATCTGGAATT TTCTGGGCCG TGAGAATGAG AAAAATnGAC nTCATGAACA GTGATTGCGA 360
 ATGGATGTGG GTTAAGCTnC AAGATTCAAA CACCTTGCTnT 400

15 (2) INFORMATION FOR SEQ ID NO: 4493:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 265 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4493:

25 TGATCCAGAG ATTTCCGAAT GGGGAAACCC AGCATGAGTT ATGTCATGTT ATCGATATGT 60
 GAATACATAG CATATCAGAA GGCACACCCG GTAGAACTGA AACATCTTAG TACCCGAGG 120
 30 AAGAGAAAGA AAATTGnTT CCCTTAGTAG CGGCGAGCGA AACGGGAAGA GCCCAAACCA 180
 ACAAGCTTGC TTGTTGGGGT TGTAGGACAC TCTATACGGA GTTACAAAGG AnGACATTAG 240
 ACGAATCATC TGGAAAGGTG AATCA 265

35 (2) INFORMATION FOR SEQ ID NO: 4494:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 293 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4494:

45 CATTACTAAA AAAGATAATC AAGGTATGAT TTCACGCGAT GTTTCAGAAT ACATGATTAC 60
 TAAGGAAGAG ATTTCTTGA AAGAGCTTGA TTTTAAATTG AGAAAACAAC TTATTGAAAA 120
 50 ACATAATCTT TACGGTAACA TGGGTTTCAGG AACAATCGTT ATTAAAATGA AAAACGGTGG 180
 GAAATATACG TTTGAATTAC ACAAAAAACT GCAAnGAGCAT CGTATGGGCA GACGTCATAG 240
 ATGGGCCCTA TATTGATACC ATTGGAGGTG AATnTAAATA ACCATGCACT CTC 293

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4495:

ACTTACAAAG TTCTGTGAAC CAAGTACCAT CAACTGCTGG TATGACGCAA CAAAGTATTG 60
 ATAACTATAA TGC GAAGAAG CGTGAAGCAG AAACTGAAAT AACTGCAGCT CAACGTGTTA 120
 TTGACAATGG CGATGCAACT GCACAACAAA TTTCAGATGA AAAACATCGT GTGCGATAAC 180
 GCATTTAACA GCATTnAAAC CAAGCGAAAC ATGAnTTTAA CTGCAGATTA CACATGCCTT 240
 AGGAGCAAGC AGTGCA 256

(2) INFORMATION FOR SEQ ID NO: 4496:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4496:

GTCATCAGAA ACCCTTGTCA CACAAGGCTT GTATTTTTTA TACTTATTTT TTAAATTAAA 60
 TTCATCATTa TCTAATTTAA AACAAATATAC TAAACGTTTC ATAATTATCG CCTGTACAAT 120
 ACGCACAAAA ACATGTCTTG AAACGCCTTT CATTACTCTA AnATACCCAA TATACTTTTT 180
 ATATCGTTTC GATTCTGAGT ATTCAGACG ATTTTCTGCA TAnAAATAAA CGTGTITCAA 240
 GGCAATATAT TGCA 254

(2) INFORMATION FOR SEQ ID NO: 4497:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 269 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4497:

AATCGGCTGT CTGATTCTGA ATCGCTATCT GAGTCCGAAT CGnTATCTGA ATCCGAGTCG 60
 CTATCCGAGT CTGAGTCGCT ATCTGAATCC GAGTCACTGT CGGAGTCGGA ATCACTATCT 120

GAGTCACTGT CGGAATCTGA ATCGCTATCT GAATCCGAAG TCACTGGTCG GGAATCTGAG 240
 TCACTGTnGG AATCTGAATC GCTATCTGA 269

5 (2) INFORMATION FOR SEQ ID NO: 4498:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 273 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4498:

CACCCCGGCA CTATAAAAAT GGAGCAGAAG ACGGGATTCTG AACCCGCGAC CCCAACCTTG 60
 GCAAGGTTGT ATTCTACCGC TGAACACTTT CTGCATATGC GGGTGAAGGG AGTCGAACCC 120
 20 CCACGCCGTA AGCTTAGnAT ACCTCAAGTC TAGTGCGTCT GCCAATTCCG CCACACCCGC 180
 AAATGGTGAG CCATAGAGGA TTCGAACCTC TGACCCTCTG ATTAAAAGTC AGATGCTCTA 240
 CCAACTGAGC TAAATGGCTC TnCAGGTGC CGG 273

25 (2) INFORMATION FOR SEQ ID NO: 4499:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 314 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4499:

GTAATAAAC GCATTTAGTG ATTGAAACAG GCAAGATAGA CGCGGGATAT CACGGCAATT 60
 TAGGGATTAA TATCAAGAAT GACGCTATTG CATCGAATGG TTATATCACA CCAGGTGTTT 120
 40 TTGAATATTA AAAGGAGAAT CGATTTGAAG TGCnnCATAA GACAATACGG ACTTATCAAA 180
 TCAACGAAGG AGACAAACTA GCTCAATTGG TTATCGTGCC TATATGGACA CCTGAACTAA 240
 AGCAAGTGGA GGAATTCGAA GTTGTTCAa CGTGGAGAAA AGGCTCGGAG AGCGGGTGAA 300
 45 AGCATCTTAG TCGA 314

(2) INFORMATION FOR SEQ ID NO: 4500:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4500:

5 ATTGTAAGGC TATCATGTCA AAGATTATAA CAATAAATCT GGTGAGATT TGGTGGCGGG 60
 GCGATGGAAG CTATCTATTT GACCATCCAT TTGGCAAAGG TTTGGGAGTT ACACAGGTGG 120
 ACTTAACTTT AATGGCGGTC GTCATATGG TATCGACTTT GGTATGCCTA CAGGAACGAA 180
 10 CCATTTATGC TGTTAAAAGG CGGTATAGCT GATAAAGTAT GGnCTGATTA CGGTGGCGGT 240
 AATTCTATAC AAATTAGGAC CGGTGCTAAC GAATGGAnCT GGTATATGCA TTTATCTAnG 300
 CATT 304

15 (2) INFORMATION FOR SEQ ID NO: 4501:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4501:

25 TTCCTTCATT CTCATAAAG TTGCATCATG ATCAGATCAG TTTTAGAAAA ACTATTTCTA 60
 TCTTTAAGAA TCGATTTTTG TTCTTCATAT TTATTTTTTC TTTCGGnATA ATCATCAAAT 120
 TTCTTTTGA ACTTCTTAAT CTCAGTTATT TTTTACGGG TCTGTTTTCT AATTGAGCA 180
 30 CAATCTTCGT TCTCAATAAG AATGATTAA ATCTnCGATT TCTTTATCTA AATGGACTAC 240
 CAATTAAATC TAT 253

35 (2) INFORMATION FOR SEQ ID NO: 4502:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4502:

45 AGTTCGGTCC CTATCCGTCG TGGGCGTAGG AAATTTnGA GGAGCTGTCC TTAGTACGAG 60
 AGGACCGGGA TGGACATACC TCTGGGTGAC CAGTTGTCGT GCCAAnGCAT AGCTGGGTAG 120
 CTATGTGTGG ACGGGATAAG TGCTGAAGAT GCTTAAGCAT GAAGCCCCC CAAGATGAGA 180
 50 TTTCCCAACT TCGGTTATAA GATCCCTCAA AGATGATGAG GTTAATAGGT TCGAGGTGGA 240
 AGCATGGTGA CATGTGG 257

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(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4503:

ATACGTTTAA TACACAAAA ACTGCAAAGC ATCGATGGCA GACGTCATAG ATGGCACTAA 60
 TATTGATAAC ATTGAAGTGA ATATAnAATA ATCATGACAT TCTCTAAATA GAAGCTGTCA 120
 TCGGAAAAAC AAGAAGTTAA GTGACAAGnT TTACATGTTG CTTAGCTTCT TTTATTATGC 180
 GTAATGATGT AAAAAGACGA ATATTCATTT GTTTGTA AAA GTGGCATTTC TATGTCCTAA 240
 AAGTGACGAA ACTTCAAATG TGCCAAGTGT 270

(2) INFORMATION FOR SEQ ID NO: 4504:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4504:

TACCTTGACC GAAGTTCTTA CCTACATCAC CTAAATTAAT GACATGTCCA CCAGTCATAT 60
 ACTCTAATCC ATGGTCGCCG ATACCTTCAA CGACAACATC TACACCACTA TTTCTAATAC 120
 AGAATCTTTC TCCTGCACTA CCGTTAATAA ATGCCTTACC ACTTGTCGCA CCATAGAATG 180
 AGACGTTACC AGCAATAATT TCATTTTGTC GTTCTTCAAA AGGTGCTTTG ACAATGACCG 240
 TACCACnGn T 251

(2) INFORMATION FOR SEQ ID NO: 4505:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4505:

AGAAGTTAAG CTCCTTAGCG TCGATGGTAG TCGAACTTAC GTTCCCGCTA GAGTAGAACG 60
 TTGCCAGGCA AATGACAAAT CGGAGAATTA GCTCAGCTGG GAGAGCATCT GCCTTACAAG 120

TAGCTCAATT GGTAGAnCAC TGA CT TGTAA TCAGTAGGTT GGGGGGTCAG TCCTCTGGCC 240
GGCACCATCT TTTGnCCATA 260

(2) INFORMATION FOR SEQ ID NO: 4506:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 313 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4506:

TTCITTAGTA GATACTAAGG CGTTATTAGA CGCATTAGAC AATGGTGTGA TTAAAGGTGC 60
AGCACTTGAT ACGTATGAAT TTGAACGCAA ACTTTTCCCA AGTGATCAAA GGGGCAAAAC 120
ACTGAACGAT CCATTGTTAG AATCGTTGAT TGACAGGGAA GATGTCATAT TAACACCACA 180
TATTGCGTTT TATACTGAAG CTGCAGTTAA AAATCTATTG TCGTGCATTA GGTGCAACAT 240
TAGGTGTATT GCAGCTTGGG GAACTTnGnT ACGGGTAAAT TTAAAATCGG CTGTGGGTAT 300
TTTGnTTTT GGG 313

(2) INFORMATION FOR SEQ ID NO: 4507:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 252 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4507:

GnCAATACGG CCAATTCCTA AGATTGCTAC TTCTGGGTGG ATTGATAACT GGAGTGAACC 60
ATTGTCCACC AGCTGnAACC GATATTACTG ATTGTGCATG TAGCACCTTT CATTTTCATCG 120
GCTGTTAATT TACCATCACG TGGCTTTAAC AGCTAATTCA TTAATTTTCAT CTGAAATTTG 180
GGAAAATAGA CTTACGGATC AGCATGTTTA ACAACAGGTA CTAATAATCC TCTATCAGTG 240
TCTGCTGCAA TT 252

(2) INFORMATION FOR SEQ ID NO: 4508:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 268 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4508:

5 CATCGAACCA GATGTACTCG CACTTGTTGA GTCTGATGTT GAATCACTAA CACTATCAGA 60
 TAATGACGTT GAATCACTCA TACTTGTTGA TGTACTTGTC GAAAGCGACA TACTTTGTGA 120
 ATCACTAGTA CTTGTACGCA TCGAAGTACT AGTTGAAGCT GATGTACTAC GAGAGTCACT 180
 10 TGTTGATGTT GATGTACTTG CTGATCCTGA TGCACCTGTA CTTCTTGATG TGCTTTGTGA 240
 ATCGGATTTC GCTCGTGcT GGTACTnG 268

(2) INFORMATION FOR SEQ ID NO: 4509:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 296 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4509:

25 CGAGAGTGCG TTAATTCCGT TACTGCTATC ACgTAAGGGG CGGAAACCCC CTAACACTTA 60
 GCACTCATCG TTTACGGCGT rGACTACCAG GGTATCTAAT CCTGTTTGAT CCCCACGCTT 120
 TCGCACATCA GCGTCAGTTA CAGACCAGAA AGTCGCCTTC GCCACTGGTG TTCCTCCATA 180
 30 TCTCTGCGCA TkTCAACGCT ACACATGGAA TTCCACTTTC CTCTGCTGGC ACTCAAGTTT 240
 TCCAGTGTCC AATGACCCTC CACGGTTGAG CCGTGGGCTT nCACATCACA CTTAnA 296

(2) INFORMATION FOR SEQ ID NO: 4510:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4510:

45 TTACTACTTA CTGAGTGACC TGTACCTGCT TTCGGAGTAA TTGTGATTGA TGAATTTGGT 60
 TTTATAGTAT TGGCATTGAA CGTCACTTTA CCAGTTTGTG CATCTAACGT TACATAGTCA 120
 GGCTTATTCG CAATTGTCCA TTGnTTATTT TGACCACGAA CAACATTAAT TGTCCTACTA 180
 50 TGTTGCTGCA CCATTACCCA CThTTCAGT GTAAGCAATA TCCATTGCTT GAGTTGGGAT 240
 TAATTAAATG GTCCTGA 257

(2) INFORMATION FOR SEQ ID NO: 4511:

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(A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4511:

10 AAAATCACAT CAGCCTGCAT TAACGACGTC GTTAATTTAT ATACATCTCC TGTAGTATCT 60
 AGATAATTCT TTCCAACGCT AAATTCTAAT TCAAGTTCTC GTAAATCCAT CAACTCTATT 120
 TGATGTCCCT CATTGATGAC TTCTAGTTCA TTTTAAAT CATCCATAGC AATTCTCGTT 180
 15 TTAGAACCTA CTGTGGAACC TGACAATAAT ACAATATTCA nGanGACGCC CCTCCTATTT 240
 TGATAAATGC 250

20 (2) INFORMATION FOR SEQ ID NO: 4512:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4512:

30 AGCTGGnTTC GAACCAACGA GTGACGGAGT nAAAGTCCGT TGCCTTACCG CTTGGCTATA 60
 GCCCAATATA TAGATGGTGG AGGGGGGCGAG ATTGGAAGT CCGAACCCGA AGAGCGGATT 120
 TACAGTCCGC CGCGTTTAGC CACTTCGCTA CCCCTCCAGC TTATTCATAT AATTTAATAA 180
 35 TCAAAATGGT GGAAGAATGA CGGGTTCGAA ACCGCCGACC CTCTGCTTGT AAGGCAGATG 240
 CTCTCCCCAG CTG 253

40 (2) INFORMATION FOR SEQ ID NO: 4513:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4513:

50 GnCGACCCCTT AATAACTTAA TCTATGTTTC CACCATTTTT ATAAGTCAAA CGTTAACATG 60
 nAAGTTACGT TCTTTTATAA AAAGATTAA ACGCGTTATT AATCTTGTC AGTGTCTTTT 120
 55 CGAACACTAG CGATTATTTT TTATGAATTC AAGCTTATTT AAAACTCTTT ATTCACTCGG 180

GTGGAGACTA GC

252

(2) INFORMATION FOR SEQ ID NO: 4514:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 244 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4514:

15 GTCATTGAAT ATGGAACTT TAGAATTACA AGGCGCTAAA TTACGATACC ACCAAGTCGG 60
 ACAAGGACCC GTGCTCATCT TTATTCCTGG TGCAAACGGT ACCGGAGACA TTTTCTGCC 120
 TCTTGCAGAA CAGTTAAAAG ACCATTTTAC TGTGTAGCC GTTGATCGTC GTGATTATGG 180
 20 AGAAAGCGAG TTAAGTGAAC CACTCCCTGA TTCCGCTTCA AACCTGACA GTGATTATCG 240
 TGTC 244

(2) INFORMATION FOR SEQ ID NO: 4515:

- 25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4515:

35 TATTAGGCAA ATCCGGTACT CGTTAAGGCT GAGCTGTGAT GGGGAGAAGA CATTGTGTCT 60
 TCGAGTCGTT GATTTACAC TGCCGAGAAA AGCCTCTAGA TAGAAAATAG GTGCCCCGTAC 120
 CGCAAACCGA CACAGGTAGT CAAGATGAGA ATTCTAAGGT GAGCGAGCGA ACTCTCGTTA 180
 40 AGGAACTCGG CAAAATGACC CCGTAACTTC GGGAGAAGGG GTGCTCTTTA GGGTTAACGC 240
 CCA 243

(2) INFORMATION FOR SEQ ID NO: 4516:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4516:

55

GATTGTCCTT TGGACAATGG TAGGAGAGCG TTCTAAGGGC GTTGAAGCAT GATCGTAAGG 120
 ACATGTGGAG CGCTTAGAAG TGAGAATGCC GGTGTGAGTA GCGAAAGACG GGTGAGAATC 180
 5 CCGTCCACCG ATTGACTAAG GTTTCAGAG GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT 240
 CCCTAACCT GAGGCCGCAA nnGTAGG 267

(2) INFORMATION FOR SEQ ID NO: 4517:

10

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 319 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4517:

20 TTGAATCTGA CGAAACGAGA AAAGAGCGCA ACGAGTTTAG TAGAGCTAAA TGAGTAAGCG 60
 AGAGCCGAAG AGAGGAAAGA AGCAAGCGAT TGTACAAGT CAAGAAAGGT CTTTAGCGAC 120
 GATGGTAGCC AACTTACGTT CCGCTAGAGT AGAACGTTGC CAGGCAAAA ATGGGATGCG 180
 25 ATGAGCCGCA TTGGAGACCG CAGTCCTnTn TnTTTTTTTA TGGCCTTAAA ACGTCAAAAT 240
 TAAAAAGTTA AACACAAAGA AAATGGGCTT TGGCGAGTGG AAACGTTTGT AATCTGGACG 300
 GAACGAGAAA GAGCGCACG 319

30

(2) INFORMATION FOR SEQ ID NO: 4518:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 259 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4518:

40 GGTATAATAG ATGACTATGT ACTATTTCCG GTACATCCTT GGCAATATCA GCATATTCTG 60
 CCGAACGTCT TTGCGAAAGA GATTAGTGAA AAGTTGGTTG TACTATTACC GTTAAAATTT 120
 45 GGAGATTATC TGTCGTCTTC AAGTATGCGT TCATTAATTG ATATTGGCGC ACCGTATAAC 180
 CATGTCAAnG TACCATTTCG AATGCAGTCA TTAGGCGCAT TAAGGCTAAC GnCTACGGTT 240
 ACATGAAAAA CGGGGAACA 259

50

(2) INFORMATION FOR SEQ ID NO: 4519:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 253 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4519:

ATAGGGTGTT GCTGAATAGG GCGTTTAGTA TTTGGTCGTA CCGnnAACCA GGTGATCTAC	60
10 CCTTGGTCAG GTTGAAGTTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA	120
AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGG AGATAGCTGG	180
TTCTCTCCGA AATAGCTTTA GGGCTAGCCT CAAGTGATGA TTATTGGAGG TAGAGCACTG	240
15 TTTGGACGAG GGG	253

(2) INFORMATION FOR SEQ ID NO: 4520:

(i) SEQUENCE CHARACTERISTICS:
20 (A) LENGTH: 245 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4520:

AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT	60
30 TTTTCTTTGT GTTACTTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG ACCTCACGGT	120
CTCAACTTGC CTGGCAACGT TCTACTTAG CGGAACGTAA GTTGGChACC ATCGTCGCTA	180
AAGACCTTTC TTGACTnGTG ACAATCGCTT GCTTCTGTCC TCTCCTTCGG CTCTCGCTTA	240
35 CTCAT	245

(2) INFORMATION FOR SEQ ID NO: 4521:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 251 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4521:

GGGCCTAAGT GGA CTCGAAC CACCGACCTC ACGCTTATCA GCGTGCGCT CTAACCAGCT	60
50 GAGCTATAGG CCCATTAATT TGAATGAACA AACATTCAAA ACTGAATACA ATATGTCACG	120
TTATTCCGCA TCTTCTGAAG AAGATGTTCC GAATATATCC TTAGAAAGGA GGTGATCCAG	180
CCGCACCTTC CGATACGGCT ACCTTGTTAC GACTTCACCC CAATCATTTG TnCCCACCTT	240

55

(2) INFORMATION FOR SEQ ID NO: 4522:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4522:

```

nATAGAACCT GAAACCGTGT GCTTACAAGT AGTCAGAGCC CGTTAATGGT TGATGGCGTG      60
CCTTTTGTAG AATGAACCGG CGAGTTACGA TTTGATGCAA GGTAAAGCAG TAAATGTGGA      120
GCCGTAGCGA AACGATGTCT GAATAGGGCG TTTAGTATTT GGTCGTAGAC CGAAACCTGG      180
TGATCTACCC TTGGTCAnGT TGAAGTTCAG GTAACACTGA ATGGAGGACC GAACCGACTT      240
ACGTTTGAA                                         249
  
```

(2) INFORMATION FOR SEQ ID NO: 4523:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4523:

```

TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGAGGACCG      60
GGATGGACAT ACCTCTGGTG TACCAATTGT CGTGCCAAng CATAGCTGGG TAGCTATGTG      120
TGGACGGGAT AAGTGCTGAA GATCTnAAGC ATGAAGCCCC CCTCAAGATG AGATTTCCCA      180
CTTCGGTTAT AAGATCCCTC AAAGATGATG AGGTTAATAG GTTCGAGGTG GAAGCATGGT      240
GACAGTGG                                         248
  
```

(2) INFORMATION FOR SEQ ID NO: 4524:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4524:

```

AACGTTAAGA TCCCTATTAA ATTATCTTAG GAATCATCAT GGGCATTAT GATGTCTTAA      60
  
```

AAATTAGTAA TCTGAATCTG CTTCTAAACC TTGTCATAAT TTGA_nCGGCT GTGGCTCG_nA 180
 CCAATACGGG TCGGACCTGC TThAACCATT TTATTGGAAA TCTTCTAAAT TACGGACGGC 240
 5 ACCCGGATGC TTTTACTTCT ATATCAGCAC CTACTGTATC TTTCATTAAT TTAACGGCTT 300
 CTGCAGTCGG ACCGGCAACT GCAAAA 326

(2) INFORMATION FOR SEQ ID NO: 4525:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4525:

20 AAGAGCACCC TTCTCCGAGT TACGGGGTCA TTGCGCGTT CCTTAACGAG AGTCGCTCGT 60
 CACCTTAGAT TCTCATCTTG ACTACCTTGT CGGTTTGCGG TAnGGCACCT ATTTTCTATC 120
 TAGAGGTTTT CTCGGCATGT GAAATCAACG ACTCGAGACA CAATGTCTTC TCCCATCACA 180
 25 GTCAGCCTTA ACGAGTACCG GATTTCCTA ATACTCAGCC TACTGCTTAG nGGCATCCAT 240
 CGCAGTThGC TATCCACTGG TCCCCCTCGA TTAAACGATT ATAGGTGGTA CAGATATCAA 300
 C 301

(2) INFORMATION FOR SEQ ID NO: 4526:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4526:

40 TGATATTATG AGCTGTGTTT TTAGCTTTAG AACCGAAGTC CCCTGCTTTT TTACCAAGAT 60
 TTTCAGTAAC TTGTnCCATC CATTTTTTCT TTTCGTACC ACCATGGAAT TTTGGCAAAA 120
 45 CACCCATCCG CTGTA_nCTTC AGAGTGT_nCAT TGGCATTTAT TACACTATCT CCAACTCCTA 180
 GTGGAACAAC CACATCTCGT CCTTGGGGTG CATGGAATGT nCCGTCAGCC CTGTGAATTA 240
 T 241

(2) INFORMATION FOR SEQ ID NO: 4527:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4527:

	CGATCACACT CTTCCGTCGT CATCGCCATT GGCTTTTCAC ACAATACATG GACACCATGG	60
10	TGTCAATGCT TCTATAGAAA GATCAGCATG GAATTTATTA GGTGTACAAA TGACCACCGC	120
	ATCAACAAGT TTAAACAGCT CGCTAGGTGT CTCAACTGCA TGAGGTATAT TGAAAGCGCT	180
	TCGCAACCAT nCAATCATCT GGCACGTGTTA TTGAATATCT TGTGACTGGC AACTTAATGA	240
15	GnACTGTGTC TTTTGGAGTT TCCAGnCAAT GCCGGGAATT ATGGACGGGT CTTGGTGGCA	300
	ATACCACCCA ACACCT	316

20

(2) INFORMATION FOR SEQ ID NO: 4528:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4528:

30	GTCCCAAGGG TTGGGCTGTT CGCCCATTAAGCGGTACCG ACGACTGGGT TCAGAACGTC	60
	GTGAGACAGT TCGGTCCTTA TCCGTCGTGG GCGTAGAAAT TTGAGAGGAG CTGTCCTTAG	120
	TACGAGGAGG AnCGGGATGG ACATACCTCT GGTGnACCAG TTGTCGTGCC AACGGCATAG	180
35	CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAAGCAT CTAAGCATGA AGCCCCCTC	240
	AAGATGAGAT T	251

40

(2) INFORMATION FOR SEQ ID NO: 4529:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 318 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4529:

50	AGTACGTGAC GTTCACTACT CTCACATATGG CCGTATGTGT CCAATTGAAA CACCTGAGGG	60
	ACCAAACATT GGATTGATTA ACTCATTATC AAGTTATGCA CGTGTAATG AATTCGGCTT	120
	TATTGAAACA CCATATCGTA AAGTTGATTT AGGATACACA TGCTATCACT GATCAAATGA	180

55

ATGGTCGTTC AGGTGATGAG TGTATGCGTT CGGGnACnAT CAGTATGCAA GAAAAGGTTT 300
GTGACGCGAC AGTGTcNA 318

5 (2) INFORMATION FOR SEQ ID NO: 4530:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 240 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4530:

15 TAGCTGTGTG ATAAATTGCA AGTGCGGCAC CACATAAGCC GAACATCATC GTAATAAAAC 60
GGCCTGACAT ACAGCGTGAC ACACCTGAAT AATACTTCGT CACATCTGGA TCACCAAGTT 120
20 GAGCAAAGAn GATGTTCTnC GTACCTTGAA CTAAGTGCCC TTTGACTTCT AAAGTACCAC 180
CAAGTGCCCGT CTGCCAAAAC GGTAAGTAAA AAATATGGTG TAAACCGAGT GGACCTAACA 240

(2) INFORMATION FOR SEQ ID NO: 4531:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 254 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4531:

CGGCTCTTCT GGGACGTTAA CCCTAAAGTG CACCCCTTCT CCCGAATTAC GGGGTCATTT 60
35 TGCCGAGTTC CTTAACGAGA TTCGACTCGn TCACCTTAGA ATTCTCATCT TGACTACCTG 120
TGATCGGTTT GCGGTTAGGG GCACCTATTT TCTATCTAGA GGCTTTTCTC GGCAGTGTGA 180
40 AATCAACGAC TCGAAGACAC AATGTCTTCT CCCCATCACA GcncAGCCTT AACGAGTACC 240
GGATTTGCCT AATA 254

(2) INFORMATION FOR SEQ ID NO: 4532:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 238 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
50 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4532:

55

TGAATAAACCC GAATGTGGCT AAAGTCGTTA ACGCAAAATA TGACGTCATC TATAACGGAC 120
 ATACTTTTGC AACATCTTTA CCAGCGnAAT TTGTAGTAAA AGATGTGCAA CCAGCGAnAC 180
 5 CAACTGTGAC TGAAACAGCG GCAGGAGCGA TTACAATTGC ACCTGGAGCA AACCAAAC 238

(2) INFORMATION FOR SEQ ID NO: 4533:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4533:

GGTCATTAAT AAAATATCTA AAGCCATTAC TGCATAAAAA TCTCATCAAG CCAATACCTA 60
 20 CATTGTACTA CTGGnCACTT TAGACAGGnC AAGGGTGTAG CTACCGATAA TTCAGGAGCA 120
 TTAACGCAAC CGACATTTGA CTGTATTAAA TGATAGAGGT TCTGGAAAAC GCCCCAGGTG 180
 GTGGAGTTCA AGAAATAATT CACAGGGCTG ACGGAACATT CCTGCACCCC AAGGACGAGA 240
 25 TGTGGTTGTT CCACTAGGAG TTGGAA 266

(2) INFORMATION FOR SEQ ID NO: 4534:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4534:

TACTCAGAGG ATACCCCGAC GTAATGCATT CAATTCAATT TTAAACGTA TTATTTCAAT 60
 40 GAGCAGAAAG AAAATTATGG CACCAAACCT TAATATTTTT TTCAATGTCA TTCTTTTGAn 120
 GGGAGTGGGA CAGAAATGAT ATTTTCGCAA AATTTATTTT GTCGTCCAC CCCAACTTGG 180
 CATTGTCTGT AGAAATTGGG AATCCAATTT CTCTTTGTnG GGGCCCATCC CCAACTTGCA 240
 45 CATTATTGTA AGCTGACTTT TCGT 264

(2) INFORMATION FOR SEQ ID NO: 4535:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4535:

5 GCGAATGGAT AACAGTTGAT ATTCCTGTAC CACCTGATAA ATCGTTTTAA TCGATGGGGG 60
 GACGCATAGG nATAGCGAC TGCCGATTGG ATTGCACTCT AAGCAGTAAG GCTGAGTATT 120
 AGGCAAATCC GGTACTCGTT AAGGCTGAGC TGTGATGGGG AGAAGACATT GTGTCTTCGA 180
 GTCGTTGATT TCACACTGCC GAGAAAAGCC TCTAGATAGA AAATAGGTGC CCCGTACnGC 240
 10 AAACCGACAC 250

(2) INFORMATION FOR SEQ ID NO: 4536:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4536:

20 AATGACGGGT TCGAACCGCC GACCCTCTGC TTGTAAGGCA GATGCTCTCC CAGCTGAGCT 60
 25 AATTCTCCGA TTTAAACTG CCTGGCAACG TTCTACTCTA GCGGAAnTAA TTCGAACTAC 120
 CATCGACGCT AAGGAGCTTA ACTTCTGTGT TCGGCATGGG AACAGGTGTG ACCTCCTTGC 180
 TATAGTCACC AGACATATGA ATGTAATTTA TACATTCAAA ACTAnATAGT AAGTA 235

(2) INFORMATION FOR SEQ ID NO: 4537:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4537:

40 TGCATCTTCA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 60
 TACGCCTTTC GTGCGGGTCG GAACTTACCC GACAAGGAAT TTCGCTACCT TAGGACCGTT 120
 45 ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTTCGTAGC TTCGCAGAAG CTAACCACTC 180
 CTCTTAACCT TCCAGCACCG GGCAGGCGTC AGCCCTATAC ATCACCTTAC GGTT 234

(2) INFORMATION FOR SEQ ID NO: 4538:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4538:

5 ACCCTCTGCT TGThAGGCAG ATGCTCTCCC AGCTGAGCTA ATTCTCCGAT TTAAAACTGC 60
 CTGGCAACGT TCTACTCTAG CGGAACGTAA GTnGACTACC ATCGACGCTA AGGAGCTTAA 120
 CTTCTGTGTT CGGCATGGGA ACAGGTGTGA CCTCCTTGCT ATAGTCACCA GACATATGAA 180
 10 TGTAATTTAT ACATTCAAAA CTAGATAGTA AGTAAAAGTG ATTTTGCTTC GCAAACCATT 240
 TA 242

(2) INFORMATION FOR SEQ ID NO: 4539:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 20 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4539:

25 TCATTAACAC CATCACCATA AATAAACCT TCCATATCTG TTCCTGTGCC AATAAGCCA 60
 TATTGCGTTT GGnCTGTCGT GCCAGTGCAA GATTCCAAC GATAATTTCT AGGCGTCACT 120
 GCTGGCGAAC CATCTAATGG ATAATCATAA TCCATCGTGC GTCCAAGAAG TACTTGnTTT 180
 30 ATTTAAAGTT TGTATTGTGG AATCCTGTGC ACATGTTCTC ACTCCTCTGT ACCT 234

(2) INFORMATION FOR SEQ ID NO: 4540:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4540:

ACACAAAGAA AAATGGCTTG GCGAAGTGAA AAcnGTTGAA TCTGACGAAA CGAGAAAAGA 60
 45 GCGCAACGAG TTTAGTAGAG CTAAATGAGT AAGCGAGACC GAAGAGAGGA AAGAAGCnAG 120
 CGATTGTCAC AAGTCAAGAA AGGTTCTTAG CGAGGATGGT AGCTAACTTA CGTTCCGCTA 180
 GAGTAGAACG TTGCTAGACA AGAAATGAAT GCGATGAGCC GCATTGAGTG TGAAATTGAT 240
 50 AT 242

(2) INFORMATION FOR SEQ ID NO: 4541:

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(A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4541:

10 GCCCTTAATA ACTTAATCTA TGTTTCACC ATTTTATAA GTCAAACGCT CACATACGGC 60
 TTCGTTTTCA TTATTTTAAA TGCTCATTTA CATAAGTAAA CTCTGCTTTA AAATAATTTA 120
 ACTCATTGTC TGCTAAACGT TTTCTTTTAT AAAAAGATTT AAACGCGTTA TTAATCTTGT 180
 15 GnAGTGTCTTCT TTCGAACATA GGCGATTATn TCTTATGAAT TCAAGCTTAT TTAAAACTCT 240

(2) INFORMATION FOR SEQ ID NO: 4542:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 242 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4542:

AAGCTAGCAA TGATGTCAAG CAATGGCAAC ATGTGCTCAn TTAGCTAATA TGCAAGCACA 60
 30 TGGTGAATAT GACGAGGTTG CAACTTCAAC GGCGAGGnTG ATGAATGCCT TACGTTTGCG 120
 TGAGACAGTA GCTATGGGCC GCGGTATTAC AGGTGGTAAT GGCATACTGA GCTGACGATT 180
 ATGATATTGT CACGTTTTCT TCTCTGTATG CAGAAGCGAT TTACACGTAC GAGGTACACA 240
 35 TG 242

(2) INFORMATION FOR SEQ ID NO: 4543:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4543:

TGGTGAGCCA TAGAGGATTC GAACCTCTGA CCCTCTGATT AAAAGTCAGA TGCTCTACCA 60
 50 ACTGAGCTAA TGGCTCTTCC ATGGTGCCGG CCAGAGGACT TGAACCCCCA ACCTACTGAT 120
 TACAAGTCAG TTGCTCTACC AATTGAGCTA GGCCGGCAAT ATGTAAGATT AAATGGTGGA 180
 55 GAnTGACGGG TTCGAACCGC CGACCTCTG CTGTGAAGGC AGATGCTCTn CCAGCTGAG 239

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4544:

10 ATAGAGGATT CGAACCTCTG ACCCTCTGAT TAAAAGTCAG ATGCTCTACC AACTGAGCTA 60
 ATGGCTCTTC CATGGTGCCG GCCAGAGGAC TTGAACCCCC AACCTACTGA TTACAAGTCA 120
 GTTGCTCTAC CAATTGAGCT AGGCCGGCAA TATGTAAGAA TAAATGGTGG AGAATGACGG 180
 GTTCGAACCG nCGACCCTCT GCTTGTAAGG CAGATGCTCT nCCAGCTGAG CTAAATTCT 239

(2) INFORMATION FOR SEQ ID NO: 4545:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4545:

20 AATTCATGCT TTCAAAGAC GATATACTAC GACACTCCTA CGAACTTGTC CAAGGATTAC 60
 30 GAAAAGACCT AAGGTTATGT AATTGGCCTA AATTTATTAA TCGTTTAAAT TCAGTTAGTA 120
 AAAAGTCTGT GAGTAAGGGT GTATGGAAAG TGGTTAATA TTATAGAAAA CATCAAAGGA 180
 35 TGTTAAGAAA TACnATTTAT TACCCAGCAT TTAATAATGG TGCTATAGAA GGA 233

(2) INFORMATION FOR SEQ ID NO: 4546:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 247 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4546:

45 ACTTTGTTGT CTTCCATCAA CTTGAGACTT CATAACGTTT TGCATCTTCG CCACCTTCAC 60
 CACTATTACT CTTTCCACCT AATTGGTTCA TGGCTTGTC TAnTTTTTCA TGTGCTTCCG 120
 50 CTGAAATCGA TCCATAACTC ATCGCCCTG TATTAAAGCG TTTGACAATG TCACCTACCG 180
 GTTCAACTTG GnCGATGTCA ATCGGTGTAC ATGCTTTAAA TTCAAGTAAA TGTCTAATGT 240

(2) INFORMATION FOR SEQ ID NO: 4547:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4547:

GAGGAAATTA CTGAAAACAA TCATCATATT TCTCATTCTG GTTTAGGAAC TGAAAATGGT 60
 CACGGTAATT ATGGCGTGAT TGAAGAAATC GAAGAAAATA GCCACGTGGA TATTAAGAGT 120
 GAATTAGGTT ACGAAGGTGG CCAAAATAGC GGTAATCCAG TGCATTTGAG GAAGACACAG 180
 AAGAAGTTTA AACCGAAATA TGnAACCAAG GTGGGCATTA TCGTTGGTTA TCGATTTTCG 240
 ATAGTGTAAC TCAAATTTCA TGGGTCCAAA TTAATGGTTA ACCCATCCAT TCGAnGnAGG 300

(2) INFORMATION FOR SEQ ID NO: 4548:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 306 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4548:

TTGCTATAGT CACCAGACAT ATGAATGTAA ATTATACATT CAAAAC TAGTAAGTCA 60
 AAGTGATTTT GCTTCGCAA CATTTATTTT GATTAAAGTCT TCGATCGATT AGTATTCGTC 120
 AGCTCCACAT GTCACCATGC TTCCACCTCG AACCTATTAA CCTCATCATC TTTGAGGGGA 180
 TCTTGATAAA CCGnAAGTTG GGGAAATCTC ATCTTTACGG GGGGGCTTCA TGCTTAGGAT 240
 GGCTTTnCAG CACTTTATGC CCGGTnCCAC ACATTAGGCT TACCCAGCCT ATGCCCCGTTT 300
 GGCACG 306

(2) INFORMATION FOR SEQ ID NO: 4549:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4549:

CTTCTACTTT TGTACCATCA ATAAGATTTT GCTTTAAACA TTGACTATGA AACTGGATAA 120
 ATAAAGATTG AATTAACGCA TCAGTATTAG GATTCACTCT AATACGATTA ATAGTTTTAT 180
 5 AAGAAGGTGn TTGATTTTGA GCTAACCACA TCATTGGAAT ACTGTCATGn AG 232

(2) INFORMATION FOR SEQ ID NO: 4550:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4550:

CTGGGTTTCAG AACGTCGTAT GnAGTTCGGA TCCCTATCCG TCGTGGGCGT AGGAAATTTG 60
 20 AGAGGAGCTG TCCTTAGTAC GAGAGGACCG GGATGGACAT ACCTCTGGTG TACCAGTTGT 120
 CGTGCCAAng CATAAGCTGG GTAGCTATGT GTGGACGGGA TAAGTGCTGA AACATTCTTA 180
 AGCATGAAGC CCCCCTCAAG ATGAGATTTT CCAACTTCGG TTATAAGATC CCTCAAAGAT 240
 25 GATGAAGTTA ATAAGTTC 258

(2) INFORMATION FOR SEQ ID NO: 4551:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4551:

TTACAGGCAT GCGAGTTGGG GTGAGGGCCC ACACAGAAGC TGACGAAAAG TCATGACAAT 60
 40 AATGTGCAAG TTGGGGATGG GCCCACAAAG AGAAATTGGA TTCCCAATTT TACAGACAAT 120
 GCAAGTTGGG TGGGACGACG AAATAAATTT GCGAAAATAT CATTTCTGTn CCCTCCCTCA 180
 AAAGATGACA TTGAAAAAAT ATTAAAGTTG GTGCCATATT TTCTTCTGCT CATGAATATA 240
 45 CGTTAAATTT GATTGATCAT CGCGAATTGA TATTATTCTC ATTATAAAAA TACTTATTAC 300
 ACTTACCGTA TGATAGTTTG nTATATACTC TGATAAAGTC AAACCTAATA GCGTTTCTAG 360
 50 CTGTGnGTGT TTCATAATTA TATACATTAT CAGGCTTTAA 400

(2) INFORMATION FOR SEQ ID NO: 4552:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4552:

	ATAGGAAACT GCCAATTGGA CGGTTGCCGC ATTCAAACCC AGCACGATTA CGGCGAATTG	60
10	CACGTGAAnC ATTTCTACAG CTTGATCTTG ACCTATGATT TTACTTCTTA AACGATTAGA	120
	AATATTTTTT AAACGTTCAA TATCGTTATC ATCCATTGG AGAACTGGG AATACCATTG	180
	AATCGTTGnA ATAGTATCTG GAAATATCAT GGAACGTAG CAACAGCAGT GTGTTGCACC	240
15	ATTnACTGAT TTTGCTAATT TATCTTGGTG AATGGATTG GATTGCAATT TTGGAATGTG	300
	CGTGCAGCTT TT	312

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(2) INFORMATION FOR SEQ ID NO: 4553:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 254 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4553:

30	AGCAGCGATC AAAAATAATC CGCAATACGC TGGCAAACCTA CCAATACCAA ACCATAGAAC	60
	AACAAATGGT GCCCATGCTA TCGGAGATAT CGGCCTAATC AATTGAAATA GCGGTTGAT	120
	AGCGTTGTAT AGCCAACGAT TCCTTCCAAG CAAGAAGCCC AATGGAATAG CAACCAACAA	180
35	TGCGACAACA AAGnCCGCTA CAAATCTCCA TGAACCTAATT GCTAAATGTG GnGAATTTCT	240
	CCAGTAACAA TGGA	254

40

(2) INFORMATION FOR SEQ ID NO: 4554:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4554:

50	GGTCTGAATC GCTATCTGAG TCTGAATCGC TATCTGAGTC TGAATCACTG TCTGAGTCCn	60
	AGTCACTGTC TGAATCTGAC TCACTATCTG ATTCTGAGTC GCTATCTGAT TCTGAGTCGC	120
	TGTCTGGAAT CTGAATCACT GTCTGGAATC CGAATCGCTA TCTGGATCTG AGTCGCTATC	180

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CTGGGGCTTG G

251

(2) INFORMATION FOR SEQ ID NO: 4555:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4555:

TACACAAAGA GATAAATTAC TTATGCAAAG GCGGAGGAAT CACATGTCTA TTA CTGAAAA 60
 ACAACGTCAG CAACAAGCTG AATTACATAA AAAATTATGG TCGATTGCGA ATGATTTAAG 120
 AGGGAACATG GATGCGAGTG AATTCCGTAA TTACATTTTA GGCTTGATTT CTATCGCTTC 180
 CTATCTGAAA AAGCCCTACC AGAATATGCA GTGCCCTGTC AAGnGAAGAC ATCACGTTCC 240
 AGAAGCATGG C 251

(2) INFORMATION FOR SEQ ID NO: 4556:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 243 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4556:

AGCTACCCCG GGGATAACAG GCTTATCTCC CCCAAGAnTT CGCATCGACG GGGAGGTTTG 60
 GCACCTCGAT GTCGGCTCAT CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT 120
 TCGCCCATTA AAGCGGTACG GAGGCTGGGT TCCGAACGTC GTGAGnCCGT TCGGTCCCTA 180
 TCCGTCGTGG GCGTAGGAAT TTGAGAGGAG CTGTCCTTAG TACGAGAGGA CCGGGTGGAC 240
 ATA 243

(2) INFORMATION FOR SEQ ID NO: 4557:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4557:

TCATTATTTT AAATGCTCAT TTACATAAGT AAACCTCTGCT TTAAAATAAT TTAACCTCATT 120
 GTCTGCTAAA CGTTTTCTTT TATAAAAAGA TTAAACGCG TTATTAATCT TGTGAGTGTT 180
 5 CTTTCGAACA CTAGnCGATT ATTTCTTATG AATTCAAGCT TATTTAAAAC TCTTG 235

(2) INFORMATION FOR SEQ ID NO: 4558:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4558:

CCGTTAAGCA CTAAATCCGC TTAATAACGG CTTTCTATCG CGCGCAACAT CTCGTTTGAC 60
 20 TGCTTTTTCT TTCAAAGCTT GACGTTATCA TATTTTTTCT TACCTCGTGC ACACCAAGTA 120
 ATACTTTACA ATGTCCATGC TTCAAATAAA GCTTTAACGG ACAATCGAAT AACCAAnCTC 180
 ACGTGTGTTGA TCACCCAATT TAATGATTTT ACGCTTGTC AATAATnATT TTCGAGACGA 240
 25 GAGGATCGGA TTAAAACGAT CCCCTCCTCG TATGG 275

(2) INFORMATION FOR SEQ ID NO: 4559:

(i) SEQUENCE CHARACTERISTICS:
 30 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4559:

TTATATGGAT GTATCGCCGA AGCAAGTTGT TTCAGCAGCG ACAnATGTAT TCCGATGACT 60
 40 CAAACCGTGC ATTGATGGGT GCGAACATGC AACGTCAAGC AGTGCCTTTG GATGAATCCA 120
 GAAGCACCAT TTGTTGGTAC AGGTATGGAA CACGTTGCAG CACGTGTATT CTGnGTGCGG 180
 CTATTACAGC TAAAGCACAG AGGTCGTGTT GAACATGTTG GAATCTAATG AAAT 234

45

(2) INFORMATION FOR SEQ ID NO: 4560:

(i) SEQUENCE CHARACTERISTICS:
 50 (A) LENGTH: 232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTCACGG TCTCAACTTG CCTGGCAACG 60
 TTCTACTCTA GCGGAAnTAA nTGGCTACCA TCGTCGTAA AGACCTTTCT TGA CTGTGTGA 120
 5 CAATCGCTTG CTTCTTTCCT CTCCTTCGGC TCTCGCTTAC TCATTTAGCT CTA CTAAACT 180
 CGTTGCGCTC TTTTCTCGTT TCGTCAGATT CAAACGTTTT CACTTCGCCA AG 232

(2) INFORMATION FOR SEQ ID NO: 4561:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4561:

20 TCAAAGGACG CATACCATTA CGGGTCTGCT ACTTGTAAGC ACACGGTTTC AGGTTCTATT 60
 TCACTCCCCT TCCGGGGTGC TTTTnACCTT TCCCTCACGG TACTGGTTCA CTATCGGTCA 120
 CTAGAGAGTA TTAGCCTTA GGAGATGGTC CTCCAGATT CCGACGGAAT TTCACGTGCT 180
 25 CCGTCGTACT CAGGATCCAn TCAAGAGAGA CAACATTTTC GACTACAGGA TTATTACCTT 240
 CTTTGATTCA TCTTGTC 257

(2) INFORMATION FOR SEQ ID NO: 4562:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4562:

40 TACCTAATAA GTTGTGAATT TGAACAGCGG CTGCTTTACA nTGGAAGTGC TGATTCAGTT 60
 GCCACAATTA CCATACCAAT TTTCTTTTTG TCTTCGTCTG TnATAATGTC CTTAGCAGCG 120
 TTAGCTCCGA TTGAAACGAT GTCTTGGTTT ACAGGACTAA CAGCCATTTTC AGTTTGACCA 180
 45 ATTCCAATTA AAAATTTGTT TGGGTCTACT TGGCGTGGCT TCCTGCTGAA TTTAGCCATG 240

(2) INFORMATION FOR SEQ ID NO: 4563:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4563:

CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 60
 5 TAGTGCCAAG GCATCCACCG TCGGCCCTTA ATAACTTAAT CTATGTTTCC ACCATTTTTA 120
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTATTTT AnATGCTCAT TTACATAAGT 180
 nGACTCTGCT TTAATAAAT TTAATCATT GTCTGCTAAA CGTTT 225

(2) INFORMATION FOR SEQ ID NO: 4564:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4564:

TGTTAATTGG nGAATTTGGA TACTGGTTAT ATTCAGCTGC ACCGCAAGCA ACTTCTATTG 60
 ATGGCCTAAC TGCCTTTTTA CCTCAAGCAA TGGGTATGGT AATTGTTGCA GTCATTTATG 120
 25 GCTTTATGAA TATGAAAGCA GAGGAATCCC ATTCCCGTAA TAAAATTACG GTGGTTACAA 180
 AATTATTTCA GGTTCCTTTC TTTTGCATTT GGGTGCTTTA ACCATATCTT nTT 233

(2) INFORMATION FOR SEQ ID NO: 4565:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4565:

AGCTCAGATA GCGCTCAGAC TCAGACAGCG ACTCAGATTC AGATAGCGAT TCAGACTCAG 60
 ACAGCGACTC AGACTCAGAC AGCGACTCAG ACTCAGATAG CGACTCAGAT TCAGATAGCG 120
 ATTCAGACTC AGACAGCGAC TCAGATTCAG ATnGCGATTC GGAnTCAGAC AGCGATTCAG 180
 45 ATTCAGACAG CGACTCAGAC TCGGATAGCG ATTCAGATTC AGATA 225

(2) INFORMATION FOR SEQ ID NO: 4566:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4566:

CCAACTGGAG CTAATGGCTC TTCCATGGTG CCGGCCAGAG GACTTGAACC CCCAACCTAC 60
 5 TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCGG CAATATGTAA GAATAAATGG 120
 TGGAGAnTGA CGGGTTCGAA CCGCCGAnCC TCTGCTTG TG AAGGCAGATG CTCTCCCAGC 180
 TGAGCTAATT CTCCGATT TA AACTGGCCT GGGCAACGTT CTACTCTAGC GGGAAC T 237

10

(2) INFORMATION FOR SEQ ID NO: 4567:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 300 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4567:

GTTGGAGATA GTGTAATAAT GCCAATGAGC CACTCTGAAG TTACAGCGGA TGGGTGTTTT 60
 GCCAAAATTC CATGGTGGTA CGAAAAAGAA AAAATGGATG GAAACAAGTT ACTGAAAATC 120
 25 TTGGTAAAAA AGCAGGGGAC TTCGGTTCTA AAGCTAAAC ACAGCTCATA ATATCAAAAA 180
 GGTGCAGAGG AAATGGTTGA nnGGCAGCGG ATAAATCAAG ATGGTGCACT TGGTTAGCGT 240
 TAAATCGCGA TGTGTGGGTT AnTACACATC CGGGAAC TAG TAATAAGTAT GTCAGTTTAA 300

30

(2) INFORMATION FOR SEQ ID NO: 4568:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 250 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4568:

ATCCCGTGGA GGTTCAGTC CTCTCGGCCG CATCAAAATT CTTAATTTAA ATAAGCGGGT 60
 GTAGTTTAAT GGCAAAACCT CAGCCTTCCA AGCTGATGTT GTGGGTTCGA TTCCCATCAC 120
 45 CCGCTCCATA GATAATTTTA ATGAACATTG AAACTGAAT GACAATATGT CAACGTTAAT 180
 TCCAAAAACG TAACTATAAG TTACAAACAT TnATTTTAGT ATTTGATGGA GCCTnAATCC 240
 AAACATTCCA 250

50

(2) INFORMATION FOR SEQ ID NO: 4569:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4569:

GATCCCCTAG CTTTACGTTT AACTTTATAT GGGTATAACT CGAATATAAT TTGGCGCTCT 60
 10 ATGTCATGGG ACAACGAGTA GACATTTAAT AACGGATCAG GTTCTGGTGA CGGTATCGAT 120
 AAACCAGTTG TTCCTGAACA ACCTGGTGAG CCTGGTGAAA TTGAACCAAT TCCAGAGGnT 180
 TCAGATTCTG ACCCAGGTTT AGATTCTGGG CAGCGnTTCT AATTCAGATA GCGGT 235

15

(2) INFORMATION FOR SEQ ID NO: 4570:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4570:

25

AATCTATTTT TTCTATTGTT AAATCGCTAT CTCCATCTTC TTTTATCTCT GGTATTATTT 60
 TTTCTTCAAC TAAGTCACGA TATAATGTTT TTGAATTTTC GTTCAATTTT GATTCGTGAT 120
 30 TTTGAATACT TTTCTTCCAC ACAAATGTAT ACCTATTGGC ATTAGCnTCT ACTTTTGTAC 180
 CAnCAATAAG ATTTTGCTTT AACATTGAC TATGAAACTG GGA 223

(2) INFORMATION FOR SEQ ID NO: 4571:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4571:

CATGATATTT TGAACCGCAT GGTAAAGTT GCAAAGACGG TCTTGCTGTC ACTTATAGAT 60
 45 GGATCCGCGC TGCATTAGCT AGTTCGTAAG GTAACGGCTT ACCAAGGCAA CGATGCATAG 120
 CCGACCTTAG AGGGTGATCG GCCACACTGG nACTAAGACA CCGTCCAGAC TCCTACGGGA 180
 50 GGCAGCAGTA GGGAATTTTC CGCAATGGGC GAAAGCTGTA CGGCGCAACG TCGTGTGnAG 240
 TGCTGCAGGT TCTTCGGATC GTAAAT 267

(2) INFORMATION FOR SEQ ID NO: 4572:

55

(A) LENGTH: 221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4572:

10 AATnCAACTT TTA~~C~~TTACTA TCTAGTTT~~T~~G AATGTATAAA TTACATTCAT ATGTCTGGTG 60
 ACTATAGCAA GGnGGTCACA CCTGTTCCCA TGCCGAACAC AGAAGTTAAG CTCCTTAGCG 120
 TCGATGGTAG TCGAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAT AATATTAATC 180
 15 CACAGTAGCT CAGTGGTAGA GCTATCGGCT GTTAACCGAT C 221

(2) INFORMATION FOR SEQ ID NO: 4573:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 230 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4573:

GCAGAAATGC CAGCCGCATT GAGTGAACAC AGAGTTACAG GGTATTCTGT AGCCGAACCA 60
 30 TTCGGTGCA~~n~~ TGGGGGAAAA GTTAGGCAAA GGTAAGACTT TGAAACATGG TGATGACGTT 120
 ATACCTGATG CGTATTGCTG TGTGCTAGTA CThAGAGGGG AATTGCTTGA TCAACACAAG 180
 GATGTAGCGC AAGATTTGTA CAAGGTTATA AAAAGTCTGG CTTTAAAATG 230

35

(2) INFORMATION FOR SEQ ID NO: 4574:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 230 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4574:

45

TCACATATCG ATAACATGAC ATA~~A~~CTCATG CTGGGTTTCC CCATTCGGAA ATCTCTGGAT 60
 CAAAGCTTAC TTACAGCTCC CCAAAGCATA TCGTCGTTAG TAACGTCCTT CATCGGCTTC 120
 50 TAGTGCCAAG GCATCCACCG TGCGCCCTTA ATA~~A~~CTTAAT CnATGTTTCC ACCATTTT~~T~~A 180
 TAAGTCAAAC GCTCACATAC GGCTTCGTTT TCATTAnTTT AAATGGCTCA 230

(2) INFORMATION FOR SEQ ID NO: 4575:

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(A) LENGTH: 309 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4575:

10 CTTACAATAG TGTGCAAGTT GGGGTGGAGC CCCGACACAG AGAAATTAGC TCCTCAATTT 60
 CTACAGACAA TGCAAGTTGG CGGGGCCCCA ACACAGAAGC TGGCGAAAAG TCAGCTTACA 120
 ATAGTGTGCA AGTTGGGGTG GGACGACGAA ATAAATTTTG CGAAAATATC ATTTCTGTCC 180
 15 CACTCCCAAA AAGACCGCAG TAGGATAATT CCATTTGGAA ATACCTTACT GCCnGTTTTT 240
 AAAGTAATAG CnAATATTTT GGAATTAnGT TTCCTAGTTA ACCATACCAA CTAATGGCCT 300
 CCTTAAATT 309

20

(2) INFORMATION FOR SEQ ID NO: 4576:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 240 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4576:

30 TGATTCTAGG AATTCAAGCT TATTTAAAAC TCTTTATTTCA CTCGGTTTTG CTTGGGTAAA 60
 ATCTATATTT TACTTACTTA TCTAGTTTTT C AATGTACAAA TAATGGTGGG CCTAAGTGGA 120
 35 CTCGAACCAC CGACCTCAG CTTATCAGGC GTGCGCTCTA ACCAGCTGAG CTATAGGCCC 180
 ATTTTTTTGA ATGTAAATA AACATCnAAA CTGGnATACC ATATGTCACG GTAATCCGCA 240

(2) INFORMATION FOR SEQ ID NO: 4577:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4577:

50 CTTCTGTGTTA AAATTTGATG CACAATGGTC ATCATTTTTTA TCTTTCCAAT AAGTACTGTC 60
 TGGGTAAAAA TnTATTAAIT GGGTGGTTCG TGAAATGCAA TCTTTTTTAAC GACTTCAGGG 120
 TAATCTTTTA ACACATGCAT CGCAACGATT GAACCTnAAC TTGAACCTAA TATATAGACA 180

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(2) INFORMATION FOR SEQ ID NO: 4578:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4578:

TAGGCATACC AAAGTCGATA CCATAGTGAC GACCGCCATT AAAGTTAAGT CCACCTGTGT	60
AACTCCCAAA CCTTTGCCAA ATTGGATGGT CAAATAGATA GCTTCCATCG CCTCCGCCAC	120
CAAAATCTTC AAACCACGAT TTACTTTGnC TACTAATTTT TTTTGTAGCA ATGAGTACGC	180
GCCTTAGCAA TTTTAnGTAG CGTAGTCCGC TCCAAAATAA TATTAACTG ACATACTTAT	240
TACnAGTTCC CTGGATGTGT ACATAATCCA CACATCGCGA TTTATCGCTA ACAGAGCACA	300
CTTGATTACG CGCGCTCAAC ATTC	324

(2) INFORMATION FOR SEQ ID NO: 4579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4579:

AATGTAAAAA CTGATTCTA TTAATTATTT GATAGAAATC ACTTTTTTGT ATTTTATAAT	60
GTACAGCTCG TTGCATTCAT ATAGCTTGAA GTCACGTTTA AAACCATATC TATCATTATG	120
GTATGCATAT CGTTTAAAAAC CTATTCTTTT GTTAnTAGGA CATATAAATT CATCATTAAT	180
TCGTCAATATT TCCAATTTTG AGTGThAAAA ATGTCACTTT TAAACTTTC	229

(2) INFORMATION FOR SEQ ID NO: 4580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4580:

CGGGGACTCn AACCCGTGTT GACCGCCGTG GAAAGGGCGG TGTCTTAACC GCTTGnACCA	60
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CTCTACCACT GAGCTACTGT GGATTAATAT TATGCCTGGC AACGTTCTAC TCTAGCGGAA 180
 CGTAAGTTTCG ACTACCATCG ACGCTAAGGA GCTTAAC TTC TGTGTTCCGC ATGGGAACA 239

5 (2) INFORMATION FOR SEQ ID NO: 4581:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 233 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4581:

CCGnACGAAT TTACACGTGT TCCGTCGTAC TCAGGATCCA CTCAAGAGAG ACAACATTTT 60
 CGACTACAGG ATTATTACCT TCTTTGATTC ATCTTTCCAG ATGATTCGTC TAATGTCGTC 120
 20 CTTTGTAAC TCGTATAGAG TGTCCTACAA CCCCACAAG CAAGCTTGTT GTnTTGGGCT 180
 CTTCCCGTTT CGCTCGCCGC TACTAAGGGA ATCGAATTTT CTTTCTCTTC CTC 233

(2) INFORMATION FOR SEQ ID NO: 4582:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4582:

35 TTAGTAAAA GTCTGTGAGT AAGGGTGAT GGAAAGTGGT TAAATATTAT AGAAAACATC 60
 AAAGGATGTT AAGAAATACA ATTTATTACC CAGCATTTAA TAATGGTGCT ATAGAAGGAA 120
 TTAATAATAA GATAAAATTA ATCAAGTGAA TTTCTTTTGG TTACAGAAAT TTCAnCanCT 180
 40 TTAAAGCACG TATAATGATG GATTTTCAGC TTGTACAA 218

(2) INFORMATION FOR SEQ ID NO: 4583:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 251 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4583:

TAATAAACAT GCCATACGTA ATAAGTGGCG TTGTATTAAA ATCATCTATA ATAGCCATAT 60

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ATTTTGAAT CATTGTAAA AATGGAATTA AAGTTCTAGT GATCTGTTGG GTTTTGGAAA 180
 TAGGTCATAG GGTnAAAACn TTTTGTAGAA TTTGTCGCTA TTTGTAAAT TGTATCCCGG 240
 5 CTTGAAGTTG G 251

(2) INFORMATION FOR SEQ ID NO: 4584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4584:

TTTAGGACCG TTATAGTTAC GGCCGCCGTT TACTGGGGCT TCGATTGTA GCTTCGCAGA 60
 nTAACCCACT CCTCTTAACC TTCCAGCACC GGGGCAGGCG TCACCCCTAT ACATCACCTT 120
 ACGGTTAGCA GAGACTGTGT TTTTGATAAA CAGTCGCTnG GCCTATTCAA TGGGGGCTCT 180
 TCTGGGGGTT AAACCTAAAG AGCAACCCTT CTCCCGAAGT TACGGGGTC 229

(2) INFORMATION FOR SEQ ID NO: 4585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4585:

TTATAAAAAG ATTTAAACGC GTTATTAATC TTGTGAGTGT TCTTTCGAAC ATAGCGATTA 60
 TTTCTTATGA ATTCAAGCTT ATTTAAACT CTTTATTCAC TCGGTTTTGC TTGGTAAAT 120
 CTATATTTAC TTAATTATCT AGTTTCAAT GTACAATTnC TTTTGTAGCA AGCGCTCGCA 180
 TACTGCTnTA TTTTCAAAA ATCAAATGCT CATTTACA 218

(2) INFORMATION FOR SEQ ID NO: 4586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4586:

5 GGAATTCCAC TTTCTCTTC TGCACTCAAG TTTTCCAGTT TCCAATGACC CTCCACGGTT 120
 GAnCCGGGGC TTTTCACATC AGACTTAAAA AACCGCCTAC GCGCGCTTGT ACGCCCAATA 180
 ATTCCGGATA ACGCTTGCCA CCTACGTATT TACCGCGGGC TGCTGGCACG TATTnAGCCG 240
 T 241

10 (2) INFORMATION FOR SEQ ID NO: 4587:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 253 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4587:

20 CAGCCACCTG TTGCCACCAG CTACACTTGC ATTGTTTGCT ACGACACGCC CAAACAATGC 60
 TGAAGTGAAT AAGAAATCAA TCATTTGCTC TTCTGTAAAA TCATGTGTTT TTTCTAATTT 120
 AAAAAGTGCA CCGGGAATGG TACCCGAGGA ACCAGCTGTT GCGTTGCAC AAATAATACC 180
 25 CATCGCAGCA TTGACTTCAT TGTTGCAAGG CACnTTGAC TCGGCAATC ATTCATATCC 240
 GACnAAGCAG ATG 253

30 (2) INFORMATION FOR SEQ ID NO: 4588:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4588:

40 ATGAACGGGT GGTAGCGAGT GGACGAAAAA CATCAATGAA AAGCTAGCTG TAGTTGCAAG 60
 AGAAACTGGC TTACGATGGC ATTGGATCAA CACATGCGGC ATTGAGAAAT CCACGCATGG 120
 CTGAGACGTT TACGATTGCG CGAAAAATGA ATCCTGAAGG CATTTTAGCA ATGTTGGTGC 180
 45 GGACGTACCA GTAGAAAAGG CTTTGGAAGC AGTTGAAT 218

(2) INFORMATION FOR SEQ ID NO: 4589:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 55 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4589:

5 GCCATGGCTC CACAGGTAGG ACTCGAACCT ACGACCGATC GGTAAACAGC CGATAGCTCT 60
 ACCACTGAGC TACTGTGGAT TAATATTATG CCTGGCAACG TTCTACTCTA nCGGAACGTA 120
 AGTTTCGACTA CCATCGACGC TAAGGAGCTT AACTTCTGTG TTCGGCATGG GAACAGGTGT 180
 GACCTCCTTG CTATAGTCAC CAGACATATG nATGTA 216

(2) INFORMATION FOR SEQ ID NO: 4590:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4590:

20 AGATTTAAAT AATCAAAAGT GCACATTATT AAAATATCAA TTTCACACTC AATGCGGCTC 60
 ATCnATTCA TTTCTTGTCT AGCAACGTTT TACTCTAGCG GAACGTAAGT TAGCTACCAT 120
 25 CCTCGGCTAA GAACCTTTCT TGAATTGTGA CAATCGGCTT GCTTCTTTCC TCTCCTTCGG 180
 CTCTCGCTAC TCAATTAGC TCTACTAAAC TCGGTTGCGG CTCTTTTCTn GTTT 234

(2) INFORMATION FOR SEQ ID NO: 4591:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4591:

40 AATTGACTGA CTTCGTTTTA CCGCGTGTTT AATATTGTTA TACATATATT CTAATTGCAC 60
 ATTTAAACTT CGTAAATGCC AATGTGnGTG GGACAGAAAT GATATTTTCG CAAAATTAT 120
 TTCGTCGTCC CACCCCAACT TGnCACATTA TTGTAACCTG ACTTTCCGCC AGCTTCTATG 180
 45 TTGGGGCCCC GCCAACTTGC ACATTATTGT AAGCTG 216

(2) INFORMATION FOR SEQ ID NO: 4592:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4592:

5 ATTCGGATA ACGCTTGCCA CCTACGTATT ACCGCGGCTG CTGGCACGTn TTAGCCGTGG 60
 CTTTCTGATT AGGTACCGTC AAGATGTGCA CAGTTACTTA CACATATGTT CTTCCTAAT 120
 AACAGAGTTT TACGATCCGA AGACCTTCAT CACTCACGCG GCGnTGCTCC GTCAGGCTTT 180
 10 CGCCATTGCG GAAGATTCCC TACTGCTGCC TCCCCG 216

(2) INFORMATION FOR SEQ ID NO: 4593:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4593:

20 TTGGACTAGA ACCAATGAAG GACGTTACTA ACGACGATAT GCTTAAAGGA GCTGTAAGTA 60
 AGCTTTGATC CAGAGATTTC CGAATGGGGA AACCCAGCAT GAGTTATGTC ATGTTATCGA 120
 25 TATGTGAATA CATAGCATAT CAGAnGGCAC ACCCGAGAA CTGAAACATC TTAGTACCCn 180
 GTGGAAGAGA AAGAAAATTC GATTCCCTTA GTAGCGGCGA GCAGAACG 228

(2) INFORMATION FOR SEQ ID NO: 4594:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 252 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4594:

40 CAATCGTTGA AGGAAATGTA CCAGCAGCAA TCAAAGACAA AGAAATTATT TCTGTAGACA 60
 TTTCATCATT AGAAGCTGGA ACGCAATATC GTGGTGCTTT TGAAGAAAAT ATTCAAAAAT 120
 TAATCGAAGG TGTAAATCT TCACAAAATG CCGTACTATT CTTTGATGAA ATCCATCAAA 180
 45 TTATCGGTTT AGGTGCCACA GnaAGTGGAT TCCAGGTTAG CCAAGGGGT TAATCTGGAT 240
 TAATTTTTTT Tn 252

(2) INFORMATION FOR SEQ ID NO: 4595:

(i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4595:

5 ACTCTCTAGT GACCGATAGT GAACCGAGTAC CGTGAGGAGA AGGTGAAAAG CACCCCGGAA 60
 GGAGnTGAAA TAGAACCTGA AACCGTGTGC TTACAAGTAG TCAGAGCCCG TTAATGGGTG 120
 10 ATGGCGTGCC TTTTGTAGAA TGAACCGGCG AGTTACGATT TGATGCAAGG TTAAGCAGTA 180
 AATGTGGAGC CGTAGCAGAA GCACGGTCTCT GGAATAGGGG CGTTTTAGTT ATTTTGGGTC 240
 GTTACCCGGG AGnAAAGG 258

(2) INFORMATION FOR SEQ ID NO: 4596:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4596:

25 CCTACCGCTG CAGCCGCTGG ATCTGCTGGA GTTGCAATTAG GATCTGCCGG TGCCGCACGT 60
 CTACTTCTCT TTTTCGGTCT ATTAGATGCT GGTTCAAGAA TTGCAACTAG CTCTGGTTTA 120
 30 TTTGAAGAAT GACGAACATC TTCTTGAATT TCCTTTAAAG TAGATGTCCT CCTGAACCAT 180
 TnCATTTGTTT AGTTGGGTAC ATTAATGCnG TATTATCGAC ACTACATCA 229

(2) INFORMATION FOR SEQ ID NO: 4597:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4597:

45 GCTCACCTTA GAATTCTCAT CTTGCACTCA CCTGGTGGTC GGTTTGGCGG GTAGGGTCAC 60
 CTATTTTCTA TCTAGCAGGC TTTTCTCGGC AGTGTGAAAT CAACGACTCG AAGnCACAAAT 120
 GGTCTTCTCC CCATCACAGC TCAGCCTTAA CGAGTACCGG ATTTGCCTAA TACTCAGCCT 180
 50 TACTGCTTAG ACGTGCAATC CAATCGCACG CTTCGCCTAT CCTACTGnGG TCCCCCATC 240
 GATTAA 246

(2) INFORMATION FOR SEQ ID NO: 4598:

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(A) LENGTH: 223 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4598:

10 AAGAAAATAA AGAATGCTAC AATTACGATT GCAATCAAAC CAAAGAACCA TAATGATGTG 60
TACCAAGTGC TGCACCTTTA GTAATGACAA CGTTTAACT TAGCAACATA ACTACTAGAA 120
CAATTAGCCC TGCAACGTCA AATTTATGTG TATTGGTAAT TTCTGATTTC GTTTCAGGCG 180
15 TCCCTTTGAT GAGTAGCATT GAAAGTACGG NAACGATGnG TTG 223

(2) INFORMATION FOR SEQ ID NO: 4599:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4599:

nTnTCACTGT TTGACCCGGT ACCGTGTCAG ATAATCCCGC ACGCAATGCA ATCGTTCGTG 60
30 CAATGTTTTG GCCTTGTAAT CCTTCTGGAA AAGCCGTACC AACAATGACA TCTTCAATCA 120
TATTCTTATT GAATTTTCCG TCAATACGTT TCAATACGCC TTGTAATACT TTGGCTGCGA 180
CATCATCAGG TCTTTCGTGG AATAATGCGC CTGCTTTGC 219

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(2) INFORMATION FOR SEQ ID NO: 4600:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 208 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4600:

AAGGTTAAGA GGAGTGGTTA GCTTCTGCGA ATACCGAATC GAAKCCCCAG TAAACGGCGG 60
CCGTAACCTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC CGACCCGCAC 120
50 GAAAGGCGTA ACGATTTGGG CACTGTCTCA ACGAGAGACT CGGTGAAAAT CATAGTACCT 180
GTGAAGATGC AGGTTACCCG CGGACAGG 208

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(2) INFORMATION FOR SEQ ID NO: 4601:

(A) LENGTH: 286 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4601:

10 AGTGCCAGTG ATTAAGTGCA TTTTCAATA GATCAGGGAA GACTACCAAG CTTATGTTGA 60
 AGGACATCTT TTGGCGTTAC CGGTTGGGCA GGTATGTTGT ATTACCGTTC ACAACAGCAT 120
 CACTGAACA ACATTTGTTA ACGGATTATT TGGCAATTCG TTATTGTCGA ACAnTGChAG 180
 15 TTGGTGAGAT TTAATCATCG CTAAAGATGT GAAATAGATC GAAAATGGTT TAAGCAAACG 240
 TTGCTCAGGT GTTACTACGT GATATGCCTA GCGAGTATAC TACAAC 286

(2) INFORMATION FOR SEQ ID NO: 4602:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 264 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4602:

30 ATATGGCTAT GGTATTCACA TATCGATnAA CATGGACATA ACTCATGCTG GGTTTCCCCA 60
 TTCGGGAAAT CTCTGGGATC AAAGCTTACT TACAGCTCCC CAAAGCATAT CGTCGTTAGT 120
 AACGTCCTTC ATGGCTTCTA GTGCCAGGCA TCCACCGTGC GGCCTTAATA ACTTAATCTA 180
 35 TGGTCCACC CATTTTTATA GGTCAAACGG TAACATGAGG TAGGGTCTTT TATAAAAAGG 240
 nTTAAACGGG GTATTAATCT TGTG 264

(2) INFORMATION FOR SEQ ID NO: 4603:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4603:

50 GAAACGTTAG CACAAGCCAT GAACCAATTA GGTGGAAAGA GTAATAGTGG TGAAGGTGGC 60
 GAAGATGCAA AACCGTTATG AAGTACAAGT TGATGGAAGC AACAAAGTAA GTGCGATTAA 120
 ACAAGTTGCT TCTGGGCGTT TTGGTGTAnc TAGTGATTAT TTACAACATG CCAAAGAATT 180

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(2) INFORMATION FOR SEQ ID NO: 4604:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4604:

ATTAAC TAAC ATGGGCATCT ACGATGGAAA CAGACGTGGT ATCCTCGCTA TTATCCAGCT 60
 AnCGCCATGC TGGCTCGTTT TTCAAATCAA GCCATTTTAA ATTTTGAAA GGTGTATGGA 120
 CCAAGCCCTA TGACATTGCA TTCACCGATT GAACACGATG TTATCGCCAT GTCTCATGGA 180
 GAAAATCAAG AGCATCATTC AGCAGTATCG CGATGCTACA TTACGCGCGA TTAAAGCAGn 240
 TTTGATGG 248

(2) INFORMATION FOR SEQ ID NO: 4605:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 246 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4605:

CAAGTTTTCC AGTTTCCAAT GACCCTCCAC GGTTGAGCCG GGACTTnTCA CATCAGACTT 60
 AAAAAACCGC CTACGCGCGC TTTACGCCCA ATAATTCCGG ATAACGCTTG CCACCTACGT 120
 ATTACGCGCG CTGCTGGCAC GTATTAGCCG TGGCTTTCTG ATTAGGTACC GTCAAGATGT 180
 GCACAGTTAC TTAACACATG ATGTTCTTCC CCTAAATGAA CAGAGTTTTG TTTTGTnTTn 240
 TGGGTT 246

(2) INFORMATION FOR SEQ ID NO: 4606:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4606:

TGTATCTGCA GTTAAATCAT GTnTCGCTTG GTTTAATGCT GTTAATGCGT TATCGACACG 120
 ATGTTTTTCA TCTGAAATTT GTTGTGCAGT TGCATCGCCA TTGTCAATAA CACGTTGAGC 180
 5 TGCAGTTATT TCAGTTTCTG CTTACAGCTn CT 212

(2) INFORMATION FOR SEQ ID NO: 4607:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4607:

TAGTCAAGAT GAGAATTCTA AGGTGAGCGA GCGAACTCTC GTTAAGGAAC TCGGCAAAAT 60
 20 GACCCCGTAA CTTCTGGGAGA GGGGTGCTCT TTAGGGTTAA CGCCAGAAG AGCCGCATGA 120
 ATAGGCCCAA GCGACTGTTT ATCAAAAACA CAGGTCTCTG CTAAACCGTA AGGAnTGTAT 180
 AGGGGCTGAC GCCTGCCCGG TGCTGGAAGG TTAAGAGGAG TGGTTAGCTT CTGCGAGTAC 240
 25 GGAATCGAAG CCCAGTAAA CGGCGG 266

(2) INFORMATION FOR SEQ ID NO: 4608:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4608:

TTCACTACGT AAATACGCAC GTGAAAAAGG TGTTAnATTA AAGCAGTTTC TGGATCTGGT 60
 40 AAAAATGGTC GTATTACAAA AGAAGATGTA GATGCATACT TAAATGGTGG TGCACCAACA 120
 GCTTCAAATG AATCAGCTGC TTCACTGACA AGTGAAGAAG TTGCTGAAAC TCCTGCAGCA 180
 CCTGCAnCAG TGAACATTAG AAGGCGACTT CCCAG 215

45 (2) INFORMATION FOR SEQ ID NO: 4609:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 241 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GGGTTTCATAC ATGTCAATAG TAACCGTCTT AACTTGTTGT CGATTTTTTTA AATCGAATCG 60
 CTCGAAATAG GCACGCAAGA ATCTTGTA GT TCTATTTTCT AAAATATCTA TAACATCATG 120
 GTATCATTAT CTATAAAAAT GAAACTCATT GATCCAGTTA CATTTTTAAAC GCTTTTAAAT 180
 TCATCCATAG CGATGTGGTT CCTGCCAACC ATTAAAGGGG TTAATTCTnGA ATnGATTAGC 240
 C 241

(2) INFORMATION FOR SEQ ID NO: 4610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4610:

ATTCATTCTT TGTCTAGCAA CGTCTACTC TAGCGGAACG TAAGTTAGCT ACCATCCTCG 60
 CTAAGAACCT TTCTTGACTT GTGACAATCG CTGCTTCTT TCCTCTCCTT CGGCTCTCGC 120
 TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCAAACG 180
 TTTCAnTTCG CCAAGCCATT TTTCTTTGGT GnTTA 215

(2) INFORMATION FOR SEQ ID NO: 4611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4611:

GTGCCATCTT TCTTCATCAA TTCATTAATA ATTGCTGGGA CGCCACCAGC TTCATGCACA 60
 TCATGCATTG AATACGATGA ACTAGGTGCT ATTTTGTGATA AATATGGCGT GCGTTTGGCA 120
 ATAGCATTAA TGCCTCTAA GTCATAATCA ATACCAGCTT CATTGGCAAT GGCTAACGTA 180
 TGCAGTACCG TGTTTGTGTA ACCACGGCAC ATCTTCGCCA ATTTCTTCTT TAAACAAGTT 240
 TAAATTATCT TGTGATTCAG GTAAATCCAT CTTGTTAGCT ACTACGATTT GAGGTCTATC 300
 TTCTAAACGT TGCTCGTACG GCGGCTAATT CTGGATTAAT GACTTTATAA TCTTCAATAG 360
 GGTCTCTACC TTCAGAACCG CTCCATATCC ATCCTGTGGA 400

(2) INFORMATION FOR SEQ ID NO: 4612:

(A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4612:

10 AATACTATTA AGAAGTCCTG AAAAATTCAC ATTAGCAGTT GGATTGTTCA ACTTTATTAA 60
 TGATAAGTAT GCAAATAATT TCACAGTGTT TGCAGCAGGG GCAATTATGA TTGCAGTACC 120
 TATAGCAATC GTATTCTTGT TCTTGCAACG CTATTTAGTA TCAGGTTTAA CAACAGGTGC 180
 15 CGACCAAAGG GTTAGTTTGA ATTTAGGAGT GGGGCCAGAT TGGTTAAGGA CCnCCTAATG 240
 ACCGTTAAGG TThAAAGG 258

(2) INFORMATION FOR SEQ ID NO: 4613:

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(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4613:

30 GACTTCGTTT CAGTGTA AAA TTTTCTAAT GTAACAGATA TGCTATTATT CATTGGAATG 60
 ATTAGTGCTT CATCTTTTTT ACCCCAATAT TTTATAAGTG CAATTCGTAT GTGCACGTGC 120
 TTTGCCACTT TTAATCAACG CTTAACCTCC TAAATTCTCA ATCCAAGTAT GTGCTGCACC 180
 35 AGCTTTTTTC TACAGCTTTT ACAATATThn 210

(2) INFORMATION FOR SEQ ID NO: 4614:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4614:

TAGCGTATTA ATCGGCGGAT CGGCTGAGCG TATCTGAGTC TGAATCGCTG TCTGAGTCTG 60
 50 AGTCGTATCC GAGTCTGAGT CGCTGTCTGA nTCTGAATCA CTGTCTGAAT CCGnATCGCT 120
 ATCTGAATCT GAATCGCTAT CCGAGTCTGA GTCGCTGTCT GAATCTGAAT CGCTGTCTGA 180
 GTCCGAATCG CTATCTGAAT CTGAGTCGCT GTCTGAGTCT GAATCGCTAT CTGAA 235

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- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4615:

ATGTGCGTGG TTTATTTTAA TAGGTTAGTA ATATATTAGG TCATGTTATG TTAAAnTTTA 60
 TAATGAATAA ATAATTTAGA AATATGCTTC CGATTGTTTCG ATGCTTTAAT TCAGTTAGAA 120
 GCATCATAGA ATGCATGATT ACTGTTGTAA AGATACGTAA TGTTTTGTAT TGA CTGTATG 180
 TChTTGGATA GAGTTACAAA CTTATTTTG 209

(2) INFORMATION FOR SEQ ID NO: 4616:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4616:

ATGCGCAAGA TATGGAGAAC ACCATCGCGA AGCGACTTTC TGGTCTGTAA CTGACGCTGA 60
 TGTGCGAnAC nTGGGGATCA AACAGGATTA GATACCCTGG TAGTCCACGC CGTAAACGAT 120
 GAGTGCTAAG TGTTAGGGGG TTTCCGCCCC TTAGTGCTGC AGCTAACGCA TTAAGCACTC 180
 CGCCTGGGGA GTACGACCGC AAGTTGGAAA CTCAAAGGAA TT 222

(2) INFORMATION FOR SEQ ID NO: 4617:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 258 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4617:

CAGTTTGCAA CACCCCAATT CTTGCCAGTC AGCATGATTC TGTCATTTC TGCGATTTCT 60
 TTGTCGATAT TTTCAAATCT TGTTGGACTT GATCTAAATC AATTGGTGCT TCTTCTTCGA 120
 ATGTATCAAC ATATCGCGGT ATGTTTAAGT TGTAATCGTT ATCGGnGATC TCTTGTAATG 180
 TCGCGCTGTG GCTATATTTA TCAATCGTGG CTTTACGCTT ATATGGGGCT ATAATACGTT 240

(2) INFORMATION FOR SEQ ID NO: 4618:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4618:

TCTAATTGAT AGTGAATATA ATTAGAGTTh GAGGCTGGGA CATAAATCCC TAAATTTCAh 60
 CAGTAAGATA ATTTTCAATT AGAAAATATC TTACTGCTGT TCTCTATTTA TACAATACTT 120
 CATTGGAATG GCTTCGCTTT CCTAGGGTGC CGTCTCAGCC TCGGTCTTCG ACTGGGCACT 180
 GCTCCCTCAG GGGTCTCGCC ATTTAATACT ACGTAT 216

(2) INFORMATION FOR SEQ ID NO: 4619:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4619:

ATGTATCGCG CCGAGCAACA CAAGATAAGC ATTGTAGATG TGGATGCCTT AACTGGGCAA 60
 GCGATTnGTC GTCCTAAAAC AGGTACATAT GCGCTATCTG ACCTAGTCGG TTTAGATATT 120
 GCAGTGCTCTG TAATTAAAGG CATGCAACAA GTACCTGAAG AAACACCCnT ATTTTCATGA 180
 TGGTCAAAAT TTGTAAATAC GTTGTTTTGA CAATGGGCGC ACCTCGGACC GTAAAACG 238

(2) INFORMATION FOR SEQ ID NO: 4620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4620:

AACCATTGAA GCACCCCAT TACGTTTTGGC TGACACGnAC GTATATCGCC TGCCCAAGCA 60
 GATGCGACCT TATTAACACC TGAACCACTT CGAACGCCAC TACCTTTAAG TGACTTCAAC 120
 CATTTTTCCT GGATCTTTAG CTGTATGCAT TGCCCTGGAT GCGACCCCTG nCATCAATTG 180

TTGACCAGC

249

(2) INFORMATION FOR SEQ ID NO: 4621:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 267 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4621:

TGGACCTGTA AAAGGAGACT CGATTGTAGA AAAAGAAGAA ATTCCATTCA AGAAAGAACG 60
 TAAATTTAAT CCTGATTTAG CACCAGGGAC AGAAAAAGTA ACAAGAGAAG GACAAAAAGG 120
 TGAGAAGACA ATAACGACGC CAACACTAAA AAATCCATTA ACTGGAGAAA TTATTAGTAA 180
 AGGTGAATCG AAGAGAAATC ACAAAGTCCG TTnTGGnTTA CAGGTACGGC AGAACGATAC 240
 ACAGTCTCGG GCGATTGTCG AGTCCAC 267

(2) INFORMATION FOR SEQ ID NO: 4622:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 231 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4622:

CAAAAGGTAG TTAAATTAG GAGTGGGGAA ATTGATAAGA CCACTAATGA CGATAAAGAT 60
 TAAAAGGAnG ACGTTATGAT GACGATTAAA GTTGGATCAT TGGGTGTGGT GGTATTCCAA 120
 TGGCAAGCAC ATGCCAAGTT TACAAAAAGT TGAAATGTTG AAATGAnCGC ATTTTGTGAC 180
 GTAGACATTT CGAAGCAGCG AGTGCGGCAG AAGCATACGG ACTGACAATG C 231

(2) INFORMATION FOR SEQ ID NO: 4623:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4623:

CGAAACCGGC CCGACCCGGA CnACCCGAG GAAAGGTACC CnAAAGnTGA AGCCCGGGAA 60

5 CCCAACACCC ACCCGGACAC CAGAAGTGCC GGAGTGAGCC AGAAACTCCA ACACCGCCAA 180
 CACCAGAGGT ACCAGCTGAA CCTGGTAAAC CAGTACCACC TGCCAAAGAA GAACCTAAAA 240
 AGCCTTCTAA ACCAGTGGAA CAAGGTAAAG TAGTAACACC TGTATTGAA ATCAATGAAA 300
 A 301

10 (2) INFORMATION FOR SEQ ID NO: 4624:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4624:
 20 CGAGGTGCTG CAGAAGGTGT CATTCTGCGT TATTTAATTG AAGAAAAGAA CTACTTAGAA 60
 GCTGTGATTG GTTTGCCAGC GAATATTTTC TATGGGACAA GTATTCCAAC ATGTATTTTA 120
 GTATTTAAAA AATGTCGCCA ACAAGACGAC AACGTACTAT TTATCGATGC ATCCAATGGT 180
 25 TTTGAAAAAG GGGnAAATCA TAATCATThG GCGATGCCCA AG 222

(2) INFORMATION FOR SEQ ID NO: 4625:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 301 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4625:
 TGGAAAGTGA ATCAAAGAGG TAATATCCGT AGTCGAAATG TTGTCTCTCT TGAGTGGATC 60
 40 CTGAGTACGA CGGAGCACGT GAAATTCCGT CGGAATCTGG GAGGACCATC TCCTAAGGCT 120
 AAATACTCTC TAGTGACCGA TAGTGAACCC AGTACCGTGA GGGAAAGGTG AAAAGCACCC 180
 CCGGAAGGGG AAGTGAAATT AGGAACCCTG AAAACCCGTG TGCTTTACCA AAGTTAnGTT 240
 45 CAAGAGGCCC CGTTTAAATT GGGGTnnAAT TGGCGGTGCC CTTTTTTGGT AGGAATTGAA 300
 A 301

50 (2) INFORMATION FOR SEQ ID NO: 4626:

 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 223 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4626:

5 GAATGAAGGA AGACCATATG AAAAATGGCC AACTTAAGCC AGGATACAAT TTACAAATAG 60
 CGACAAATTC TCAATTTGTT TTATCCTATG ACCTATTTCA AAACCCAACA GATACTAGAA 120
 10 CATTAATCCC ATTTTAnCA ATGATTCAAA ATACCTTCGG TTATTTACCA GAGTATATTG 180
 TAGCTGATGC AGGTTATGGT AGTGAGCAAA ACTATATGGC nAT 223

(2) INFORMATION FOR SEQ ID NO: 4627:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 221 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4627:

TTGTGGGGC CCCGCCnGCG nCATTGCCTG TAGAATTTCT TTTCGAAATT CTCTGTGTTG 60
 25 GGGCCCCTGA CTAGAATTGA AAAAAGCTTA TTACAAGCGC ATTTTCGTTC AGTCAATTAC 120
 TGCCAATATA ACTTCGTAGA TCATAGAACA TTGATTTATT TCCCAGCCTA TTCTTTTCAT 180
 30 AAAAAAAGA CGGATTAATT ATCCGCTTTT TCCTTATATC T 221

(2) INFORMATION FOR SEQ ID NO: 4628:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4628:

ATATATTCGT ATTTATAGTA AAATTAAATA AAGAGnATTA TATAACACGA GGTGTAGTAA 60
 GTATGAAATT TGAGnAAATA TATAGATCAC ACTTTATTGG AAGCCTGAGT CAACACGTAC 120
 45 GCAAATCGAT CAAATCATCG ATGAAGCGAA GCATACCAAT TTAAATCTG TATGTGTGAA 180
 TCCACCACAT GTTAAATATG CAGCAGAG 208

50 (2) INFORMATION FOR SEQ ID NO: 4629:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 305 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4629:

5 ACAATAATGC ATCATAATGC GCAACAACAA TCAATACTGC GAAAACAGAA GCACAACAAG 60
 TGATTAATAA TGAGCGTGCA CACCACAACA AGTTTCTGAC GCACTAACTA AAGTTCGTGC 120
 ACACAACTAA GATTGATCAG CTAAAGCTTA CTTCAAAATA AAGAGATATA GCCATTAGTA 180
 10 ACGTTAAAAT AACTTACAAG nTCTGTGACC AGTACCTCAC TGTGGTATGA CGCACAAGTA 240
 TTGATACTnT ATCGAGAGCG TGAGnGAACT GAATACTGCG CTCACGGTAT TACATGCGTG 300
 CACTG 305

15 (2) INFORMATION FOR SEQ ID NO: 4630:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4630:

TCGACTACCA TCGACGCTAA GGAGCTTAAC TTCTGTGTTT GGCATGGGAA CAGTGTGACT 60
 CCTTGCTATA GTCACCAGAC ATATGAATGT AATTATACAT TCCAACTAG ATAGTAAGTA 120
 30 AAAGTGATTT GCTTCGCCAA ACATTTATTT TGATTAAGTC TTCGATCGAT TAGTATTCGT 180
 CAGCTCCACA TGTCACCATG CTTCCAnCTn GAA 213

(2) INFORMATION FOR SEQ ID NO: 4631:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 40 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4631:

45 GAnGTGAAAT AGAACCTGAA ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA 60
 TGGCGTGCCT TTTGTAGAAT GAACCGGCGA GTTACGATTT GATGCAAGGT TAAGCAGTAA 120
 ATGTGGAGCC GTAGCAAAAA CnAAGTTCTG AATAGGGCGT TTAGTATTTG GTCGTAGCCG 180
 50 GAAACCAGGT GATCTACCCT TGGTCAAGTT GAA 213

(2) INFORMATION FOR SEQ ID NO: 4632:

55

(A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4632:

10 GCTTTTAAAT CAAATGATAG CGGAAGGGnA TTTTAAAT ATTCTGAACCA TTATTTACAG 60
 CAGCAGATGG ATGGATTGGT GTCACAATTA TCTTTGGTGC CTTTGCATTA TTCTGGTTTG 120
 TAGGTATTCA TGGTCCGTCA ATTGTAGAGC CAGCAATTGC AGCCATTACA TATGCGAATA 180
 15 TCGAAGCGAA CTTCAAGTTG CTTCA 205

(2) INFORMATION FOR SEQ ID NO: 4633:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 204 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4633:

AGTTATATTG ACAGTAGTTG ATGGGGCCCC AACATAGAGA AATTGGAACA CCAATTTCTA 60
 30 CAGACAATGC AAGTTGGGGT GGGCTCTAAC ATAAAGAAnt ACTTTTTCTn TAGAAATTAG 120
 TATTTCTTAT ACATGGGTTT TACTCAGTAT TTCCTATTCT TAAGTCACA TTAGCAGCGG 180
 CTAATGTGTT AAGAACTACT ACAT 204

35

(2) INFORMATION FOR SEQ ID NO: 4634:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4634:

GCCGATGGAT TAGAGTATAT GACGTGGTGG CATGTCATTA ATTTAGGTGA TGTAGGTAAG 60
 AACGTTnGGG CAAGGTATGA GTGGTGGTAT TGC GTTACGT TAGCCCGTCT GATGTAGAAG 120
 50 CTTTTGTGTA AAATAATCAA CTAGATACGC TTTCGTTTAC AAAGATTAAA CACCAAGAAG 180
 AAAAAGCATT CATTAGCAA ATGCTGGAAG AnCCATGTGT CACACA 226

55

(2) INFORMATION FOR SEQ ID NO: 4635:

(A) LENGTH: 208 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4635:

10 CATATAGTTT TGCTCACTAC CATAACCTGC ATCAGCTACA ATATACTCTG GTAAATAACC 60
 GAAGAGTTGT TGAATCATTG TTA AAAATGG GATTAATGTT CTAGTATCTG TTGGGTTTTG 120
 AAATAGGTCA TAGGATAnAA CnGTACGGAG AATTTGTCGC TATTTGTAAA TTGTATCCTG 180
 15 GCTTAAGTTG GCCATTTTTC ATATGGTC 208

(2) INFORMATION FOR SEQ ID NO: 4636:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4636:

TTTTTCTTTG TGTTTATTTT TATTTTGAAC GTTTTAGGAC ATAAAAAAA GTAGACCTTG 60
 30 CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGTTCTAC TCTAGCGGAA 120
 CGTAAGTTGG CTACCATCGA CGCTAAGAAC CTTTCTTGAC TTGTGACAAT CGCTTGCTTC 180
 TTTCCGCTTC TTCTGCTCGn GCTTACTCAT TGAGCnCTAC TAAACTCG 228

35

(2) INFORMATION FOR SEQ ID NO: 4637:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4637:

CATGGTTCAA AAGTGAAAGA CGGTCTTGCT GTCACTTATA GATGGATCCG CGCTGCATTA 60
 GCTAGTTGGT AAGGTAACGG CTTACCAAGG CAACGATGCA TAGCCGnCCT GAGAGGGTGA 120
 50 TCGGCCACAC TGGAGCTGAG ACACGGTCCA GACTGCTACG GGAGGCAGCA GTAGGGnATC 180
 TTCCGCAATT GGCgAAAGCT GTACGGGCAA CG 212

55

(2) INFORMATION FOR SEQ ID NO: 4638:

(A) LENGTH: 256 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4638:

10 ATnTtATTAA ATAGAGAACA GCAGTAAGAT ATTTTCTAAT TGAAAATTAT CTTACTGCTG 60
 TTTTTTAGGG ATTTATGTCC CAGCCATTTT TGTATTCATA TTAAATTTTC GATAATTTTT 120
 CAGGAAGCAT TTAAATTTTA CTAATGAAGC CATATTTTTA GATTAACCAA AATTAATATT 180
 15 TACATTTTCT AACCATTTT ATGTAACATT TACAGTTCCA AAAATGGGGG TAATAATCCA 240
 GGTTAGGATA AAGAGG 256

(2) INFORMATION FOR SEQ ID NO: 4639:

20

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4639:

30 AnAGnAACCA CTACATAATA AATCATTAGT GGCTCTTTAT CATTTCTGTC CCACTCCCCCT 60
 GAGAAGTTTA AAATTTTATA TGTTGGCTTG TTATGTTAAG GGAATTAACA TGGTTGTCTT 120
 GTTTATATTA TGTGATTCCA ACATTACTAG TCCTGGTAA TCTAATTCCG TAAATGCTA 180
 35 AATCTAACCA TCTATTAAAT TTAAAACC 209

(2) INFORMATION FOR SEQ ID NO: 4640:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 224 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4640:

nGnAAAGGTG AAAAGCACCC CGGAAGGGAG GTGAAATAGA ACCTGAAACC GTGTGCTTAC 60
 50 AAGTAGTCAG AGCCCGTTAA TGGGTGATGG CGTGCCTTTT GTAGAATGAA CCGGCGAGTT 120
 ACGATTTGAT GCAAGTTAAG CAGTAAATGT GGAGCCGTAG CAGAAGCATG GTCTGAATAG 180
 55 GTGCGTTTAG TATTTGGTCG TAGCCGCGAG AACCAGGGTG ATCT 224

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4641:

CACTCACnCA GATTTTTTAAG TCCTGTGCGT CTGCCAGTTC CGCCACCCCG GCACTATAAA 60
 AATGGAGCAG AAGACGGGAT TCGAACCCGC GACCCCAACC TTGGCAAGGT TTTATTCTAC 120
 CGCTGAACTA CTTCTGCATA TGCGGGTGAA GGGAGTCGAA CCCCCACGCC GTAAGCTAnG 180
 ATCCTAAGTC TAGTGCGTCT GCCAA 205

(2) INFORMATION FOR SEQ ID NO: 4642:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 235 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4642:

AGCTGACATG ATCAGTCAGC TTACAACAAT GTGCCGGTTG GGGTGGCTGG ACACGGCACC 60
 CTGAGGGAAG GGCACCCGTC ATCAAAATT CTATTATAG AATTTTACAG TAATGTGACA 120
 GACGGGCAAA GCGAACCATT CAATACGAAG TATTGTATAA ATAGAGAACA GCAGTAAGAT 180
 ATTTTCTAAT TGAAAATTAT CTTACTGCTG TnTTTTTAGG GATTTATGTn CCCAG 235

(2) INFORMATION FOR SEQ ID NO: 4643:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 260 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4643:

AGnAAGGTGG GGATGACGTC AAATCATCAT GCCCCTTATG ATTTGGCTAC ACACGTGCTA 60
 CAATGGACAA TACAAAGGCA GCGAAACCGC TAGTCAAGCA AATCCCATAA ATTGTTCTCA 120
 GTTCGATTGT AGTCTGCGAC TCGACTACAT GAAGCTGGAA TCGCTATAAT CTAGATCAGC 180
 ATGCTACGTG ATAGTTCCGG GTCTnTACAC ACGCCCGTCA CACCACGGAG GGTTTTACAC 240

(2) INFORMATION FOR SEQ ID NO: 4644:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4644:

CAGCAGGCCA CCAAAATTGT GGTCCGAGAT GTTCATATAA AACTTTATAT AATTCATCAG 60
 TTCCTAACAT TTACACCCCTC CATTTTAGAG GGAGTGGGAC AGAAATGATA TTATCGTAAA 120
 ATTTATTTTCG TCGTCCCACC CCAACTTGCA TGTCTGTAGA AATGGGGATC CAATTCnCTT 180
 GTTGGGGGCC CGCGGGCAAG GTnACTAGAA TGAAAAAGC CTGTTACAAG CGATTTTCGG 240
 TTCAGTCCAC TACTGGCAAT ATAAGTTGTA GAGCTAGGAC ATTGG 285

(2) INFORMATION FOR SEQ ID NO: 4645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 206 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4645:

GCTATTACTC TGCTATCAAT GTACCTAAAG CTACCGATGA TTTCCGAGAC ATAGACCGTG 60
 CGCTTGnTG GGGGTTCAAC TGGAACTTG GTCCATTCCA ATTATGGGAT GCAATGGGGn 120
 TACGAACGTG TTAACAAGT ATGGAAGACG AACTTGGAGA CTTACCACAA TGGGTTAGTG 180
 ATTTAGATGG TGGCTTTTGA TAAACA 206

(2) INFORMATION FOR SEQ ID NO: 4646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4646:

ACAGTTACCG ATACAACTGA AGATGATAAC GATGCAGATG GTGGCGACGT TGACGTCACA 60
 CTTACGGATC ATGATGATTT CAACTTGAT AACGGATACT TCGAGATGAT ACATCAGACA 120

CnGACAGTGA TTCAGATTCA GACAGCGACT CAGATTCnGA TA

222

(2) INFORMATION FOR SEQ ID NO: 4647:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4647:

GTACTATTCTG TGTGTGACAA TGTCTTCCA GCATTGCTT AATGAATGCT TTTCTTCGT 60
 TTAATCTTTG TAAACGAAAG CGTATCTAGT TGATTATTTT CAACAAAAGC nTCTACATCA 120
 GnCGGGATAA CGTAAGCAAT ACCACCACTC ATACCTTGAC CGAAGTTCTT ACCTACATCA 180
 CCGAAATTAA TGACAGTCCA 200

(2) INFORMATION FOR SEQ ID NO: 4648:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4648:

CCACCATTAA TTTAATACCT ATTTGGGGGC TTAGCTCAGC TGGGAGAGCG CCTGCTTTGC 60
 ACGCAGGAnG TCAGCGGTTC GATCCCCTA GTCTCCACCA TTATTTGTAC ATTGAAAAC 120
 AGATAAGTAA GTAAATATA GATTTTACCA AGCAAAACCG AGTGAATAnA GAGTTTTTAA 180
 TAAGCTTGGA ATTCATTAAG A 201

(2) INFORMATION FOR SEQ ID NO: 4649:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4649:

AGTAAATACA GATGGAATAA ATCTTTTAAG GCTTATAAAC GCTCATCTGn CATTGTAGCA 60
 ATTCATGCTT TCAAAAGACG ATATACTACG AACTCCTAC GAACTTGTCC AAGGATTACG 120

AAAGTCTGTG AGTAAGGGTG TATGGAAAGT GGTnAAAT

(2) INFORMATION FOR SEQ ID NO: 4650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4650:

GTGGCGGTGC	GACTGTCAGA	AGCACGTTAA	ATTAATGAAA	GATACAGTAG	GTGCTGATGT	60
AGAAGTAAAA	GCCATCAGGT	GGCGTACGTA	ATTTAGAAGA	TTTCAATAAA	ATGGTTGAAG	120
CAAGTGCAC	ACGTATTGGT	GCGAGCGCAG	GTGTTCAAAT	TATGCAAGGT	TTAGAAGCAG	180
ATTCTGATTA	C	TG				202

INFORMATION FOR SEQ ID NO: 4651:

PHYSICAL CHARACTERISTICS:

- LENGTH: 209 base pairs
 PE: nucleic acid
 RANDEDNESS: double
 (D) TOPOLOGY: linear

DESCRIPTION: SEO ID NO: 4651:

ACCGGCGC	AA CACGTGGATA ACCTACCTAT AAAACTGGnA TAACTTCnGG	60
ATACACCGGA	TTATTTTTA AACCGCATGG TTCAAAAGTA AAAGACGGTC	120
TTATAGATGG	ATCCGCGCTG CATTAGCTAG TTGGTAAGGT AACGGCTTAC	180
CGACGGAAG	CGCC GACCTGAGA	209

(2) INFORMATION SEQ ID NO 2:

UENGLIC

- 10 LAM: ... re pa
 11 TYPE: nu ... i
 12 DED: ... double
 13 BY: ... near

(xi) SEQUENCE L. NO: 4652:

TGAAGAT G TGC GACAGGACGG TCG TGGAGCTTTA CTGTAGCGTG 60

ATATTGAAG TCGGCACAGL TCGGCTGGn TAGGTAGGAG CCTTTGAAAC GTGGAGCGCT 120

CCACTTATCG TGGTTGGAGA CA

202

(2) INFORMATION FOR SEQ ID NO: 4653:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 205 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4653:

CCGTGCGACC CCTTTGGTCC CAAACCAAGT GCTCTACCAA GCTGAGCTAC GTTCCCGGTA 60
 TAATTAACGC GCCCGATAGG AGTCGAACCC ATAACCTCTT GATCCGTAGT CAAACGCTCT 120
 ATCCAATTGA GCTACGGGCG CATATGTTTT TATTGAAAAT GGTGCCGAGG ACCGGAATCG 180
 AACCGGTACG TGATCACTCA ACnGn 205

(2) INFORMATION FOR SEQ ID NO: 4654:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 264 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4654:

AGACGAAACC TTGTTGTTGC GAAGATAAAT CGCACAGCGA TTGAGCCTAT CTGCTGCACC 60
 ATTAAGTGGT GAAGTAACAC CATTATCAGA AGTGCTGAT CAAGTGTTCA GCGAAAAAAT 120
 GATGGTGACG GTATCGCTAT CAAACCTTCA CAAGGTGAAG TTCGTGCACC ATTCAACGGT 180
 AAAGTACCAA TGATTTCCCA ACCAAACATG CCATTGGTCC TGTATCAGAT AGTGGTTAGn 240
 CTATTAATCC ACACGGGTTA GAnG 264

(2) INFORMATION FOR SEQ ID NO: 4655:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 211 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4655:

GACGATTACA TATCATCGCT AATAACTTAG CATTAAAACC GCTTGATGCG CCACCACAAG 60

AACACAACGA ACTGGGnACA TGCTTCGGTT AAATCCATCA ATTTCAACGC TTGTnACGCG 180
 AAATCAGTTT GCTCTTGGCT GCAGTAAATC G 211

5 (2) INFORMATION FOR SEQ ID NO: 4656:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4656:

TTTACATTTA TCGGTTTAGT CAGATTCAAA CGTTTTCACT TCGCCAAGCC ATCTTTCTTT 60
 GTGTTTGCTT TTATTTTGAC GTTTTAGACA TAAAAAAGA GACCTTGCGG TCTCAATGCG 120
 20 GCTCATCGCA TCCACTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AAGTTCGACT 180
 ACCATCGACG CTAAGGnGCT TAACTGnTGG GT 212

(2) INFORMATION FOR SEQ ID NO: 4657:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4657:

35 TGGGTTTCGAA nTCCACTTAG GACCCACCAT TAACTTAATA CCTATTGGG GGCTTAGCTC 60
 AGCTGGGnAG AGCGCCTGCT TTGCACGCAG AGGTCAGCGG TTCGATCCCG CTATCTCCAC 120
 CATTATTTGT ACATTGAAAA CTAGATAAGT AAGTAAAATA TAGATTTTAC CAAGCAAAAC 180
 40 CGAGTGAATA AAGAGTTTTA 200

(2) INFORMATION FOR SEQ ID NO: 4658:

(i) SEQUENCE CHARACTERISTICS:
 45 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4658:

TACAGTATAT CGGGAAGACA GGATTCGAAC CTGCGACCCC TTGGTCCCAA ACCAAGTGCT 60

55

CTCTTGATCC GTAGTCAAAC GCTCTATCCA ATTGAGCTAC GGGCGCATAT GTTTTTATTG 180

AAAAan 185

5

(2) INFORMATION FOR SEQ ID NO: 4659:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4659:

AAGTGTTAGG GGGTTTCCGC CCCTTAGTGC TGCCAGCTAA CGCATTAAAGC ACTCCGCCTG 60

GGGAGTACGA CCGCAAGTGT ATAACTCAAA GGAATTGACG GGGACCCnCA CAAGGTTGGA 120

20

GCATGTGGTT TAATTCGAAn CAACGCGCAG TAACCTTACC AAATCTTGAC ATCCTTTGAC 180

AACTCTAGAG ATAGAGCCTT CCCCTTCG 208

25

(2) INFORMATION FOR SEQ ID NO: 4660:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 365 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4660:

ACGTCGCGAG AACGCAATTA GCTGAAAAAG ATTACAACAT TAGAACAAGA TTAAAGTCA 60

CATTTAGTGA ACATCAAAGG CCGAATAACA TCATAAATTA CGATTAGATA TAACAAAAGA 120

GCTTGGGACA TAAGTCCTAA AGTCTTAGGC AAGTAAAAAA GTGATTTCTA TTATTTATTT 180

40

GATAGAAATC ACTTTTTGAT ATGTATTTnT ATGTACAGCT CGTTGAGCnC TATTTTCCTT 240

ATATTAGTGC CATAATACAA ACCTAGCTCT TGTTTAACTT TATTATTCCG AACTGACATC 300

45

GGTGAACCCA ATAGCCTCAT AAGCAAACAG CTTACATCAT TTTCTTGAnT GGTTTTTCGTT 360

CTGTC 365

(2) INFORMATION FOR SEQ ID NO: 4661:

50

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4661:

AAAGTATTTTC TTTATGTTGG GGGGCACCCC ACTTTGnCAT TGTCTGTAGA AATTGGGAAT 60
 5 CCAATTCTCC ThATGTTGGG GCCCCGCAGT TCAACTACTG CCAATATAGT GTTGTAGTGT 120
 CTAAGACATA AAAGTTCATC TCAGTCACAA TTACTTTATA GCCTATCCAT CATCTTTTCT 180
 ACATGAAATT TTTCCAAGTG ATATATTTT 209

(2) INFORMATION FOR SEQ ID NO: 4662:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4662:

TTATGGCACT TAAAACCAGC GATGACGATT GCAGTATCAC ATGGTATCTT CAACATAACA 60
 AATACTTTGA TTCAATTACC ATTTGTAGCA GGTTTAGCAT GGATTGTTAC AAAGCTTGTC 120
 25 CCAGGTAAAG ATATTGCTGA TGACTATAAA CCTCAGCACT TAAACCAAGG TCTGTTATCA 180
 CGCACCTGGT GTTGCATAC CAGGAACTCC AAAAGGATTA CCAAATGTnG GGGCAGAnTG 240
 GCCTAA 246

(2) INFORMATION FOR SEQ ID NO: 4663:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4663:

AATGGTGTAT TATGAGTAGT AATAATTAGC AAAGAGGTAA ATTAAGTGAT GTCGCGTCAT 60
 TTAAGGAAGC GATTACAAT CGAGAATCAC AAAGTACAAC TGGTATCGGC GAAGGTATnG 120
 45 CCATTCCACA TGCCAAAGTG GCCGCAGTTA AGTCACCAGC TATTGCGTTT GGTAAATCTA 180
 AAGCAGGCGT AGATTATCAA AGnTTTTGGT ATGCAACCAG CACACT 226

(2) INFORMATION FOR SEQ ID NO: 4664:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs
 55 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4664:

5 TTCCGTCTCG GCACCATTTT AGCGCCGTAG CTCAATTGGA TAGAGCGTTT GACTACGGAT 60
 CAAGAGGTAT GGGTTCGACT CCTATCGGGC GCGCATTTTT AAATTAATTG AATAACGGGA 120
 GTAGCTCAGC TTGGTAGAGC ACTTGGTTTG GGACAAGGGC GCAGGTTCGA ATCCTGTCTC 180
 10 CCGATTACTT CTAAATCCAT TTATGGGGCT ACTCACTGGG nACGCCTCTT nCAC 234

(2) INFORMATION FOR SEQ ID NO: 4665:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4665:

GTACATCTAA AATCATCCAT GAAGGTTTGT TACCTGAATT ACGGAATGAT TCAACAACCTT 60
 25 CTAAACGTTT AATTnACCAG TAAGTCTTTG CCAAGTAGCT GATTCCAACCT CATCGCGTAC 120
 AATTTAAGTC TTCGTCAAGA TCAATCCTCT TCAAGTAAAT CTTTAATAAC CTTCTGCACC 180
 CATTTTTGCA CGAATT 196

30

(2) INFORMATION FOR SEQ ID NO: 4666:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 226 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4666:

CCGCCGAACA ACTACTTTGT TTGTTGATTC TCTCCACCTG TTTCAGTAGT TCAGATTTCT 60
 TAGATTGTGG TTTTnTAGTT GGTGCCATGC TTnAACCTTT TCATTGATTT CAATAACAGG 120
 45 TGTTACTACT TACCTGTTCC ACGGTTTAGA AGGCTTTTAG GTTCTTCTTG GCAGTGGTAn 180
 GGTTTACCAG TTCAGCGGTA CCGCGGTGTT GGnCGTGTG GATTTC 226

50

(2) INFORMATION FOR SEQ ID NO: 4667:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 187 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4667:

5 GTTCTGAATA GGGCGTTTAG TATTTGGTCG TAGCCGAnAA CCGGTGATCT ACCCTTGGTC 60
 AGGTTGAAGT TCAGGTAACA CTGGAATGGG AGGACCGAAC CGACTTACGT TGAAAAGTGA 120
 GCGGATGAAC TGAGGGTAGC GGAGAAATTC CAATCGAACC TGGAGATAGC TGGTTCTCTC 180
 10 CGAAATA 187

(2) INFORMATION FOR SEQ ID NO: 4668:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4668:

CTAAGTGGAG TTGTCACAAC ATCTTTAAAC GTTCCAGGTA AATAGTCTTT TGCCATTCT 60
 25 GAAAATGCTT TTGCCAACGT TTTATAAATA TCCAGTCTG AACGCGATTC CCATAACGGA 120
 TCAATGGCAG GATTGAAAGG ATGTACATAT GGATGCATAT CCGTTGATGA TAAATCATGn 180
 30 TT 182

(2) INFORMATION FOR SEQ ID NO: 4669:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 182 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4669:

AGTTACGTTA AAAGATGAAA ACGACAAAGT TTTAAAAACA GTTACAACAG ATGAnAATGG 60
 TAAATATCAA TTCACTGATT TAAACAATGG AACTTATAAA GTTGAATTCG AGACACCATC 120
 45 AGGTTATACA CCAACTTCAG TAACTTCTGG GAAATGATAC TGCAAAAAGA TTCTAATGGT 180
 TT 182

(2) INFORMATION FOR SEQ ID NO: 4670:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4670:

5 GGGGCAAAGT CATTnCATAG ATTAATGGTT CTCCGATACC TAGGAAACCA ACTGGCAATG 60
CACCTTTTAA AGTATTACGT AATGTTGTGT TGC GTTTACA TCTTACCCAA AGTGCTAATG 120
CGGCACCTAC TTGTCCAGCA CCAGCCATCG CTGCAATTGG CAATAAGTAA GTAGCACCTG 180
10 ATTGG 185

(2) INFORMATION FOR SEQ ID NO: 4671:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 200 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4671:

CTGACGAACG AGAAAAGAGC GCAACGATTT AGTAGAGTAA ATGAGTTAAG CGAGACCGAA 60
25 GAAGAGGAAA GAAGCAAGCG ATTGTCACAA GTCAAGAAAG GTTCTTAGCG TTCGATGGTA 120
GCCAACTTAC GTTCCGCTAG AGTAGAACGT TGCCAGGCAA AAAAATGGAT GCGATGACCG 180
30 CATTGAGACC GCAAGGnTnT 200

(2) INFORMATION FOR SEQ ID NO: 4672:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 base pairs
35 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4672:

CCCCGGGTAC AGTTATTCCC CAGAGTCAAC GCGGGGGTTG GACTCGATGT CGGTCATCGC 60
ATCCTGGGCT GTAGTCGGTC CCAAGGGTTG GGCTGTTCGC CATTAAAGCG nACGnTGCTG 120
45 GGTTCAGACG CGTGAGCAGT CCGTCCCTAT CCGTCGTGGG CGTAGGAAAT TTGAGAGGGC 180
TGTCCTTAGT ACGAGAGGCC GGGATGGCAT ACCTTGGTGT ACCATTGTCTG TGCCACGCAT 240
50 AGTGGGTAGT ATGTGTGGAC G 261

(2) INFORMATION FOR SEQ ID NO: 4673:

(i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 184 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4673:

	ATAGGGCGTT TAGTATTTGG TCGTAnCCAG AAACCAGGTG ATCTACCCTT GGTCAGGTTG	60
10	AAGTTCAGGT AACACTGGAT GGAGGACCGA ACCGACTTAC GTTGAAAAGT GAGCGGATGA	120
	ACTGAGGGTA GCGGAGAAAT TCCAATCAAA CCTGGAGATA GCTGGTTCTC TCCGAAATAG	180
	CGTT	184

15

(2) INFORMATION FOR SEQ ID NO: 4674:

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 203 base pairs
	(B) TYPE: nucleic acid
20	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4674:

	CCCAGTCAAA CTGCCCCCCT GACACTGTCT CCCACCACGA TAAGGTCGTG GGTGAGAAA	60
	GCCAACACAG CTAGGGTAGT ATCCCACCAG CGTnCTCCAC GTAAGCTAGC GCTCACGTTT	120
30	CAAAGGCTCC TACCTATCCT GTGACAAGnT GTGCCGAATT TCAATATCAG GCTACAGTGA	180
	AAGCTCCACG GGGTTCTTTC CGT	203

(2) INFORMATION FOR SEQ ID NO: 4675:

35

(i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 229 base pairs
	(B) TYPE: nucleic acid
	(C) STRANDEDNESS: double
40	(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4675:

45	nnGTTTGTAA ATAATATGGT GGAGACTAGC GGGATCGAAC CGCTGACCTC CTGCGTGCAA	60
	AGCAGGCGCT CTCCCAGCTG AGCTAAGCCC CCATAATAAT TACAGTATAT CGGGAAGACA	120
	GGATTCTGAAC CTGCGACCCC TTGGGTCCCA AACCAAGTGC TCTACCCAGC TGGAGCTTAC	180
50	TTTCCCGGTA TTATTTAACG CGGCCCGATA GGGAGTCGGA ACCCATTAA	229

(2) INFORMATION FOR SEQ ID NO: 4676:

(i) SEQUENCE CHARACTERISTICS:

55	(A) LENGTH: 178 base pairs
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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4676:

TCTAAAAATC GCGCACTTAA ACCGCTTATG ACAATCATTA TTACCTCAAT ATGCTTGTCA 60
TCACTTGCCT TTATCGTCGT TCATTGGCTA TATAGTTAAT ATGAAAAGAC GCTCAAACAC 120
TTACAAATTT AGTGTGChGA GCGTCTTATT TTTATACTTT AAAAGTCGTA TTGGTTGT 178

(2) INFORMATION FOR SEQ ID NO: 4677:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 286 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4677:

GCAAGTAAGC ATAATGTGGA GCCGTAGCGA AACAGTCTGA ATAGGGCGTT TAGTATTTGG 60
TCGTAGACCG GAAACCAGGT GATCTACCCT TGGTCAGGT GAAGTTCAGG TAACACTGAA 120
TGGAAGGACC GAACCGACTT ACGTTGAAAA ATGAGCGGAT GAACTGAAGG TAACCGGAGA 180
AAATCCCAAT CGAACCCTGG GAGATAAGCT TGGGnTCTCC TCCCGAAAAT AAGCCTTTTA 240
GGGGCTTAAG CCTCCAAAGT GGATGATTTA ATTTGGAAGG TAAAn 286

(2) INFORMATION FOR SEQ ID NO: 4678:

35

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 229 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4678:

CACACGGCTT ATGGTAACAA AAAATTCCTT TGGAGCATTA TGGAGCGAA GATAGGTTTA 60
CACCTATACC TCGTTCCGGA AGGAnTGTTT TAAAAGTGAA CTACTCCCGC AATATTAAAT 120
ATGGAGCGGA GATAGGATTT ACACCTATAC CTCATTCCAG AGGATGTATT CTAAGAGTGA 180
AATACTCCCC ATATATTAAA TATGGAGCGG AGATAGGATT GACCATACh 229

(2) INFORMATION FOR SEQ ID NO: 4679:

55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 173 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4679:

ATGACTGCTT TTTATTATAC TTTACATTTC TCGTTTCGTC AGATTCAAAC GTTTTCACTT 60
CGCCAAGCCA TCTTCTTTG TGTTCGCTTT TATTTTGACG TTTTAGACAT AAAAAAAGAG 120
ACCTTGCGGT CTCAATGnGG CTCATCGCAT CCACTTTTTC CCTGGCAACG TTC 173

(2) INFORMATION FOR SEQ ID NO: 4680:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 183 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4680:

AAAAGTAACA AGAGAAGGAC AAAAAGGTGA GAAGACAATA ACGACGCCAA CAAAAATCCA 60
TTAACTGGAG AAATTATTAG TAAAGGTGAA TCGAAAGAAG AAATCACAAA AGATCCCATT 120
AATGnATTAA CAGAATACGG ACCAGAAACG ATAACACCAG GTCATCGAGA CGAGTTTGAT 180
CCC 183

30

(2) INFORMATION FOR SEQ ID NO: 4681:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4681:

CGGTGCTTTC ACTTTCCTAC AGACTGGTTA CTATCGGTCA GAGAGAGATT TAGCnTTAGG 60
AGATGGTCCT CCCAGATTCC GACGAATTTC ACGTGTCCG TCGTACTCAG GATCCACTCA 120
AGAGAGACAA CATTTCGAC TACAGGATTA nTACCTTCTT TGATTCATCT TTCCAGATGA 180
TTCGTCTAAT GTCGTCCTTT GTA 203

50

(2) INFORMATION FOR SEQ ID NO: 4682:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4682:

GGGTCACACC TGTTCCTCATG CCGAACACAG AAGTTAAGCT CCTTAGCGTG CGATGGTAGT 60
 5 CGAACTTACG TTCCGCTAGA GTAGAACGTT GCCAGGCAAA AAGTGGGATG CGATGGAGCC 120
 GCATTGGAGA CCGCAAGCCT CTGTTCTTTG ATGTCTAAAA CGTnCAAAAT AAAAGCGAAC 180
 10 ACAAAGA 187

(2) INFORMATION FOR SEQ ID NO: 4683:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs
 15 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4683:

GGCTACACTG GTCATGATGC TGCTAAACTA CGTGATTATn ATGAAACACA TCATGCTTTG 60
 TCTGGATATG AAATGATTGA CGCAGCAAAG GTGCCATTGC AACAAATGAA GTCAATGCTG 120
 25 CGATGGGTAT ATTTGTGCAA CGCCAACAAC TGGTTCCTCC GGTACCATCC CGGTGCAGTT 180
 TTAAATT 187

(2) INFORMATION FOR SEQ ID NO: 4684:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4684:

AGTGCCAAGG CATCCACCGT GCGCCCTTAA TAACTTAATC TATGTTTCCA TCCTACAGGA 60
 AACCGTTATT AATCTTGTGA GTGTTCTTTC GAACACTAGC GATTATnTCT TATGAATTCA 120
 45 AGCTTATTTA AAACCTCTTTA TTCACTCGGT TTTGTAAAAT CTATATTT 168

(2) INFORMATION FOR SEQ ID NO: 4685:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4685:

5 ACGGGAAGTA GCTCAGCTTG GTAGAGCACT TGGTTTGGGA CCAAGGGGTC GCAGGTTCGA 60
 ATCCTGTCTT CCCGATTACT TCTTAAATTC CATTTTATGG GGGCTTAGCT CAGCTGGGAG 120
 AGCGCCTGCT TTnCACGCAG GAGGTCAGCG GTTCGATCCC GCTAGTCT 168

(2) INFORMATION FOR SEQ ID NO: 4686:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4686:

20 ATGATTCAAG CTTATTTAAA ACTCTTTATT CACTCGGTTT TGCTTGGTAA AATCTATATT 60
 TTACTTACTT ATCTAGTTT CAATGTACAA TTTCTTTTGA GTCAAGCGCT CGCATACTGC 120
 nTTATTTTCA AAAAATCAAA TGCTCATTGA CAAAAGTAAA CTCCGCTTTT AATT 174

(2) INFORMATION FOR SEQ ID NO: 4687:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 base pairs
 30 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4687:

35 TGTTGTTGAA TATGAAGAAG ATACAAACCC AGGTGGTGGT CAGGTTACTA CTGAGTCTAA 60
 CTTAGTTGAA TTTGACGAAG AGTCTACAAA AnGTATTGTA ACTGGCGCAG TGAGCGATCA 120
 40 TACCACAGTT GAAGGTACGA AAGAATATAC AACTGAAGTA ATCTGA 166

(2) INFORMATION FOR SEQ ID NO: 4688:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 189 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4688:

50 AGAACCTTAC CAAATCTTGA CATCCTTTGA CAACTCTAGA GATAGAGCCT TCCCCTTCGG 60

55

GCAACGAGCG CAACCCTTAA GCTATTGCCA TCATTAAGTT GGGCATCTAA TTGACTGCCG 180
 GTGACAAAC 189

(2) INFORMATION FOR SEQ ID NO: 4689:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4689:

TAACCACTCC TCTTAACCTT CCAGCACC GG GCAGGCGTCA CCCCTATACA TCACCTTACG 60
 GTTTAGCAGA GACCTGTGTT TTTTGATAAC AGTCGCTTnG GGCTATTAC TGCGGCTCTT 120
 CTGGGCGTTA ACCCTAAGAn ACCCTTCTCC CGAAGTACGG GGGCATTITG CGAGTCCTAA 180
 CGAGGTCGTC GTCACCTAGA TTCTCATCTT GATACTGTGT GGTTCG 227

(2) INFORMATION FOR SEQ ID NO: 4690:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4690:

AGATAATGCA CCATCAACTA ATGGATATTT ATGTCCAGTT GGGGGCCAGA AATCATAAAC 60
 GTCTTCAGTG TAAGCAACAG CATCTTCATT TnGCAGCCAA AATGCTTGGA TTATGTGCAA 120
 TAACCATCGC AACTGCGCCA CACCTTGTGT TGGCTCGCCG CCTGAAGTGG GGTG 174

(2) INFORMATION FOR SEQ ID NO: 4691:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4691:

TTTTTTTTTA AAAAAAGGGA AGGGAAAAAn AAAAGGGAAA AAAATTTAAC CCAAGGGTTT 60
 TTAAAGGGGG CCAATTTTT CCCTAAAAAA AAACCCTTTG GGTAAATTT TTTTAAAAA 120

GTTAAATTTT TTTAAAAAGG GTTCCCTTTT AAATTTTGGG AAAAACCCCC TTTTTTTTTT 240
 TTAAGGGAAT TTAaaaaATT TAAGGCCCTC CCCTAAATTA AAATTAAAGG TGGGAAAAAA 300
 5 AAAATTAATT AAAaAACCCA TTTTTTTTTT TTAATTTTTT AACCCAAAGG GGGTAATTTG 360
 GCC 363

10 (2) INFORMATION FOR SEQ ID NO: 4692:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 210 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4692:

20 TAGTGTCAAT TTTATTGATA TTTGCAATTA AACTGAAATT TAATTTTTTCG GATGTATTTT 60
 nTTTACTTAA AGTAAATAG AACACGATTT TGATGTCTGG GAATAGTGGA AATGATAAAA 120
 ACTACTAATG ATTGATTAAG TAGTGGTTCT TAACATTAGC CTCAGCTAAT TGTTACTTAA 180
 25 AAATAGGAAT ACATGAGTAA AACTCAnTGG 210

(2) INFORMATION FOR SEQ ID NO: 4693:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4693:

ATAGTAGTAA AGTATTTTCT TCCAAACATT TATTTTGATT AAGTCTTCAT CATTAGTATT 60
 40 CTCAGCTCCA CATGCACCAT CTTCCACCTC AACCTATTAA CCTCATCATC TTTAGGATCT 120
 TATAACCAAT TGGAAATCTC ATCTTGAGGn nGCTTCATCT TAGATGCTTT CACACTTATC 180
 CCTCCACACA TAGCTACCCA GCTATCCGT 209

45 (2) INFORMATION FOR SEQ ID NO: 4694:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 222 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

55

GCACATTAAC CnAAGCACCA GGCCATATAG CAATTGTTGA TACAGTATTT AAATATTTAG 60
 CATGTGACGG AATAGTTACA TATGTATTCA CTAAGGCCAT AATGACAAAT CCATTAAAAA 120
 5 GTTGGATGCT TATTCGACCC TGCTAGATGA TCTGATGAAC GGAACGCATA TTAAATAAGT 180
 ACGTGGTTAT GGATCAGTAA GATACTCTAC CAGTTACCAG nG 222

(2) INFORMATION FOR SEQ ID NO: 4695:

10

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 159 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4695:

20 TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60
 TCTATTTCTT CTATTGTTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120
 TCTTCAACTA AGTCACGATA TAATGTTTTT GAATTTTCG 159

25

(2) INFORMATION FOR SEQ ID NO: 4696:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4696:

35

AATATGGTAG TTTTAACTT ATCTATTAAG GTACAATTGA CCAAATCGAT AAAACAAATA 60
 ATACGTATCG TCAGACAATT TATGTCAATC CAAGTGGAGA TAACGTTATT GCGCCGGTTT 120
 40 TAACAGGTAA TTAAAACCA AATACGGATA GTAnTGCATT A 161

(2) INFORMATION FOR SEQ ID NO: 4697:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 170 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4697:

CCAAACTCAA TATGGCTTTA TTGGCACAGG GAACAGATAT GGAAGGTTTT ATTTATGGnT 60

55

ATATGGGATC AACACACAAA GCCGGACGCA GTGAATATTA CGCAAAATGA

170

(2) INFORMATION FOR SEQ ID NO: 4698:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4698:

CCACGGCTAA CTACTGCCAG CAGCCGCGTA ATACGTAGTG GCAAGCGTTA TCCGGAATTA 60
 TTGGGCGTAA ACGCGCGTAG GnGTTTTTTTA AGTCTGATGT GAAACCCACG GTCAACCGGA 120
 GGGTCATTGG AAAC TGAAA CTTGAGTCAG AAGAGGAAGT G 161

(2) INFORMATION FOR SEQ ID NO: 4699:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4699:

TAAATCTTCA TCAATATGAT CTAACCAATA TTGATAAAAC CTTGATGTGT TTCGTGTCAA 60
 TGACATACCA TATCGACTAG GTACCTTTTT AGAATGTTGA TTAATCACAA CAAATATCAT 120
 GGGCAAGGTC ATCTTGCAAA ATGGATTGCA TTCAAGTGGG AGGGnCGATG ATGGACGTGC 180
 TGCATGCACT GATGACCCTT TTTGCCCAT CTGGCAAATC CCACCATGAA ATGACTGACG 240
 CGGACGCh 248

(2) INFORMATION FOR SEQ ID NO: 4700:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4700:

CCCGACGAAG CGAACGTTTG GCACTGTCTC AACGAGAGAC TCGGTGAAAT CATAGTACCT 60
 GTGAAGATGC AGGTTACCCG CGACAGGACG GAAAGACCCC GTGGAGCTTT ACTGTAGCCT 120

(2) INFORMATION FOR SEQ ID NO: 4701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4701:

TACAGGGTAG TGAGATTTCG AAACAATATG GAGAAGCAGG ACTTCCTGGA AAATACAATT 60
 AATGTTTATA CGAATGGTCA TGCTGGTCAA AGTTCCTGCA GGCATATGCA CCGAAAGCTT 120
 AATGATTCAT CATACTGGAG ATGCGAATGA CTATGTTGGG TAAAGGATTT ATCTGGT 177

(2) INFORMATION FOR SEQ ID NO: 4702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4702:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTCGTTAA 60
 GGCTGAGCTG TGATGGGGAG AAGACATTGT GTCTTCGAGT CGTTGATTTC ACACTGCCGA 120
 GAAAAGnCTC TAGATAGAAA ATAGGTGCCC GTACCG 156

(2) INFORMATION FOR SEQ ID NO: 4703:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4703:

CTTGAAAAAG ATGGTTATTC TGTGAAGTA ATTGACTTAC GTACTGTTCA ACCAATCGAT 60
 GTTGACACAA TTGTAGCTTC AGTTGAAAAA ACTGGTCGTG CAGTnGTCAG CAAGACGCAC 120
 AACGTCAAGC TGGTGTGGT GCAGCAGTTG TAGCTGAATT AAGTGA 166

(2) INFORMATION FOR SEQ ID NO: 4704:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4704:

GCGGTGTCTT AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGnCT CGAACCTACG 60
ACCGATCGGT TAACAGCCGA TAGCTCTACC ACTGAGCTAC TGTGGATTAA TATTATGCCT 120
GGCAACGTTC TACTCTAGCG GAACGTAAGT TCG 153

10

(2) INFORMATION FOR SEQ ID NO: 4705:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 163 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4705:

AGGTAGAGCA CTGTTTGGAC GAGGGGCCCC TCTCGGGTTA CCGAATTCAA ACAAACTCCG 60
AATGCCAATT AATTAACTT GGGAAGTCAG ACACATGGGT GATAAGGTCC GTATTGAAAA 120
nGGAAACAGC CCAGACCACC AGCTAAGGTC CCAAATATA TGT 163

25

30

(2) INFORMATION FOR SEQ ID NO: 4706:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 203 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4706:

TAAGGTTGGG ATTGTTTGTG GGCTCGTTGC CACCCATTGT ACGGCACTCA TCAnTTCAAG 60
CCACCAGCTA CAGTATATCT CCTTGACCAG CCATAATTG ATTGGCTGCA GTCGCGATGG 120
TTTGTAAATCC TGATGAGCAG TAGCGATTCA TGTTTGACn GTACCCGTCA GATATCCGCA 180
GCAATGCAAT GTTGTGCAAG TTT 203

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45

(2) INFORMATION FOR SEQ ID NO: 4707:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 153 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4707:

CGGGTGAGAA TCCGTCCACC GATTGACTAA GGTTCACAGA GGAGGCTCGT CCGCTCTGGG 60
 5 TTAGTCGGGT CCTAAGCTGA GGCGCAGnGT AGGCGATGGA ATAACAGGTT GATATTCCTG 120
 TACCACCTAT AATCGTTTTA ATCGATGGGG GGC 153

(2) INFORMATION FOR SEQ ID NO: 4708:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 150 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4708:

20 nCTATAATGA ATAAATAATT TAGAAATATG CTTCCGATTG TTCGATGCTT TAATTCAGTT 60
 AGAAGCATCA TAGAATGCAT GATTACTGTT GTAAAGATAC GTAATGTTTT GTATTGACTG 120
 TATGTCTTTG GATAGAGTTA CAAACTTATT 150

25 (2) INFORMATION FOR SEQ ID NO: 4709:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4709:

AAAATTCGGG TTCTCAAATC ATCGGAACAT AACAAAACAA CCTAAGCAAC ATGTAGGCCG 60
 TTGTCACTTA ACTTCTTGTT TTTCCGATGA CAGCTTCTAT ThAGAGAATG TCATGATTAT 120
 40 TTTATATTCA CTTCAATGTT ATCAGTATTA GTGCCA 156

(2) INFORMATION FOR SEQ ID NO: 4710:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 base pairs
 45 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4710:

GTTGATATTC CTGTACCACC TATAATCGTT TAATCGATGG GGGGGACGCA TAGGATAGGC 60
 55

TCGTTAAGGC TGAGCTGTGA TGGGGAGAA

149

(2) INFORMATION FOR SEQ ID NO: 4711:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4711:

15 TTGACTTCAA TACCATGGGC CAGGTACnCT TTAAATGTTG TTGTCTCAGT TAATATTAAT 60
 TGGCTTTTCT TTTGCATAAT TGACAAATGGC TTCTGCCAAT GGGTGTTTCT AATCTTTTTC 120
 AGCAGTAGCA AGTAGTTGGT AGCGTTTGAT TGGTCACCAG 160

20 (2) INFORMATION FOR SEQ ID NO: 4712:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4712:

30 ATAGTGAACC AGTACCGTGA GGACnAGGTG AAAAGCACCC CGGAACGACG TGAAATAGAA 60
 CCTGAAACCG TGTGCTTACA AGTAGTCAGA GCCCGTTAAT GGGTGATGGC GTGCCTTTTG 120
 TAGAATGAAC CGGCGAGTTA CGATTTGATG C 151

35

(2) INFORMATION FOR SEQ ID NO: 4713:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4713:

ACCAGTTGAT CTACCCTTGG TCAGGTTGAA GTTCAGGTAA CACTGAATGG AGGACCGAAC 60
 CGACTTACGT TGGAAAAGTG AGCGGGATGA ACTGnGGGTA GCGGAGAAAT TCCAATCGAA 120
 CCTGGGAGAT AGCTGGTTCT CTCCG 145

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(2) INFORMATION FOR SEQ ID NO: 4714:

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(A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4714:

10 TGTnACGCAG AGATCGCGGG TTCGATTCCC GTCGAGACCG CCATTTAATT TTATAATTAA 60
 TAGCGATGTA CCTATAATAA TGGAGGAATA CCCAAGTCCG GCTGAAGGGA TCGGTCTTGA 120
 AAACCGACAG GCCTTAACGG GCCGCGGGGG T 151

15 (2) INFORMATION FOR SEQ ID NO: 4715:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4715:

25 TCGTATTGAA TGGCTTCGTT TCCTAGGGTG CCGTCTCAGC CTCGGTCTTC GACTGGCACT 60
 GCTCCCTCAG GAGTCTCGCC ATTAATACTA CGTATTAACG TGTAATTTTA CTTTGnAATA 120
 30 CTTTAAAAAA ATAAGACACT TTGCCAACTT G 151

(2) INFORMATION FOR SEQ ID NO: 4716:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 152 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4716:

GCTGTCATCG GAAAAACAAG AAGTTAAGTG ACAAGGGTTT ACATGTTGCT TAGCTTCTTT 60
 45 TATTATGCGT AATGATGTAA AAAGACGAAT ATTCATTTGT TTGTAAAAGT GGCATTTCTA 120
 TGTCTTAAAA GTGACGAAAC TTCACnCTGT GC 152

(2) INFORMATION FOR SEQ ID NO: 4717:

50 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4717:

5 GGATACTAGT AAAACCATAT TTAGTAAATA CAGATGGAnT AAATCTTTTA AGGCTTATAA 60
ACGCTCATCT GACATTGTAG AATTCATGCT TTCAAAAGAC GATATACTAC GACACTCCTA 120
CGAACTTGTC CAAGGATTAC GAAA 144

10 (2) INFORMATION FOR SEQ ID NO: 4718:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 145 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4718:

20 ATCATAAGGG GCATGATGAT TTACGTCATC CCCACCTTCC TCCGGTTTGT CACCGCAGTC 60
AACTTAGAGT GCCCAACTnA ATGATGGCAA CTAAGCTTAA GGGTTGCGCT CGTTGCCGGA 120
CTTAACCCAA CATCTCACGA CACGA 145

25 (2) INFORMATION FOR SEQ ID NO: 4719:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 156 base pairs
(B) TYPE: nucleic acid
30 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4719:

AAATACCTTT CCACGATCTT CAGCTGGGCG CCTCTGCACT CGCAAACGCA CTTGATGCAT 60
CAACAACACC ACCAAATAGT CCCTGCAATA ACCTCACAGT ACAAACGTGA ATGGTGTCGT 120
40 ACACnATGCC ATTTAAAAAT AGCATACCGG CAAAGC 156

(2) INFORMATION FOR SEQ ID NO: 4720:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 152 base pairs
45 (B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4720:

TTAAATCGAG TCTCTTTTAC AGGTCCATAT TTTGTTACGT ATCGACCGGT GGCTAACTAC 60
55

TAACTCGGAT CAAATTCGTC TCGATGACCT GG

152

(2) INFORMATION FOR SEQ ID NO: 4721:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4721:

15

CACTAGTTCA AGTTCAAGTG GCGACGATTG GTATTTTACA AGAATTTTAT CAACAAGGAT 60

TTAATTAGCT TAAACGCGC AATCCCTGTG TTACTAGGGC GGATAACATT GGTACCACGG 120

TTACAGCTAT CTTAGCTAGT TTAGCC 146

20

(2) INFORMATION FOR SEQ ID NO: 4722:

25

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 156 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4722:

CCACACCAAT ATTTTGGCGCT AAGTAATCG CATTAAACGT TTGTCTTCCG CCATTTGAGC 60

CACACTGCTC CAGCTCATAG CGCTATATCG CAGGGAATAA TCATTCCGCC ACCACAACCC 120

35

TAACATTACC CAGCCATACA GCCATACCAG GGCCAC 156

(2) INFORMATION FOR SEQ ID NO: 4723:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4723:

ACGGTCTTGC TGTCACTTAT AGATGGATCC GCGCTGCATT AGCTAGTTGG TAAGGTAACn 60

50

GCTTACCAAG GCAACGATGG CATGAGCCGA CCTGGAGAGG GTGGATCGGG CCACACTGGG 120

AACTGAGACA CGGTCCAGAC TCCTACGGGG AGGCAGCAGT A 161

(2) INFORMATION FOR SEQ ID NO: 4724:

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(A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4724:

10 CAGAAAGCTC ACGGGGCTTT CGTCTGTCGC GGGTAACCTG CATCTTCACA GGTACTATGA 60
 TTTCACCGAG TCTCTCGTTG AGACAGTGCC CAAATCGTTA CGnCTTTCGT GCGGGTCGGA 120
 ACTTACCCGA CAAGTAATTT CGCTACCTTA GGACCGTTAT AGTTA 165

15 (2) INFORMATION FOR SEQ ID NO: 4725:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4725:

25 GGACGTTATA AGTGCTGAAA CATCTAAGCA TGAAGCCCCC CTCAAGATGA nATTTCCCAA 60
 CTTTCGGTTAT AAGATCCCTC AAAGATGATT AGGTTAATAG GTTCGAGGTG GAAGCATGGT 120
 30 GACATGTGGA GCTGGACGAA TACTAATCG 149

(2) INFORMATION FOR SEQ ID NO: 4726:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 275 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4726:

40 TTGAATTTTT GAAAAAAAAA TGCCGAAATA AAAGATGCCA AGATATCCGC CGGGTAAAAA 60
 ATTAAGTTTC CGAAAAACCA GGTGTTGGTA CCCATTGCAT CTGGGGTGGC AAAAGCATTT 120
 45 GCAGATAAAA TTGTCATCAG TGTTACGAT GGTGGTACAG GGCTTCACCC AAACGAGTAT 180
 CAGCATGCCG GTGTTCTTGG GAGATGGTTA GCAGAACACA TCAACATAAA CTAATGCTAA 240
 50 GAnCGGTAAA GTAGACAnCG GTAGTATACT GAAAT 275

(2) INFORMATION FOR SEQ ID NO: 4727:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 149 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4727:

ATCAATGAAC AACACATACA GATGGTACTG CGACGCCTAG AGTAACAAAA TAAGTTTGT 60
AACTCTATCC AAAGACATAC AGTCAATACA AAACATTACG TATCTTTACA ACAGTAATCA 120
TGCATTCTAT GATGCTTCTA ACTGAATnA 149

(2) INFORMATION FOR SEQ ID NO: 4728:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 158 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4728:

GCACGTTATT CCATTATCTT AATGGTTATC TTATCCTCAA CTAAATTGGA GGAATCACTA 60
TGACAATTAA TAAAGAACCG TTCTTGGCGC AGCACAATGG GCGCTCACTG GCAGACTTTT 120
GTGATGCTGA CTTAAAGTAA ACTATTAGAT ATTGnGTG 158

30

(2) INFORMATION FOR SEQ ID NO: 4729:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4729:

TCATTGACAT CGCTGGAATA GGTGTAAATC CTGCGATTTCG ATCTGGACCA TATTTTTTTA 60
TTGTATACAG TAATTGTGCT GCGATTATCT CTGTAACGTC TTTCCAATTT GAnCGCACGT 120
GCCCTCCCAT ACCTCGGG 138

45

(2) INFORMATION FOR SEQ ID NO: 4730:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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TAAAGACTAT ACCATTCTAT CCAATAATAA TTGGATTTCG ATTTGTCTGA ATTCGTAACC 60
 GAGAGGCCCC TCGTCCAAAC AGTGCTCTAn CTCCAATAAT CATCACTTGA GGCTAGCCCT 120
 5 AAAGTATTTT GGAGAGAACC AGCTATTTCC AGTTCGATTG GAATTTCTCC GCTACCCTCA 180
 GTTCATC 187

10 (2) INFORMATION FOR SEQ ID NO: 4731:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4731:

20 CGCATCCTGG GGCTGTAGTC GGTCCCAAGG GTTGGGCTGT TCGCCATTAA AGCGGTACGA 60
 AGCTGGGTTT AGAACGTCGT GAGACAGTTC GGTTCCTTAT CCGTCGTGGG CGTAGGAAAT 120
 TTAGAGGAG CTGTCCT 137

25 (2) INFORMATION FOR SEQ ID NO: 4732:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 30 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4732:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60
 TCTATTTCTT CTATTGTAA ATCGCTATCT CCATCTTCTT TTATCTCTGG TATTATnTTT 120
 40 TCTTCAACTA AGTCACG 137

(2) INFORMATION FOR SEQ ID NO: 4733:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4733:

TCGTTCTCAA TAGAATGATT TAAATCTTCG ATTTCTTTAT CTAAATGACT ACCAATTAAA 60

55

TCTTCAACTA AGTCACG

137

(2) INFORMATION FOR SEQ ID NO: 4734:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 153 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4734:

15 AAAACATAAA TACAAAAATA TAGCTATTAC TATAAAAAAC AGCAGTAAGC ATATTTCCAA 60
 ATTGCAAATT ATCCTACTGC TGTTCITTTT GGGCAGTGGG nACAGCAAAT GATATTTTCG 120
 ACAAATTTTA TTTCGTCGTC CCACCCCAAC TTG 153

20

(2) INFORMATION FOR SEQ ID NO: 4735:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 142 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4735:

30 TAGAAATTAC GGACCCAATT TCTCTATGTT GGGGCCCCATC CCCAACTTGC ACATnATTGC 60
 AAGCTGACTT TTCGTCACCTT GCTTTGTGTTG GGCCCCGCCA ATAAGCGTTG TAGTGCCTAG 120
 35 TACTTTGATT GATGTCCAAG TT 142

(2) INFORMATION FOR SEQ ID NO: 4736:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4736:

45 ATGTTATTCA AAGTAAATTG CTTTGCCTGA TTTTGCAGAC TGATAAATCG CTTCAAGAAT 60
 50 TTTTGTAACCT ACCATTGCTT GTTCCGGTTT CACAACTGGT TCAGTATCAT TTACAACnGC 120
 ATCAATCCAA GCTTTTG 137

(2) INFORMATION FOR SEQ ID NO: 4737:

55

(A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4737:

10 GGTCTTTTAG TATTTGGTCG TACACCGCAA ACCAGGTGCA TCTACCCTTG GTCAGGTTGA 60
 AGTTCAGGTA AACTGAAAT GGAGGACCGA ACCGACTTAC GTTGAAAAT GAGCGGATGA 120
 ACTGAGGGTA GCGGAGAAAT TCCA 144

15 (2) INFORMATION FOR SEQ ID NO: 4738:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4738:

25 GGGTAGCTAT GTGTGGACGG GATAAGTGCT GAAACATCTA AGCATGAACC CCCCTCAAGA 60
 TGAGATTTCC CACTTCGGTT ATAAGATCCT CAAAGATGAT GAGGTTAATA GGTCGAGGTG 120
 30 GAACATGGTG ACATGTnATC TGCTTTTCTA ATCATAC 157

(2) INFORMATION FOR SEQ ID NO: 4739:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4739:

40 GCTTTATGTC TAAAACGTCA AAATAAAAAG CAAACACAAA GAAAAATGGC TTGGCGAAGT 60
 45 GAAAACGGTT GAATCTGACG AAACGAGAAA AGAACGCAAC GAGTTTAGTA GAGCTAnATG 120
 AGTAAGTGAG AGCCGAAGAG AGGGA 145

(2) INFORMATION FOR SEQ ID NO: 4740:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4740:

5 TAGTAGCACC ACCCTTAGAC CTTCTTGATT TGACATCGTT GTTCTTCCTT CCTTCGGTCT 60
 CGTTACTCAT TTAGCTCTAC TAAACTCGTT GCGTCTTTTC TCGTTTCGTC AGATCAAACG 120
 TTTCACTTCG CCAAGCCATT TTTCTTGTGT TTATTTTATT TGACGTTTAG ACATAAAAAA 180
 10 GAGACCCACG TTCAACTTGC CnGCACGTTT TACTCTGCGG AnTAGTGGCT ACCA 234

(2) INFORMATION FOR SEQ ID NO: 4741:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 135 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4741:

20 GCAAGTCTTT TTAAAGGTAA CACTATCATT TATGCAATAC GGCGCATTAC CAGAGTTGCA 60
 TGGTCAAAAT ATATTGTTGT CATTTGAAGA TGGACGTGTA CAAAAATGCG TGTTACGTGA 120
 25 TCATGATACT GTCAn 135

(2) INFORMATION FOR SEQ ID NO: 4742:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4742:

35 ACCCTGGTAC AGTTGAATTC AGGTAACACT GAATGGAGGA CCGAACCGAC TTACGTTGAA 60
 40 AAGTGAGCGG ATGAACTGAG GGTAGCGGAG AAATTCCAAT CGAACCTGGA GAnAGCTGGT 120
 TCTCTCCGAA ATAGCTTTAG GGCTA 145

(2) INFORMATION FOR SEQ ID NO: 4743:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4743:

TGATTATCAT GGGTGCGGGT ATTAACCATT GGTTTAACTC AGATACGATT TATnGTGCAA 120
 TCTTAAACTT AGTTATGGTA TGTGGCGTCA A 151

5 (2) INFORMATION FOR SEQ ID NO: 4744:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4744:

TAAAGCTAAA AACACAGCTC ATAATATCAA AAAAGGTGCA GAAGAAATGG TTGAAGCGGC 60
 AGGCGATAAA ATCAnAGATG GTGCATCTTG GTTAGGCGAT AAAATCGGCG ATGTGTGGGA 120
 20 TTATGTACAA CA 132

(2) INFORMATION FOR SEQ ID NO: 4745:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 132 base pairs
 25 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4745:

CGTGCGCTCT AACCAGCTGA GCTATAGGCC CATTAAITTG AATGAACAAA CATTCAAAAC 60
 TGAATACAAT ATGTCACGTT ATTCCGCATC TTCTGAAGAA GATGTTCCGn ATATATCCTT 120
 35 AGAAAGGAGG TG 132

(2) INFORMATION FOR SEQ ID NO: 4746:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 base pairs
 40 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4746:

GTGATCCGAC TCAGATAGCG ATCCGACTCA GATAGCGACT CAGATTCAGA CAGCGATTCA 60
 50 GATTTCAGACA GCGATTCAGA TTCAGATAGC GATTTCAGATT CCGACAGTGA CTCAGATTCC 120
 GACAnTGACT CGGATTCA 138

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 185 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4747:

CATTATTGTA AACTGAACTT TTCGTCACCT GCTGGTGnTT GGGGACCCCA CCAACTTGGC 60
 ACATTATTGG TAAGCTGACT TTTGTCACCT TACTGTGTTG GGGCCCCGCC AACTTGCATT 120
 GTCTGTAGAA ATTGGGAATC CAATTCTCT ATGTTGGGGC CCACACCCCA ACTCGACATT 180
 GCCTG 185

(2) INFORMATION FOR SEQ ID NO: 4748:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 173 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4748:

ACCGAATCCC TTCAGACCGG TACTTGGGTA TTCCTCCAA ATTATATGGA CCTTGACAGT 60
 ACTCGAACCT GACGTACCGA AACGGTTATG AAGACCGTTA nCTCTAACCA ACTGAGCTAA 120
 AGGATCCTAA ATATAATTTT ACAACTAATA AATAGTGGAC GGTGGAGGGA TCG 173

(2) INFORMATION FOR SEQ ID NO: 4749:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 212 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4749:

ACACAAGGAT AAGGCATTGT TGGATGTGGG ATGCTTTAAC TGGGCAAGCG ATTGGTCGTC 60
 CTAAACAGG TACATATGCC GGCTATCTGA CCTAGTCGGT TTAGATATTG CAGTGTCTGT 120
 AATTAAAGGG CATGCAACCA AGTAnCTGAG GAAACAACTT ATTTTCATGG TGTCAAAAAT 180
 TGnTAAATAC GGTGTTTGAC AATTGCGCAC CT 212

(2) INFORMATION FOR SEQ ID NO: 4750:

(A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4750:

10 AATCTCAGGT TTTACCAAGC AAAACCGATG AATAAAGAGT TTAAATAAG CTTGAATTCA 60
 TAAGAAATAA TCGCTAGTGT TCGAAAGACn GCAGCAAGAT TAATAACGCG TTAAATCTT 120
 TTTATAAAAG AAAACGTTTA 140

15

(2) INFORMATION FOR SEQ ID NO: 4751:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 184 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4751:

ATTCGTCAGC TCCACATGTC ACCATGCTTC CACCTCGAAC CTATTAACCT CATCATCTTT 60
 GAGGGATCTT ATAACCGAAG TTGGGAAATC TCATCTTGAG GGGGGTTCAT GCTAGATGCT 120
 30 TCAGACTATC CCGTCCACAC ATGTAACCAG nATGCGTGGA CGCATGGAAC AGGGATGTCA 180
 TCCG 184

35

(2) INFORMATION FOR SEQ ID NO: 4752:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 133 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4752:

45 GGGATCTTCC GCAATGGGCG AACTGTACG GAGCAACGCC GCGTGAGTGA TGAAGGTCTT 60
 CGATCGTAAA ACTCTGTTAT TAGGGAAGAA CATATGTGTA AGTAACTGTG CACATCTTnA 120
 CGGTACCTAA TCA 133

50

(2) INFORMATION FOR SEQ ID NO: 4753:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 162 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4753:

5 GTATGCTGTG TGGCTTGTCa TGTTcGGGTT TGGTGGCGGA CCTGATTATT CCTGCGnTAT 60
 ACGCTATGGC TGGAGCAGTG TGGCCAAATG GCGGAAGACA AACGTTTAAT GCGATCTACT 120
 TGGCGCAAAA TATTGGTGTG GCTGTcGGTG CTGCAATGGG CG 162

(2) INFORMATION FOR SEQ ID NO: 4754:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 134 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4754:

20 AATTCGATTC CCTTAGTAGC GGCGACGAAA ACGGGAaNGA GCCCAAACCA ACAAGCTTGC 60
 TTTGGGGGTT TGTAGGACAC TCTATACGGG GTTAACAAAG GACGACATTA GACGAATCAT 120
 CTTGGGAAAG ATGA 134

(2) INFORMATION FOR SEQ ID NO: 4755:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 139 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4755:

35 AGAGTGCCTA ATAGCTCACT AGTCGAGTGA CACTGCGCCG AAAATGTACC GGGGCTAAAC 60
 ATATTACCGC AAGCTGTGGA TTGTcCTTTG GACATGGCTA GGAGAGCGTT CTAAGGGCGT 120
 40 TGAAGCATGn ATCGTAAGG 139

(2) INFORMATION FOR SEQ ID NO: 4756:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4756:

55

CGTGAAATGC GCAGAGATAT GGAGGAACAC CAGTGGCCGA AAGCCACTTT CTGGTCTGTA 120
 ACTGGACGCT GGATGTGCCA AACCTGGGGG ATCAAACAGG TTA 163

(2) INFORMATION FOR SEQ ID NO: 4757:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4757:

CATGAACTA GATAAGTAGT AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG 60
 TTTTAAATAA GCTTGAATTC ATAAGAAATA ATCGCTAGTG TTCGAAAGAC ATCACAnGAT 120
 TAATACCGCG TTTAATCTTT TATAAAGGAC CGTAACTTCA 160

(2) INFORMATION FOR SEQ ID NO: 4758:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4758:

TACATGGGTT TATTGTTGAA GATGACGAAA TTGTAGAAAT TTAATATTCT AAAAAGGTTG 60
 GGGACATAAA TCCCCCTAAA AAAACCAGCA GTAAGATAAT TTTCAATTAG AAAATATCTT 120
 ACTGCTGTTC TCTATTATA CCAAnATTACT TTCGTAATTG TTAAAATTTT AAAAGGA 177

(2) INFORMATION FOR SEQ ID NO: 4759:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4759:

CGGTGTGTAC AAGACCCGGG AACGTATTCA CCGTAGCATG CTGATCTACG ATTACTAGCG 60
 ATTCAGCTT CATGTAGTCG AGTTACAGAC TACAATCCGA ACTGAGAACA ACnTTATGGG 120
 ATTTGCT 127

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4760:

10

GGGCCCCCTCG TCGGGTTACC GAATTCAGAC AAACCTCCGnA ATGCCAATTA ATTTAACTTG 60

GGAGTCAGAA CATGGGTGAT AAGTCCGTGT TCGAAAGGAA ACAGCCCAGA CCACCAGCTA 120

15

AGTCCCAAAT ATATGTTAAT GAAAG 145

- (2) INFORMATION FOR SEQ ID NO: 4761:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

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- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4761:

TAAACAAGGC GCGTTGGGCC TATTCAGTGC GGCTCTTCTG GCGGTTAACC CTAAAGAGCA 60

30

CCCCCTTCTCC CGAAGTTACG GGGTCATTTT GCCGAGTTCC TTAACGAGAT TGCTCGCTCA 120

CCTTAGAATT CCATCTGACT ACGGTCGTTG CGTACGGCAC TATTTCTTCA AGCTTCCGCA 180

TTAACACACC AAAACAGCTC CCACCACCAC TAnATCGAnC AACACTAG 228

35

- (2) INFORMATION FOR SEQ ID NO: 4762:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4762:

45

TnGCCAAATC TTAGTAGTCG CTTGGTTCCG TTGTGGTGCG ACAGCTGTGA AATCATCACT 60

ACGTTGCTCA TCACTCACTG TCTCTCCGCT TCCTTGCATT GCAACAGCTT GAATTGTATC 120

50

AGCAGGGTTG 130

- (2) INFORMATION FOR SEQ ID NO: 4763:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4763:

CAACTCGTAG TCAGGGTCGA AAGACGGGAC TTAGTGATCC GGTGGTTCCG TCATGGGTAG 60
GGCCATCGTC TCAACGGTAT AAAAGCTACC CCGGGGATAA CAGGCTTATC TnCCCCAAGA 120
GTTACATCG ACGGGGAGGT TTGGCACCTC G 151

(2) INFORMATION FOR SEQ ID NO: 4764:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 128 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4764:

ACCCCAACTT GCATTGnCTG TAGAAATTGG GAATCCAATT TCTCTTTGTT GGGGCCCCGC 60
CGGCAAGGTT GACTAGAATT GACCAAAAGC TTGTTACAAG CGCATTTTCG TTCAGTCAAC 120
TACTGCCA 128

(2) INFORMATION FOR SEQ ID NO: 4765:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4765:

AATACAGCCC CAGAGCGATG AGCCGACATC GAGGTGCCAA ACCTCCCCGT CGATGTGAAC 60
TCTTGGGGGA GATAAGCCTG TTATCCCCGG GGTAGCTTTT ATCCGTTGAG CGGATGGCCC 120
TTTCCATGTG GnaAC 135

45

(2) INFORMATION FOR SEQ ID NO: 4766:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 126 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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GATTCTCACC CGTCTTTTCGC TACTCACACC GGCATTCTCA CTTCTAAGCG CTCCACATGT 60
 CCTTACGATC ATGCTTCAAC GCCCTTAGAA CnCTCTCCTA CCATTGTCCA AAGGACAATC 120
 5 CACAGC 126

(2) INFORMATION FOR SEQ ID NO: 4767:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 130 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4767:

TTAATAGTTT TATAAGAGAG GTGTTTGATC TTGAGCTAAC CACnTCATTC GAGTACTGTC 60
 20 ATGAAGTAAT TTCTCTATTC TACGACCAGA AAATACAGAT GGGGTATATG CATATAAGAT 120
 GATTTTTTAAC 130

(2) INFORMATION FOR SEQ ID NO: 4768:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 142 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4768:

GTTAACCTTA AAGAGCACCC CTTATACCGA AGTTACGGGG TCATTTTGCC GAGTTCCTTA 60
 35 AAGCGCGTTC GATCGCTCAC CTTAGGAATT CTCATCTTGA CTACCTGTGT CGGTTTGCGG 120
 TAGGGCACCT ATTTTCCTAT CT 142

40 (2) INFORMATION FOR SEQ ID NO: 4769:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4769:

CCTTGGGACC GACTACAGCC CCAGGATGCG ATGAGCCGAC ATCGAGGTGC CAAACCTCCC 60
 CGTCGATGTG AACTCTTGnG TGGAGATAAG CCTGTTATCC CCGGGGTGAG CTTTGTATCC 120

55

(2) INFORMATION FOR SEQ ID NO: 4770:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 145 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4770:

CTAAAAGTTG TATTTTAAAA ATAGTTCTTT AAATTATATA CCCACCACAT TTGGTGGAGA 60
 ACCGTTAAAC AATGCATAGT TTGCTTAACT TCCAATATTG ACTCATCATT ACAATTGACA 120
 TAGAGCTATT AAGCGTnGCC ATGAG 145

(2) INFORMATION FOR SEQ ID NO: 4771:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4771:

TCGAGTGACA CTGTCGCCGA AAATGTACCG GGGCTAAACA TATTACCGAA GCTGTGGATT 60
 GTGCCTTTGG AAATGGTGAG GnGAGCGTTC TAAGGGCGTT GGAAGCATGA TCGTAAGGAC 120
 ATGTGGGA 128

(2) INFORMATION FOR SEQ ID NO: 4772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4772:

GGGCAGATGT TCCTGCAGTC ATAGTGCCGT CAACTTTAAA TACTGTACGT AATTTGGCTA 60
 ATGCCTCCAT CGTGGnTGTC AGGGCGTATA AATTCATCTT GGGTCAAAGA TATTTGGTGT 120
 GTACTT 126

(2) INFORMATION FOR SEQ ID NO: 4773:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4773:

GTCTTTTCTC GTTTCGTTCA GATTCAAACG TTTTCACTTC GCCAAGCCAT TTTTCTTTGT 60
10 GTTTACTTTT TATTTTGACG TTTTAGGATA AAAAAAGAn ACCTTGCGGT CTCAATGCGG 120
CTCATC 126

(2) INFORMATION FOR SEQ ID NO: 4774:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4774:

25 ATTTCAATAT CAGGCTACAG TAAAGCTCCA CGGGGTCTTT CCGTCCTGTC GCGGGTAACC 60
TGCACTCTTnA CAGGTACTAT GATTTACCG AGTCTCTCGT TGAGACAGTG CCCAAATCGT 120
TACG 124

30

(2) INFORMATION FOR SEQ ID NO: 4775:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4775:

40 ACCAAGTGAG CCGGAAACAC CAACGCCACC AACACCAGAA GTACCAAGTG AGCCGGAAAC 60
ACCAACACCA CCGACACCAG AAGTGCCGAG TGAncCAGAA ACTCCAACAC CGCCAACACC 120
45 AGAG 124

(2) INFORMATION FOR SEQ ID NO: 4776:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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CCCGCTAGTC TCCACCATT ATTITTTTACA CGATGAACAT TGAAAACTnA ATACAATATG 60
 CAACGTTAAT TCCAAAAAAC GTAACATAA GTTACAAACA TTATTTAGTA TTTATGAGCT 120
 5 AATCAAACAT CATAA 135

(2) INFORMATION FOR SEQ ID NO: 4777:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4777:

(AGTGCAGAAG AGGAAAGTGG AATAnCCCCA ACATAGCGGT GAAATGCGCA GAGATATGGA 60
 20 GGAACACCAG TGGCGAAGGC GACTTTCTGG TCTGTAAC TG GACGCTGGAT GTGCGAAACG 120
 TTGGGGGTTC AAACAGGATT TAGA 144

(2) INFORMATION FOR SEQ ID NO: 4778:

25 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4778:

35 AATTTTTGAT GACGGGTCCC TTCCTAGGGT GCCGTCTCAG CCACCCCAAC CGGCACATTG 60
 TTGTAAGCTG ACTATATGTC nTTCATGTGT TGGGGCCCCT GTCTTCGACT GGCACTGCTC 120
 CCT 123

40

(2) INFORMATION FOR SEQ ID NO: 4779:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 45 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4779:

GCGCATTAAC TATCGCGATA TTAATCGCTA TTCTATATCG TCACTTTAGA GGATATCCTG 60
 AACAAATATAG CTCAGGTATT ACGTTTTTCAT CTAAATATTT ATTAAGATTT GCAATCATCC 120

55

(2) INFORMATION FOR SEQ ID NO: 4780:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4780:

GGTAATATGT TTAGCCCCGG TACATTTTCG GCGCAnTGTC CTCGACTAGT GAGCTATTAC 60
 GCACTCTTTA AATGATGGCT GCTTCTAAGC CAACATCCTA GTTGTCTGGG CAACGTCACA 120
 TCCTTTT 127

(2) INFORMATION FOR SEQ ID NO: 4781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4781:

ACACnGGGTG AGAATTTGTC GCTATTTGTA AATTGTATCC TGGCTTAAGT TGGCCAAAGT 60
 GTCTTATTTT TTAAAGTAT TTAAAGTAA AATTACATGT TAATACGTAG TATTAAATGG 120
 CGAGACTCC 129

(2) INFORMATION FOR SEQ ID NO: 4782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 136 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4782:

CTCATTCCCG TTGCATTTTA TCTTCTGCAA CAACAACATT TCGTCTTTAT CGTCTTCCAT 60
 AGTAGTAGGA TTTTCTACTA CTTGACCATT CATAATCTGT TGCATTTTCAT GTTTGnTTTG 120
 GTCAGATTTA GGACCA 136

(2) INFORMATION FOR SEQ ID NO: 4783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4783:

CATCAACATC GCGCATTA AAGATGGACG TTTTGATGAT GTACAACAAG ACATTGAAGC 60
10 AGTGGTTAAA GCTGCGAAAG GTCACACAGT AAAAGTGATT ATTGnGACGG TATTGTTGG 119

(2) INFORMATION FOR SEQ ID NO: 4784:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 127 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4784:

ATCACTAATC CATTGTGGTA AGTCTCCAAG TTCGTCTTCC ATACGTGTTT TAACCTGCGT 60
25 nATCCCAT TG CATCCATAA TTGTGAATGG ACCAAGTTTC CAGTTGAACC CCCAGACAAG 120
CGCACGG 127

(2) INFORMATION FOR SEQ ID NO: 4785:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 119 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4785:

ACACCGGCAT GCTGAATACT CGTTTTGGGT GAAGCCCCTG nACCACCATC GTAACCACTG 60
40 ATGACAATTT TATCTGCAAA TGCTTTTGCC ACCCCAGATG CAATGGTACC AACACCTGT 119

(2) INFORMATION FOR SEQ ID NO: 4786:

(i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 137 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4786:

CTTTCTAAAC CCGnCAACCAC TTTATCGTGG TGGGAGACA GTGTTGAGC GGGCCAGTTT 60
55

AATCATTCAT AGAGTGT

137

(2) INFORMATION FOR SEQ ID NO: 4787:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4787:

15 GTTTTAAACA CTGTTACCGT TTCATCTTT TAATGTTACC GTTACGCCAG AnATACCTTT 60
 TTCATCTTGG TCTTGGATAC CATTTTTATT TGTATCTTCC CAGACATAGT CACCTAAGT 119

(2) INFORMATION FOR SEQ ID NO: 4788:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 141 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4788:

30 CATGCTTCCA CCTCGAACCT ATTAACCTnC ATCATCTTTG AGGGATCTTA TAACCGCAGT 60
 TGGGAAATCT CATCTTGTAG GGGGGCTTCA TGCTTCAGAT GCTTTGCAGC ACTTAGCCCCG 120
 GCCACACATA GCTACCCAGC T 141

35 (2) INFORMATION FOR SEQ ID NO: 4789:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 139 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4789:

45 CTGGGTTTCAAG AACGTCTAAG CAGTTCGGTC CCTATCCGTC GTGGGCGTAA GAAATTTGAG 60
 AGGAGCTGTC CTTAGTACGA GAAGACCGGG ATGGACTACC TCTnGTGTAC CAATTGTCGT 120
 50 GCCAACGCAT AGCTGGGTA 139

(2) INFORMATION FOR SEQ ID NO: 4790:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 129 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4790:

CATTATTTAG TATTTATGAG CTAATCAAAC AnCATAATTT TTATGGAGAG TTTGATCCTG 60
10 GCTCAGGATG AGCGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGACGAGATG 120
CTTGCTTCG 129

(2) INFORMATION FOR SEQ ID NO: 4791:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4791:

GGGTGCTCTT TAGGGTTAAC GCCCAGAAGA GCCGCAGTGC AATAGGCCCA AGCGACTGTT 60
25 TATCAAAAAnC ACAGGTCTCT GCTAAACCGT AAGGTGATGT ATAGGGGCTG ACGGCTTCCC 120

(2) INFORMATION FOR SEQ ID NO: 4792:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 123 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4792:

CAAATTCCTT CGCTACTTGA ATGACAACAC TTTGTTTTAC GCCTGAAATG GCTTCTTGCC 60
40 AAGCAGGTGT ATATTTTGAT TCTGCATCGT CGTATCCTTT TGATCTAATT ATGATCAAAC 120
CGn 123

45

(2) INFORMATION FOR SEQ ID NO: 4793:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 130 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4793:

55

AGTTTTGAAT GTTTGTTTCAT TCAAATTAAT GGGCCTATAG CTCAGCTGGT TAGAGCGCAC 120
nCCTGATAAC 130

5 (2) INFORMATION FOR SEQ ID NO: 4794:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4794:

CACAGCCACA AGTGATTAAA GGCTTACCCA ATGATCCTGA AATGACGATA GAGTCAGTAT 60
TAACTCATTT TTCAATAGAT CAGGAAGACT ACCAAGCTTA TGTnGAAGGA CATCT 115

20 (2) INFORMATION FOR SEQ ID NO: 4795:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 224 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4795:

nTTAAAAAAA ATTCCCAATT TTTTnTGGGG GGTnGGGAAT TTAAAAATTT GGTTTTTAAC 60
CCAAAGGCCC TTTTCCCAAA AATTnTAAATT CCCTTAAAAA TTTAAAAATTT GGGAATTTTT 120
35 TTTTnGGCCC AAAATTTTTT CCCTTTTTTT AAAGGCCCCA ATTTTTTAATT TAACCCTTAA 180
AACCCCAAAA CCTTTTTTCC TTTTTTAAAA TTTTTTTAAA TGGA 224

40 (2) INFORMATION FOR SEQ ID NO: 4796:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4796:

50 TCGCGTACCG CTTTAATGGG CGAACAGCAA GACCTTGGGC ACCGACTACA GCCCCAnGAT 60
GCGATGAGCC GACATCGAGG TGCCAAACCT CCCCGTCGAT GTGAACTCTT GGGGGCAGAT 120

55 (2) INFORMATION FOR SEQ ID NO: 4797:

(A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4797:

10 AATTCGATTC CCTTAGTAGC GGCGAGCGAA ACGTGAAGAG CCCCA_nACCA ACAAGCTTGG 60
 CTGTTGTGGT TGTAGGACAC TCTATAACGG GAGTTACAAA GGACCGACAT TAGACGAATC 120
 ATCTG 125

15 (2) INFORMATION FOR SEQ ID NO: 4798:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4798:

25 CAAAATAATG ACTCCTACGG G_nCTCGAACC CGTGTTACCG CCGTGAAAGG GCGGTGTCTT 60
 AACCGCTTGA CCAAGGAGCC ATGGCTCCAC AGGTAGGACT CGAACCTACG ACC 113

30 (2) INFORMATION FOR SEQ ID NO: 4799:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4799:

40 CCGGTGGGAG GTAACCTTTT AGGAGCTAGC CGTCG_nAGGT GGGACAAATG ATTGGGGTGA 60
 AGTCGTAACA AGGTAGCCGT ATCGGAAGGT GCGGCTGGAT CACCTCCTTT CTAAGG 116

45 (2) INFORMATION FOR SEQ ID NO: 4800:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4800:

55

TCAGTGGGAT GATTCGTGAA ATTGAAACGC AAGATTTCTGA TATCGAnCAC CT 112

(2) INFORMATION FOR SEQ ID NO: 4801:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 110 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 10 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4801:

15 ATAGGATAGG CGACGTGCGA TTGGATTGCA CGTCTAAGCA nTAAGGCTGA GTATTAGGAA 60
 ATCCGGTACT CGTTAAGGCT GACTGTGATG GGGAGAAACA TTGTGTCTTC 110

(2) INFORMATION FOR SEQ ID NO: 4802:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 237 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4802:

30 GAACCAAGTT GTTATTGAAA AnTCGTTTCGT AAAGTTACGG TACGCCCACC GTGAGTGCTT 60
 TTACTTCTAT ATCAGCACCT ACTGTATCTT TCATTAAATT AACGTCTTCT GCAGTCGCAC 120
 CGCCACCTGC AAAACCTGTT GAATTTTACG AGTCCGCACC GCGCTTTGTA ATCATnCTTA 180
 35 CATTCTCTGT CACAACGCCA TACCTTCGGG ACTGACTCAC AGCTCAGCGG AACACAA 237

(2) INFORMATION FOR SEQ ID NO: 4803:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4803:

CTTGAACCCC CAACCTACTG ATTACAAGTC AGTTGCTCTA CCAATTGAGC TAAGCCGGGC 60
 50 AATATGTAAG AATAAATGGT GGAGAATTGA CGGGTTCGAA CCGCCGAnCC TCTG 114

(2) INFORMATION FOR SEQ ID NO: 4804:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4804:

GGATCAAACA GGATTAGATA CCCTGGnTAG TCCACGCCGT TAAACGCATG AGTGCTAAGT 60

10 GTTAGGGGTT TCCGCCCCCTT AGTGCTGCAG CTAACGCATT AAGCACTCCG CCT 113

(2) INFORMATION FOR SEQ ID NO: 4805:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4805:

TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTTCGC GCATCAGCGT CnGTTACAGA 60

25 CCAGGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT CTGCGCAT 108

(2) INFORMATION FOR SEQ ID NO: 4806:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 115 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4806:

TTTCAGCACT TATCCCGTCC ACACATAGTC TACCAGGCT ATGCCGTTGG CACGACAACT 60

40 GGTACACCAG AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGAnAGCTC CTCTC 115

(2) INFORMATION FOR SEQ ID NO: 4807:

(i) SEQUENCE CHARACTERISTICS:

45 (A) LENGTH: 167 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4807:

CAGCCACATA ACATAACTAA GTTAAAGATT GAACGATAAA TCGTATCTGA GTTAAACCAA 60

55 TGGTTAATAC CCGCACCCAT GATAATCATT GAACGCCTTC AGTATCGTAG GTTTGGAATT 120

(2) INFORMATION FOR SEQ ID NO: 4808:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4808:

TGCTTACATC ATTAGCTAAT TGAGCACATG TTGCCATTGC TTGCAGCTAA ATTACCTTGC 60
 ATCATTGCTA GCTTTTCTTG TATTAAGTGA TANTTACTAA TTGGTTTGCC GAATTGCT 118

(2) INFORMATION FOR SEQ ID NO: 4809:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4809:

TTGAGGTAGC CTAAAGCTAT TTCGGAGAGA CCAGCTATCT CCAGGTTTGA TTGGAATTTTC 60
 TCCnATACCT CAGTTCATCC GCTCACTTTC AACGTAAGTC GGTTCGGTCC TCATCAGTGG 120
 TACCTGACTT CAACTGACCA GGGTAGACAC 150

(2) INFORMATION FOR SEQ ID NO: 4810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4810:

AAGAAGGCCA CGATACATTA TCACCTGGTG TAACAATTAG TACGTGTATA TATCGTTCA 60
 AAACGTAAAT TCATGTTGGT GATAAGATGT GTGGTCGACA TGGTACA 107

(2) INFORMATION FOR SEQ ID NO: 4811:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4811:

AGAGTGnATT AGGTTATGAA GGTGGGCAAA ATAGGGTAAC CAGTCATTTCG AGGAAGACAC 60
 5 AGAAGAAGAC AAACCTAAAT ATGAACCAAG GTGGCATATC GTAGATATCG ATTTCCA 117

(2) INFORMATION FOR SEQ ID NO: 4812:

(i) SEQUENCE CHARACTERISTICS:
 10 (A) LENGTH: 123 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4812:

CTTTTATCCG TTGAACGATG GCCCTTCCAT GCGGAACCAC CCGATnACTA AATCCGTCTT 60
 20 TCGACCCTGC TCGACTTGTA AGTCTCGCAA TCAAGTCCCT TATGCCTTTA CACTCTATGA 120
 ATG 123

(2) INFORMATION FOR SEQ ID NO: 4813:

(i) SEQUENCE CHARACTERISTICS:
 25 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4813:

TAACCCGAGA GGGTCCCCTn GTCCAAACAG TGCTCTACCT CCAATATCAT CACTTGAGGC 60
 35 TAGCCCTAAA GCTATTTTCGG AGAGAACCAG CTATCTCCAG GTTCGA 106

(2) INFORMATION FOR SEQ ID NO: 4814:

(i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4814:

CTATTGCTTT AGATGCATAT GAATCATTGA nTGACGCGAT GCCGATGATT TCTGAACACG 60
 50 GAATCGCGAA CGTTGGCCAA CTGCCAACGA TTGGCGTGGG AATCATCCAG TG 112

(2) INFORMATION FOR SEQ ID NO: 4815:

55

(A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4815:

10 ACGTGGAGAG CATGTCCGTT CAAGCAGAGG GCGGCGGTT GAACCCGTCA TTCTGCACCA 60
 TTTATTCTTA CATATTGCCG G_nCTAGCTCA ATTGGTAGAG CAACTGACCT TGTAATCACT 120
 AGGTT 125

15 (2) INFORMATION FOR SEQ ID NO: 4816:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 20 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4816:

GTGCTGGCGC AGTTGCGATG GTTATTGCAC ATAATCCAAG CATGGCATT AATGAAGATG 60
 CTGTTGCTTA CACTGAAGAC GTTTATG_nTT TCTGGCGTCC AACT 104

30 (2) INFORMATION FOR SEQ ID NO: 4817:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4817:

40 GTCGGGTAAG TTCCGGCCCG CACGAAAGGC GTAACGATTT GGGCACTGTC TCAACG_nGAG 60
 ACTCGGTGAA ATCATAGTAC CTGTGAAGAT GCAGGTTACC CGCGGCAGGG CGGAAAG 117

45 (2) INFORMATION FOR SEQ ID NO: 4818:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4818:

55

TCGCTTACTC ATTTAGCTCT ACTAAACTCG TTGACGCTCT TTTCTCGnTT CGTCAGATTC 120

A 121

5 (2) INFORMATION FOR SEQ ID NO: 4819:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4819:

TCAGTTCGGT ATTGTGAGTC TGCAACTCGA CTGACATGAA GCTGGAATCG CTAGTAATCG 60

TAGATCAGCA TGCTACGGTG AATACGTTCC CGGGTCTTGT ACACAACGCC CGTnAAGA 118

20 (2) INFORMATION FOR SEQ ID NO: 4820:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4820:

30 CAAACAGTGC TCTACCTACA ATAATCATCA CTTGAGGCTA GCCCTAAAGC TATTTCCGAG 60

AGAACCAGCT ATCTnCAGGT TCGATTGGAA TTTCTCCGCT ACCC 104

35 (2) INFORMATION FOR SEQ ID NO: 4821:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4821:

45 TCGTAGTGGT TTCCAACCAA GTTTTTATAA GTCAAACGCT CACATACGGC TTCGTTTTCA 60

TTATTTTAAA TGCTCATTTA CATAGTnAAC TCGCTTTAAA ATAATTAAAC TCATGTCGCT 120

AACGTTTTCT TTTATAAAAG TTAAACGGTT TTATCTGTGG TGTCT 165

50 (2) INFORMATION FOR SEQ ID NO: 4822:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 113 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4822:

GAGTTTGATC CGGGCTCAGG ATGAACGCTG GCGGCGTGCC TAATACATGG CAATCGAGCG 60
10 AACGGACGAG AAGCTTGCTT CnCTGAGGTA GCGGCGGACG GGTGAGTAAC ACG 113

(2) INFORMATION FOR SEQ ID NO: 4823:

(i) SEQUENCE CHARACTERISTICS:
15 (A) LENGTH: 106 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4823:

CCGGCAACGT TCTACTCTAG CGGAACGTAA GTTGGCTACC ATCGACGCTA AGAACCTTTC 60
25 TTTGAnTTGT GACAATCGCT TGCTTCTTTC CTCTTCTTCG GCTCTC 106

(2) INFORMATION FOR SEQ ID NO: 4824:

(i) SEQUENCE CHARACTERISTICS:
30 (A) LENGTH: 108 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4824:

TAAACGGCGG CCGTAACTAT AACGGTCCTA AGGTAGCGAA ATTCCTTGTC GGGTAAGTTC 60
CGACCCGCAC GAAAGGCGTA ACGATTGGG CACTGTCTCA ACTAGAGn 108

40

(2) INFORMATION FOR SEQ ID NO: 4825:

(i) SEQUENCE CHARACTERISTICS:
45 (A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4825:

TCTAGTGACC GATAGTGAAC CAGTACCGTG AGGATAAGGT GAAAAGCACC CCGGAAGTAG 60
nTGTAATAG AACCTGAAAC CGTGTGCTTA CAAGTAGTCA GAGCCCGGTA ATGGGT 116

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 160 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4826:

ATAATATTGT AAATTAATCC ATTGATGCCA CAAGTGCCGG ACCAGAAATG ATGGTATTTA 60
 ATAATGTGCC ATCTTTATCT TTACGCCAAT CATAATTGGT AAAAATTCCC CCTTCTAATA 120
 ATCCTTGTAT TCGGTGTCAT AaAGTCTTTG CTCCTTGCAC 160

(2) INFORMATION FOR SEQ ID NO: 4827:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4827:

CGCATTGAGA CCGCAAGCTC TTTTTTTTAT GTCTAAAACG TCAAAATAAA AAGTAAACAC 60
 AAAGAAAATG GTTGCCnAG TGAAAACGTT TGAATCTGAC GAAACGAGAA AGAGC 115

(2) INFORMATION FOR SEQ ID NO: 4828:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4828:

CCAAAATAGC CTCATAATC CAAAAACAGG CTCCTTTGAC TATAGATTTT CGTTTCTGGT 60
 TCAGAAAGCT TTTGATTAACTTTAAAGTAT nCCCAATTAT AAT 103

(2) INFORMATION FOR SEQ ID NO: 4829:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 111 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

GGACCGAACT GTCTCACGAC GTTCTnAACC CATCTCGCGT ACCGCTTTAA TGGGCGAACA 60
GCCAACCCTT GGGACCGACT ACAGCCCCAT GATGCGATGA GCCGACATCG A 111

5 (2) INFORMATION FOR SEQ ID NO: 4830:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 105 base pairs
 (B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4830:

15 GTTGTGTGGGG CCCCGCCGGC AAGGTTGACT AGAATTGAGA AAAGCTTGTT ACAACGCTAT 60
TTTCGTTTCTAG TCAACnACTG CCAATATAAC TTTGTAGAGC ATTGA 105

20 (2) INFORMATION FOR SEQ ID NO: 4831:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4831:

30 ACATTGAGTC TTCGAGTCGT TGCATTTTAC ACTGCCGnGA AAAGCCTCTA GATAGAAAAT 60
AGGTGCCCCGT ACCGCAAACC GACACAGGTA GTCAAGATGA GA 102

35 (2) INFORMATION FOR SEQ ID NO: 4832:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4832:

45 TTnTAGAATG AACCGGCGAG TTACGATTG ATGCAAGGTT AAGCAGTAAA TGTGGAGCCG 60
TAGCGATAAG GAGGTCTGAA TAGGGCGTTT AGTATTTGGT CGTAGCC 107

50 (2) INFORMATION FOR SEQ ID NO: 4833:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 base pairs
 (B) TYPE: nucleic acid
55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4833:

5 TGCAACTAAT GAAAAGTAGA GTTCCGGGGA GTTAAAACCA GTGACTGTTG ACCTTGTTGT 60
 CTCCATTGGA ATGTACTACC TGATGCAAGA TAATTATCAT CACTTTGTTG ACGTGCTTnA 120
 TTTTCAGCAT CAATTTGATC AATC 144

10 (2) INFORMATION FOR SEQ ID NO: 4834:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4834:

20 GGCTCAGATG nACGCTGGCG GCGTGCCTAA TACATGCAAG TCGAGCGAAC GGCACCAGAA 60
 GCTTGCTTCT CTGGATGTTA GCGGCGGACG GGTGTAGTAA CACGTGGG 108

25 (2) INFORMATION FOR SEQ ID NO: 4835:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4835:

35 GACAATGGTA GGnGAGCGTT CTAAGGGCGT TGAAGCATGA TCGTAAGGAC ATGTGGAGCG 60
 CTTAGAAGTG AGAATGCCGG TGTGAGTAGC GAAAGACGCA GT 102

40 (2) INFORMATION FOR SEQ ID NO: 4836:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 109 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4836:

50 TTGCAGACTA CAATCCGGAA CTGGAGTAAC AACTTTATGG GATTTGnCTT GACCTCGCGG 60
 TTTGCTGGC CCTTTGGTAT TGTCCATTGT AGCACGTGTG TAGCCCAA 109

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 103 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4837:

CTCCACGTAA GCTAGCGCTC ACGTTTCAAA GGCTCCTACC TATCCTGGTA CAAGCTGTGC 60
 CGGAATTTCA ATTTGCAnGC TACAGTAAAG CTCCACGGGG GTC 103

(2) INFORMATION FOR SEQ ID NO: 4838:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 121 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4838:

TCAAACACTC nCATACTGCT TTATTTTCAT AAACAATATC ACTTTAACCA AAAAATATTT 60
 GAATGTTAAA TAAACATTCA AAAGTGAATA CAATATGTCA CGTTATTCCA CATCTTCTGG 120
 A 121

(2) INFORMATION FOR SEQ ID NO: 4839:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4839:

AAACCATGAA TTAAGAATCC AGAAACAGGA GATGTAGTTA GACCACCGGT CGATTAGCGT 60
 ACCAAAATAT GGACCTGTAA AAGGAGACTC GATTGTAGAn AAAG 104

(2) INFORMATION FOR SEQ ID NO: 4840:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

CCGTGGAGTT TATGTAGCCT GATATTGAAT TCGGCACAGT TGTACAGGTA GGTAGGAGCC 60
 TTGAAACGTG ACGCTATTA GTGnAGGCGT GGTGGGTACT ACCCTAGCTG TGTGGGCTTT 120
 CTAACCC 127

(2) INFORMATION FOR SEQ ID NO: 4841:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4841:

CATCCCACCC CGGGCAAGGT TGACTAGAAT TGGAAAAAAA CTTGGTTACA ACGTTATTTT 60
 CATTCAGTCA ACTACTGCCA ATATAATATT GnAAACTATA GGACATTTAT TAGTGTTTCA 120
 GTTCT 125

(2) INFORMATION FOR SEQ ID NO: 4842:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4842:

TGGTACGGCA TCTCACCCGT CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAnGCGCTC 60
 CACATGATCC TTACGATCAT GACTTCAACG CCCTTAGAAC GCTCGTCC 108

(2) INFORMATION FOR SEQ ID NO: 4843:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4843:

TAATGAAGGT CTTCCGATCG TAAACTCTG TTATTAAGnA GGAACATGTG TGTAAGTAGC 60
 TGTGCACATC TTGACGGTAC CTAATCAGAA AGCCACGGCT AACTACGT 108

(2) INFORMATION FOR SEQ ID NO: 4844:

(A) LENGTH: 117 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4844:

10 CGGTCTCAAT GCGGCTCATC GCATCCATTT TTTGACCTGG GCAACGTTCT ACTCTAGCGG 60
 AACCTAAGTT GGGCTACCAT CGACGnCTAA GAACCTTTCT TGACTTGTGT ACAATCG 117

(2) INFORMATION FOR SEQ ID NO: 4845:

15

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4845:

25 GACTGTTTAT CAAAACACA GGTCTCTGCT AAACCGTAAG TGATGTATAG GGGGCTGACG 60
 CCTGnCCGGG TTCTGGTAAG GTTAAGAGGA GTGGTTAGCT TCTGCGAA 108

(2) INFORMATION FOR SEQ ID NO: 4846:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 118 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4846:

40 CAATATTTGA AGCGATTGGC TTGTCTCATG ATGTGATTGA TCGTTATTTT ACTGGGACAC 60
 AGTCTAAGTT ATCTGGTATT TCGATTGATC AAATThTGCC TGAAAAAGAC GCACAAGT 118

(2) INFORMATION FOR SEQ ID NO: 4847:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4847:

55 GATCCCCGGA CGGAGTGCTT AATGCGTTAC TGACAGCACT AAGGGGCGGA AACCCCCTAA 60

(2) INFORMATION FOR SEQ ID NO: 4848:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4848:

CTGGCGATTG TGCTCTGTAA CGTGCTTTCC AATTTGGAAC GCACGTGnCC CTGCCCATAC 60
 CTACGGGACT TGACTTATAT TGTTTGGCTT TGTACGTCAT TTCAACAATA GACGCCCATG 120
 CCAGCAACGC GATTACC 137

(2) INFORMATION FOR SEQ ID NO: 4849:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4849:

GTTTAGGCTC ATCTTAAGAT GTTAGGTCCA CTCGGTTTAC ACCATATTTT TTA CTTACCG 60
 TTTTGGCAGA CGGCACTTGG TGGTACTTTA GAAGTCAAAG ACAnGGGGGG GGGGGG 116

(2) INFORMATION FOR SEQ ID NO: 4850:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 125 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4850:

TCCTTTCGTG ACGGGCTCGG TAACTTACCC GACAAGGTAA TTTCGCTACC TTAGGnACCG 60
 TTATAGTTAC GGTCCGCCGT TTA CTTGGGGC TTCGATTCGT ATCTTCGCAG CTATATCTCA 120
 CTCCT 125

(2) INFORMATION FOR SEQ ID NO: 4851:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4851:

5 AAGTTGTATT TTAAAAATAG TTCTTTAAAT TATATACCCA CCACATTGG TGGGAGAACC 60
TAAAAAAAG CACTTTCCCC AAAAATGGGA AAGTGC 96

(2) INFORMATION FOR SEQ ID NO: 4852:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4852:

ACCGTGTGCT TACAAGTAGT CAGAGCCCGT TAATGGGTGA TGGCGTGCCT TTTGTAGNAT 60
20 GAACCGGCCGA GTTCACGATT TAGATGCAAG GTTGAAGCAG 100

(2) INFORMATION FOR SEQ ID NO: 4853:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4853:

CCGACAGCGT AGnCGATGGA TAACAGGTTG ATATTCCTGG TACCACCTAT AATCGTTTTA 60
35 ATCGATGGGG GACCCATAGG ATAGCGAACC TGCGATTGGA T 101

(2) INFORMATION FOR SEQ ID NO: 4854:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 102 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4854:

GGACATCTCC TAAGGCTAAA TACTCTCTAG TGACCGTAGT GAACCAGACC GTGAGGAAAG 60
50 GTGAAAnACC CCGGAGGGGA GTGAATAGAC CTGAAACCGT GT 102

(2) INFORMATION FOR SEQ ID NO: 4855:

55

(A) LENGTH: 104 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4855:

10 ATAACCGCAA TTGGCGAAAT CTCATCTTGA GGGGGGCTTC ATGCTTAGAT GCTTTCAGCA 60
 CTTATCCCGT CCACACATAn CTACCCAGCT ATGCCGTTGG CACG 104

(2) INFORMATION FOR SEQ ID NO: 4856:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 138 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4856:

CTACTGTCTT CATTCTTTCA GTTCTTTTTT ACGGGTCTGT TTTCTAATTT GAGCACATCT 60
 25 TCGATTCTTT ATCAAATGAC TACCAATTAA ATCTATTCTT CTnTGGTAAA TCGCTAACTC 120
 CATCTCCTTA ACCCGGTA 138

(2) INFORMATION FOR SEQ ID NO: 4857:

30

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 100 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4857:

40 TCAAACGnTT GTCATCTATT AAAGAAGTAG GTCTAGATAT ATCACGTACG TAATGTGTAA 60
 TGGATGGCGC TATTGCTTTA GGTCAATCCAT TAGGTGCTAC 100

(2) INFORMATION FOR SEQ ID NO: 4858:

45

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 106 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4858:

55

CCTGTGTGTT TGATAAACAG TCGGTTGGGC CTATTCCTG CGGCTT

106

(2) INFORMATION FOR SEQ ID NO: 4859:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4859:

15

GTAACGCGCC GGTTCATTCT ACAAAGGGC ACGCCAATCA CCCATTACG GGCTCCTGAA

60

CTACTTGTTA AGCAACACGG TTTCCAGGGT TCTATTTCCTA CTTCCCCTTT CCGGGGTnGC

120

TTTTTCAACC TTTTTCCTCC TCCACGGTTA CT

152

20

(2) INFORMATION FOR SEQ ID NO: 4860:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4860:

30

GCCCGTACCG CAAACCGACA CAGGTAGTCA AGATGAnGAA TTCTAAGGTG AGCGAGCGAA

60

CTCTCGTTAA GGAACGCGC AACTGACCC CGTCACTTCG

100

(2) INFORMATION FOR SEQ ID NO: 4861:

35

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 104 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4861:

45

CAGGTAACAC TGAATGGAGG ACCGAACCGA CTTACGTTAA AAAGTAAGCG GATGAACTAA

60

AGGTAGCnGA GAAATTCCAA TCGAACCTGG AGATAGCTGG TTCT

104

(2) INFORMATION FOR SEQ ID NO: 4862:

50

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 87 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4862:

5 TTACTTATCT AGTTTTCAAT GTACAAATAA TGGTGGAGAC TAGCGGGATC GAACCGCTGA 60
CCTCCTGCGT GCAAAGCAGG CGCTCTG 87

(2) INFORMATION FOR SEQ ID NO: 4863:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4863:

ACCGTTTGAT TTCTTATCTA ATTCAAGCTT ATTTAAACT CTTTATTCAC TCGGTTTTGG 60
20 CTTGGTAAAA TCTATATTTT ACTTACTTAT CTAnTTTTCA ATGTA 105

(2) INFORMATION FOR SEQ ID NO: 4864:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 129 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4864:

AGGGAATCGA ATTTTCCTTC TCTTCCTCCG GGGTACTAAG ATGTTTCAGT TCTCCGGGTG 60
35 TGCCTTGCTG GATGATGCTA TGATATTGCA CATATCGAAT CAACAGTGGT GCATGAACCT 120
GCAnTGGCT 129

(2) INFORMATION FOR SEQ ID NO: 4865:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4865:

50 AAACCGCAAG GTCAAGCAAA TCCCATAAAG TTGTTCTCAG TTCGGATTGT AGTCTGCAAC 60
TCGACTACnT GAAGCTGGAA ATCGCTATAA ATCGTAGATC 100

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4866:

GTGATAAGAT TAGCAGAAAA TGGATGGTGT TAAGAGAGTT AATTGGTTTG GnGGTATGCT 60
 TATTTTAAAT GGCATTGTGT ACGAGAGCAT TAGAGTTTGT ACTTGTGAGG TTATT 115

(2) INFORMATION FOR SEQ ID NO: 4867:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 90 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4867:

ACACCACTCC TCATTAACCT TCCAGCACCG CAGCAGGCGT CACCCCTATA CATCACCTTA 60
 CGGTTTAGCA GAGACCTGTG TTTTGTGATAA 90

(2) INFORMATION FOR SEQ ID NO: 4868:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 87 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4868:

CACGAACGAT TGTCTTTCGT GCGGGGATTA TCTGACACGG TACCGGTCAA ACAGTGAATC 60
 GCTACTGCTC ATCAGGGATT ACAAACC 87

(2) INFORMATION FOR SEQ ID NO: 4869:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 165 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4869:

CGCTCACCTT AGAATCTATT TACTACTGGTG TTGGTAGGCA CTTTTTTCAA GCTTCCGATT 120
AACACATGAA AAGCTTCCAA AGTACTAGGA CGTTCAATAC ATGTA 165

5 (2) INFORMATION FOR SEQ ID NO: 4870:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 111 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4870:

15 AATATCATTT ATAACATTAA GTAATAACTT TTTTATCTT GTCCATTTTA TTTTThAACC 60
AAAATTTGAT TAAAAAACTG CCTGGCAACG TTCTACTCTA GCGGAACTAA G 111

20 (2) INFORMATION FOR SEQ ID NO: 4871:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
25 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4871:

30 TAGCAGAGAC CTGTGTTTTT TGATAAACAG TCGCTTGGGC CTATTCCTG CGGCTCTTCT 60
GGGCGTTAAC CCTAAAGAGC ACCC 84

35 (2) INFORMATION FOR SEQ ID NO: 4872:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
40 (C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4872:

45 ACAGTAAAGC TCCACGGGTC TTTCCGTCCT GTCGCGGGTA ACTGCATCTT CACAGGTACT 60
ATGATTTTAC CGATCTCTCh ATGAACAGTG CCAAATCGTA C 101

50 (2) INFORMATION FOR SEQ ID NO: 4873:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4873:

5 GACAGGCGTA GCGATGGAT AACAGGTTGT ATTCCTGTAC CACCTATGAT CGTTTAAATC 60
GATGGGGGGA AGCATAGGAT AGGCGAA 87

(2) INFORMATION FOR SEQ ID NO: 4874:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4874:

20 GGGAGAGCGC CTGCTTTGCA CGCAGGAGGT CAGCGGTCG ATCCCGCTAG TCTCCACCAT 60
TATTTGTACA TTGAAACTA G 81

(2) INFORMATION FOR SEQ ID NO: 4875:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4875:

30 TATGTTTCGA AATATCTTTA TCACTCTAAA ATGATATACA AGAAATCCAA GAAAAATAAG 60
35 CGAACTGAAT AAATAAGAT T 81

(2) INFORMATION FOR SEQ ID NO: 4876:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 87 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4876:

AACGCGTTAA ATCTTTTAT AAAAGACGTA ACTTCATGTT AACGTTGCTT ATAAAAATGG 60
50 TGGAACATAG ATTAAGTTAT TAAGGGC 87

(2) INFORMATION FOR SEQ ID NO: 4877:

55

(A) LENGTH: 101 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4877:

10 ACAACGGATA AAAGCTACCC CGGGGATAAC AGGCTTATCT CCCCCAAGAG TTCACATCGA 60
CGGGGAGGTT TGnCTCAAT GTGGCTCATC GGATCTTGGG G 101

(2) INFORMATION FOR SEQ ID NO: 4878:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 79 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4878:

25 ATTATTAGG TGTACAAATG ACCACCGCAT CAACAAGTTT AACAGCTCG CTAGGTGTCT 60
CAACTGCATG AGGTATATT 79

(2) INFORMATION FOR SEQ ID NO: 4879:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4879:

40 ACATCGTTTC AATGGGTCGC TAACGCTGCT AGGACATTAT AACAGACGTG TACAAAAAGA 60
AAATTGGTAT GGTAATTGTG GCA 83

(2) INFORMATION FOR SEQ ID NO: 4880:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 84 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4880:

55 CTTTCATCTG ATCCAGATCA AACTCTCCAT AAAAATTATG ATGTTTGATT AGCTCATAAA 60

(2) INFORMATION FOR SEQ ID NO: 4881:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4881:

TTGTGCAGTT GCATCGCCAT TGATCAATAA CACGTTGAGC TGCAGTTATT TCAGTTTCTG 60
 CTTACAGCTT CTTTCGATTA 80

(2) INFORMATION FOR SEQ ID NO: 4882:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4882:

TCTGATGTGA AAGCCCACGG CTCAACCGTG GAGGGTCATT GGAAACTGGA AAACCTTGAGT 60
 GCAGAAGAGG AAAGTGGGTT CCATGT 86

(2) INFORMATION FOR SEQ ID NO: 4883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4883:

TGATCGCATA TCTACGCAAC ATCGGCATAA GTnTGATGAC AAACAAGCTT CCATGACAAA 60
 AGTAATGGAC GAATATCGCA TTTGGGGAAA GTCCTCTAAA AATGCCTTTT GAAGGAACGT 120
 CGGTAA 127

(2) INFORMATION FOR SEQ ID NO: 4884:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4884:

AGTAGGAATC GAACCCACAC CAAAGTTTGT GAGACCTCTA TTCTACCTTG AACTATGCCC 60
 CTATTAAAAA TAATAAAT 78

(2) INFORMATION FOR SEQ ID NO: 4885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4885:

CTCACTATTC GAGTGACACT GCGCCGAAAA TGTACCGGGG CTAAACATAT TACCGAAGCT 60
 GTGGATTGTC CTTTGGAAT GGGT 84

(2) INFORMATION FOR SEQ ID NO: 4886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4886:

GGTATCTGTT CACTCTCCG GTGGTGCAGT TGCGACCAAC AATGGGTTGG AGATTGGATT 60
 TCATCCTTCT CAATTAATCG TTCCGTACT TTCAANTGG TACCCCATCC AAAAGGG 117

(2) INFORMATION FOR SEQ ID NO: 4887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4887:

CGGATCTGGG AGGAAATCTC CTAAGGCTAA ATACTCTCTA GTGACCGATA GTGAACCACT 60
 ACCGTGAGGA AAGGTGAAAA 80

(2) INFORMATION FOR SEQ ID NO: 4888:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4888:

AATATGCAAG CACATGGTGA ATATGACGAG GTTGCAACTT CAACGGCGAA GATGATGGAA 60

10

GGCCTTACGT TTGCGTG 77

(2) INFORMATION FOR SEQ ID NO: 4889:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4889:

TCTTCTGGGC GTTAACCCTA AAGAGCACCC CTTCTCCCGA GTTACGGGGT CTTTGGCCGA 60

25

GTTTCCTTAAC GAGAGT 76

(2) INFORMATION FOR SEQ ID NO: 4890:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4890:

GTGGGGGCCC CAACATAGGA GCTGATTTTC TGTGAGCTTA CCATnATGTG GCAAGTTGGC 60

40

GGGGGCCCCC AAACCAAGGA GCTGGCTTTC TGTCACTTTA CCATTAATGT GGCAAGT 117

(2) INFORMATION FOR SEQ ID NO: 4891:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 109 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4891:

TTAATCCnCC TGCATATGAT GACTTTGTTG AACCGTCATT GCATACTTTC AACATGAATA 60

CGCTGAACAC CTTCACTTAC TGCATATCTT AGTTCCTCGG TCTGTCTTA 109

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4892:

CTCTTAACCT TGCAGCACCG GGCAGGCGTC AGCCCGTATA CATCACCTTA CGGTTTGCAG 60
 AGACCGTGTG TTTTGTAGAA ACAGGTGC 88

(2) INFORMATION FOR SEQ ID NO: 4893:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 102 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4893:

TAGCGAATGA GATAAACGCG GCGGACTGTA AATCCGCTCC TTCGGGTTCG GCAGTTCGAA 60
 TCTGCCCCCC TCCATTTATT ATTTTnAAAA AAAGCATAGT TC 102

(2) INFORMATION FOR SEQ ID NO: 4894:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4894:

CGAGCGATTG CCACTCAGAC AATGACTCGG AATTCAGATA ACGAATCTGA CTCAGACAGT 60
 GACTCAGATT CCGACAGT 78

(2) INFORMATION FOR SEQ ID NO: 4895:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 141 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4895:

TTAGTATTTCG CACTCACATG TCACATGCTT CACTCGACCT ATTACCTCAC ACTTGGGGAC 120
TTATACCGAG TnGGAATCTC A 141

5 (2) INFORMATION FOR SEQ ID NO: 4896:

- 10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4896:

GTTCGGATTT AATTGATTC ATTTGTTGCG TAATTTTCAGA AGCCATTTTA TGAAAAGAGT 60
GATTTAATTC ATAAATTTCT 80

20 (2) INFORMATION FOR SEQ ID NO: 4897:

- 25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4897:

30 GGTATGGCTG GCGCTTTACG TGCCACATTA GATTATGTCA CTGAGCGTAA GAAGTTCGGC 60
AAACCAATTA GTA 73

35 (2) INFORMATION FOR SEQ ID NO: 4898:

- 40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4898:

45 GTGCCGAGGA CCGGAATCGA ACCGGTACGG TGATCACTCA CCGCAGGATT TTAAGTCCTG 60
TGCGTCTGCC A 71

(2) INFORMATION FOR SEQ ID NO: 4899:

- 50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 116 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
- 55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4899:

AGCCGCTGGA TTCCACGGTG TAAGCAGTAA GGCTGAGTAT TAGGCAAATC CGGTACTCGT 60

TAAGGCTGGA GCTGTnGATG GGGAGAAGAC ATGTGTGCTT ACGTAGTGCG TGGTTT 116

(2) INFORMATION FOR SEQ ID NO: 4900:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4900:

TTCCGGCCCC TGGCGGTnTC CTAGGAGTTC CACGGAACCC CAGGATTTTG TAGGACCCCC 60

CGGGCAGAGT CCCCTTCGAC TAAGAAAATC TCACATTCTT CAGGGACTTT TAC 113

(2) INFORMATION FOR SEQ ID NO: 4901:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4901:

ACTTAATGGA TTGATTAAGT AGTGGGTTCT TAACATTAGG CCTCAGCTAA TGTGGTACTT 60

AAAAATAGGG AATACATG 78

(2) INFORMATION FOR SEQ ID NO: 4902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4902:

ATGGGACATG GTGTGCCTCC TTGCTATAGT CACCAGACAT ATGAATGTAA TTTATACATT 60

CAAAACTAGA TAGTAAGTAA AAGT 84

(2) INFORMATION FOR SEQ ID NO: 4903:

- (A) LENGTH: 70 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4903:

10 TTGTCGGGTA AGTTCGACC CGCACGAAAG GCGTAACGAT TTTGGCACTG TCTCAACGAG 60
 AGACTCGGTG 70

(2) INFORMATION FOR SEQ ID NO: 4904:

- 15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4904:

25 TAAGTTGGCT ACCATCGACG CTAAGAACCT TTCTTGACTT GTGACAATCG CTTGCTTCTT 60
 TCCTCTTCTT GGCTCTGCTT CTATTTGCCT CTAATGTGGC TTTTGTGT AATAAGTTAT 120
 GCGCTTCGGT GTTATnGTGA AAAAGCGGTC A 151

(2) INFORMATION FOR SEQ ID NO: 4905:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4905:

40 TGA CT TGTAG GCGCTGGTGG GATACTACCC TAGCTGTGTT GGCTTTCTAA CCCGCACCAC 60
 TTATCGTGGT GGGGA 75

(2) INFORMATION FOR SEQ ID NO: 4906:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 112 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4906:

55

ACTCAGACAG TGA CTCAGAT CAGATAGTg CTCGGATTCA GCGATTATTC AG

112

(2) INFORMATION FOR SEQ ID NO: 4907:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4907:

15

GTAAAAACAC CCCAGCCAGG TCACTTTACG CCTACGCATC GCTTGACAC GTGCTACTAA

60

AGGTTTACCA

70

(2) INFORMATION FOR SEQ ID NO: 4908:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4908:

30

AGAAGATACA AATAAAGnTA AACCCAAATT ATTCAATTC GGTGGGACAC AATAGTGTG

60

ACTTTGAAGA AGATACACTT TCCCACCAAG TTAAGTGGGT CCATAATTGA AGGGTCCAAC

120

C

121

35

(2) INFORMATION FOR SEQ ID NO: 4909:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 70 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4909:

45

GGGAACAAAG TGGACAGGTG GTGCATGGTT GTCGTCAACT CGTGTCGTGA GATGTTGGGG

60

TTAAGTCCCG

70

50

(2) INFORMATION FOR SEQ ID NO: 4910:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4910:

5 GGACACCCGG AGAACTGAAA CATTTAGTAC CCGGAGAAGA GAAGAAATTC GTTCCCTTAG 60
TAGCGGGACG AACGGGAGAG CCCAAACCAC AGCTTGTGnG 100

(2) INFORMATION FOR SEQ ID NO: 4911:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 155 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4911:

nTCTGTGTTT GGCATGGGAA CAGGTGTGAC CTCCTTGCTA TAGTCACCAG ACAAATAAC 60
20 TTACTTATTC ATGATACACG CTTAATTAAT AAGGTGCAAT AGTTAATTTT ACACTTTGAT 120
GTAAACTTTG GCACATCAGC TTTTAGTGTG TTTCG 155

(2) INFORMATION FOR SEQ ID NO: 4912:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4912:

35 CCCGTCACAC CACGAGATTT GTAACACCCG AAAGCCGGTG GAGTGAACCT TTTAGGAGCT 60
AGCCGTCGA 69

(2) INFORMATION FOR SEQ ID NO: 4913:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
45 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4913:

50 TATGCTCTCC CAGCTGAGCT AATTCTCCGA TTAAAACTG CCTGGCAACG TTCTACTCTA 60
GCGGAACGT 69

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4914:

CAAATGCTTC TGTC AATTCG ATCAAATCAA TGTCTTCAAC AGATAGATTG CTGAGTGACA 60
 ATACTTCAT 69

(2) INFORMATION FOR SEQ ID NO: 4915:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4915:

TATTTCCGGAG AGAACCAGCT ATTTCCAGGC TCGATTGGAA TTTCTCCGGT ACCCTCAGTT 60
 CATCCGCTCA 70

(2) INFORMATION FOR SEQ ID NO: 4916:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4916:

TCACCCATTA ACGGGCTCTA ACTACTTGTA AGCACACGGT TTCAGGTTCT ATTTCACTCC 60
 CCTTCCG 67

(2) INFORMATION FOR SEQ ID NO: 4917:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4917:

TCCACCGTTG ACTAAGGTTT CAGAGAGGCT CGTCCCTCTG GGTAGTCGGG CCTAAGCTGA 120
 GGCGCACGTA GGCGATGATA CAGGTTATAT CCTnACACCT A 161

5 (2) INFORMATION FOR SEQ ID NO: 4918:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4918:

GCACGTAGTT AGCCGTTGGC TTTCTGATTA GGTACCGGCA AGATGTGCAC AGTTACTTAC 60
 ACATATGT 68

20 (2) INFORMATION FOR SEQ ID NO: 4919:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 78 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4919:

GAAAGCAAAT GTCTTCGTTG CAATTCGATC AAATCAATGT CTTCAACAGA TAGATTGCTG 60
 AGTGACAATA CTTCAGGG 78

35 (2) INFORMATION FOR SEQ ID NO: 4920:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4920:

AATTTTCGCTA CCTTAGGGAC CGTTATAGTT ACGGCCGACG TTTACTGGGG CTTCGATTTC 60
 TACTTCGC 68

50 (2) INFORMATION FOR SEQ ID NO: 4921:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 67 base pairs
 (B) TYPE: nucleic acid
 55 (C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4921:

5 AATCATAGTA CCTGTAAAGA TGCAGGTTAC CCGCAACAAG ACGGAAAGAC CCCGTGGAGC 60
TTTACTG 67

(2) INFORMATION FOR SEQ ID NO: 4922:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4922:

GGGAGCTGTA ATAAGCTTTG ATCCAGAGAT TTCCGAATGG GGAAACCCAG CATGAGTTAT 60
20 GTCATG 66

(2) INFORMATION FOR SEQ ID NO: 4923:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4923:

GTGGAGGCGC TGGTGGGATA CTACCCTAGC TGTGTTGGCT TTCTAACCCG CAACCACTTA 60
35 TCGTGGGTGG GAG 73

(2) INFORMATION FOR SEQ ID NO: 4924:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 89 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4924:

GAGGTCAGCG GTTCGATCCC GCTAGTCTCA CCATTTATTT TTTACACGAT GACATGAAAC 60
50 TGATGACATA TGCACCGTAA TTCCAAAAA 89

(2) INFORMATION FOR SEQ ID NO: 4925:

55

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4925:

10 AATGGCATCG GAGTTGTCTG AATTCGGTAA CCCGAGAGGC CCCTCGTCCA AACAGGCTCT 60
ACCTCCAA 68

(2) INFORMATION FOR SEQ ID NO: 4926:

- 15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4926:

25 ACGAAAGGCG TAACGATTG GGCACGATC TCGACGAGAG ACTCGTGAAA ATCATAGATA 60
CCTGTGAAGA TGC 73

(2) INFORMATION FOR SEQ ID NO: 4927:

- 30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4927:

40 ATTTCTATTA ATTATTTGCA TAGAAATCAG CTTTTTTGAT ATGTATTTTA TAATGTACAG 60
CTCGTTGAG 69

(2) INFORMATION FOR SEQ ID NO: 4928:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4928:

55 AGGTATGTCC ATCCCGGTCC TCTCGTACTA AGGACATCTC CTCTCAAATT TCCTACGCCC 60

(2) INFORMATION FOR SEQ ID NO: 4929:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 83 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4929:

GGCGGGGCCC CAACACAGAG GCTGGCGGAA AGTGCAGCTT ACAATAGTGT GCAAGTTGGG 60
GTGGGTCCCG ACACAGAGAA ATT 83

(2) INFORMATION FOR SEQ ID NO: 4930:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4930:

CTTGGTAGAG CACTTGTTT GGGACCAAGG GGTGCAGTT CGAATCCTGT CTTCCCGATT 60
ACTCTA 66

(2) INFORMATION FOR SEQ ID NO: 4931:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4931:

AAGAAGCTTG TTATGCTGCA ACACCAGCAA TTCAAGTAGC TAAAGATTAT TTAGCAACTA 60
GACCG 65

(2) INFORMATION FOR SEQ ID NO: 4932:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 TGCAGAAGAG GAAAGTGGAA TTCCATGTGT AGGGTGAAAT GCGCATAGAT ATGGCAGGAA 60
CACCAGTGGG CGA 73

(2) INFORMATION FOR SEQ ID NO: 4933:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4933:

TCGCTATCCG AGTCTGGGTC GCTATCTGAG TCTGAGTCGC TATCTGAGTC TGAAATCGCT 60
GTCTG 65

(2) INFORMATION FOR SEQ ID NO: 4934:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 120 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4934:

GAGCATGTGG GTTTAATTCG AAGCAACGCA GAGAACCTTG ACCAAATCTT GGACATCCnT 60
TGACAACTCT GAGAGATTAG AGCCTTGCCC CTTGCGGGGT AACAAATGTA CAGGTTGGTG 120

(2) INFORMATION FOR SEQ ID NO: 4935:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 72 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4935:

GAAGGCTCGT CCGCTCTGGG TTAGTCGGGT CCTAAGCTGA GGCCGAGCAG GTACGGCGAT 60
GGATAACGGT TG 72

(2) INFORMATION FOR SEQ ID NO: 4936:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4936:

5 CACATCAGCG TCAGTTACAT ACCAGAAAGT CGCCTTCGCC ACTGGTGTTC CTCCATATCT 60
CTGC 64

(2) INFORMATION FOR SEQ ID NO: 4937:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4937:

ATCACCTGGT GTAAACCAAT TAGTACGTGT ATATATCGTT CAAAACCGTA AAATTCATGT 60
20 TGGT 64

(2) INFORMATION FOR SEQ ID NO: 4938:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4938:

CTGGGTAGCT ATGTGTGGAC GGGATAAGTG CTGAAACATC TAAGCATGAA GCCCCCTCAA 60
35 GAT 63

(2) INFORMATION FOR SEQ ID NO: 4939:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4939:

TAGAAATCAG CTTTTTTGCA TATGTATTTT ATAATGTACA GCTCGTTGAG CTGCTATTTT 60
CCT 63

50 (2) INFORMATION FOR SEQ ID NO: 4940:

55

- (A) LENGTH: 68 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4940:

GGTAGTCGAA CTTACGTTCC GCTAGAGTAG AACTTGCCAG CAAATGACAA ATCGGAGAAT 60
 TAGCTCAG 68

(2) INFORMATION FOR SEQ ID NO: 4941:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4941:

CTGAAACATC TTAGTACCCG GAGAAGAGAA AGAAAATTCG ATTCCCTTAG TAGCGGCGAG 60
 CG 62

(2) INFORMATION FOR SEQ ID NO: 4942:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4942:

TTACAACAAT GCAATTGGCG GGGCCCAACA TAGAACTGGC AATAGTTACT TTCAATAATG 60
 TGCAAGTTGG GGTAGGGCCC AACACAGAA 89

(2) INFORMATION FOR SEQ ID NO: 4943:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4943:

AATGGACAAT ATGTCAACGT TAATTCCAAA AAACGGTAAC TATAATTTAC AAACATTATT 60

55

(2) INFORMATION FOR SEQ ID NO: 4944:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4944:

CCCGTGAAAG ATGATGAGGT TAATAGGTTT GAGGTGGAAG CATGGTGACA TGTGGAGCGT 60
GACGAATACG TAATTGA 77

(2) INFORMATION FOR SEQ ID NO: 4945:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4945:

GAATAGGTCG ATGTATTTGG CGACCGAAAC CAGGAATCTA CCCTTGGTCA GGTGAAGTT 60
CAGGTAACAC TGAAT 75

(2) INFORMATION FOR SEQ ID NO: 4946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4946:

ATCAGAAGGC ACACCCGAGA ATGAAACATC TAGTACCCGG AGAAGAGAAA GAAATTCGAT 60
TCCCTATAGC GGCGnCGAAA CGGAAGAGCC AACCACAGCT GCTTTGGTTT GACCCATCGG 120
TACAGCGCTG AACT 135

(2) INFORMATION FOR SEQ ID NO: 4947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4947:

GATTTGGGCT CTTCCATTTC GCTCGCCGCT ACTAAGGGAA TCGAATTTC TTTCTCTTCC 60
5 T 61

(2) INFORMATION FOR SEQ ID NO: 4948:

(i) SEQUENCE CHARACTERISTICS:
10 (A) LENGTH: 70 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4948:

GCTTTTGAGG AATTTAATAT CAATATATAT TCTGTGTATG AAAATATTTT TCATAAAAAT 60
20 TGTTTGAATC 70

(2) INFORMATION FOR SEQ ID NO: 4949:

(i) SEQUENCE CHARACTERISTICS:
25 (A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4949:

CTTCGACCTG ACCAAGGGTA GATCACCTGG TTTCGGGTCT ACGACCAAGT ACTAAACGCC 60
35 CTATTC 66

(2) INFORMATION FOR SEQ ID NO: 4950:

(i) SEQUENCE CHARACTERISTICS:
40 (A) LENGTH: 78 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4950:

GGGTGTTACA AAATATCGTG GTGTGACGGG GCGGTGTGTA CAAGACCCCG GGTACGTTTT 60
50 TCACCGTAGG CATGCTGG 78

(2) INFORMATION FOR SEQ ID NO: 4951:

(i) SEQUENCE CHARACTERISTICS:
55 (A) LENGTH: 61 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4951:

CCGCGATAAT AAAAAATAAT GCGGAGGAA GAGGGATTCTG AACCCCGTG GCCCGTTAAG 60

10

G 61

(2) INFORMATION FOR SEQ ID NO: 4952:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4952:

ACTTATCTAG TTTTCAATGT ACAATGTCTT TTTAGTCAGC GCTCGCATAA GCAATATCAC 60

25

TGTAACCA 68

(2) INFORMATION FOR SEQ ID NO: 4953:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4953:

ACTGACGCTG ATGTGCGAAA GCGTGGGGAT CAAACAGGAT TAGATACCCT GGTAGTCCA 59

40

(2) INFORMATION FOR SEQ ID NO: 4954:

(i) SEQUENCE CHARACTERISTICS:

45

(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4954:

50

CGTGAGCGCT AGCTGTACGT GGAGGCGCTG GTGGGATACT ACCCTAGCTG TGTTGGCTTT 60

(2) INFORMATION FOR SEQ ID NO: 4955:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 59 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4955:

AAGGCGTAAC GATTGGGCA CTGTCTCAAC GAGAGACTCG GTGAAATCAT AGTACCTGT 59

10

(2) INFORMATION FOR SEQ ID NO: 4956:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4956:

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AATAGGTGCC CGTACCGCAA ACCGACACAG GTAGTCAAGA TGAGAATTCT AAGGTGAGC 59

(2) INFORMATION FOR SEQ ID NO: 4957:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 77 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4957:

ACACGTTTAG TTCACGCGGG TTTGCTTGG TAAAATCTAT ATTTTACTTA CTTATCTAGT 60

35

TTTCAATGTA CAATTTTC 77

(2) INFORMATION FOR SEQ ID NO: 4958:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4958:

TGTCGTCAGC TCGTGTCGTG AGATGTTGGG TTAAGTCCCG CAACGAGCGC AACCCTTAA 59

50

(2) INFORMATION FOR SEQ ID NO: 4959:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4959:

GACTTGAACC CCCAACCTAC TGATTACAAG TCAGTTGCTC TACCAATTGA GCTAGGCCG 59

(2) INFORMATION FOR SEQ ID NO: 4960:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4960:

TATTAAGTGG TGACTTAGCG AGATGGACAA CGATGGCGAT ATATTTATTA TTGACCGCA 59

(2) INFORMATION FOR SEQ ID NO: 4961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4961:

ATGATTATCA TATTGCCTTA AATATCGCCA CAATTTTAGC GGGTGGTGAT TTACCAAGA 59

(2) INFORMATION FOR SEQ ID NO: 4962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4962:

CGCCGAAAAT TGTACCGGGG CTAAACATAT TACCGAAGCT GTGGATTGTC CTTTGGACA 59

(2) INFORMATION FOR SEQ ID NO: 4963:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

TTAAGCTTAG TTGCCATCAT TAAGTTGGGC ACTCTAATGT TGACTGCCGG TGACAAACCG

60

(2) INFORMATION FOR SEQ ID NO: 4964:

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- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4964:

15

TAGTTTTGGT ACGGTAACAA ATTTATTGA AGAAACAATC TCAAATAAAG AATTGTTTG

59

(2) INFORMATION FOR SEQ ID NO: 4965:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4965:

AGTTCGGTCC CTATCCGTCG TGGGGCGTAG GAAATTTTAG AGGAGCTGTC CTTAGTACG

59

(2) INFORMATION FOR SEQ ID NO: 4966:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4966:

40

TACAAAGGGC AGCGAAACCG TGAGTCAAAG CAAATCCCAT AAAGTTGTTC TCAGTTCGG

59

(2) INFORMATION FOR SEQ ID NO: 4967:

45

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4967:

CCATTGCAGC ACCGACAGCC ACACCATTTA TTTTTCGCT ATGTATATCG CATTAAACGT

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(2) INFORMATION FOR SEQ ID NO: 4968:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4968:

GCCTCCGTTA CTTTtagagg CGACGCCcag TCAAactgcc CGCTGACACT GTCTCCCACC 60

(2) INFORMATION FOR SEQ ID NO: 4969:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4969:

CAAGGAATTT CGCTACCTTA GGACCGTTAT AGTTACGGCC GCCGTTTACT GGGGCTTCG 59

(2) INFORMATION FOR SEQ ID NO: 4970:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4970:

CATCTGTCAC AGGTACTATG GATTTACCG GAGTCTCTCG TTGAGACAGT GCCCAAATCG 60

TTACG 65

(2) INFORMATION FOR SEQ ID NO: 4971:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 100 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4971:

CTAGAGTTGG CATACCAGTC CGTCGCTAAG GAACCTTTCT TGACTTGATG ACAATCGACT 60

(2) INFORMATION FOR SEQ ID NO: 4972:

- 5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4972:

AGACCCCGTG GAGCTTTACT GTAGCCTGCA TATTCGAATT CGGCACAGCT TGTACAGGAT 60
15 AGGTAGG 67

(2) INFORMATION FOR SEQ ID NO: 4973:

- 20 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4973:

TGTGTACTTA AAAATATGAA TACATGAGTA AAACTCATGC ATAAGAAATA CTAATTTTC 58

30 (2) INFORMATION FOR SEQ ID NO: 4974:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
35 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4974:

ACCTCCAATA ATCATCACTT GAGGCTAGCC CTAAAGCTAT TTCGGAGAGA ACCAGCTA 58

(2) INFORMATION FOR SEQ ID NO: 4975:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4975:

GAGCCACAT CCTTTTCCAC TTGGCGTGTG TTTTGGGACC TTGGCTGGTG GTCTGGGCTG 60
55

(2) INFORMATION FOR SEQ ID NO: 4976:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4976:

TCACTAAGTC CGTCTTTTGA CCCTGACTCG ACTTGTTAGGT CTCGCAGTCA AGCTCCCTT 59

(2) INFORMATION FOR SEQ ID NO: 4977:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4977:

TAAGTAAGTA AAATATAGAT TTTACCAAGC AAAACCGAGT GAATAAAGAG TTTTAAAT 58

(2) INFORMATION FOR SEQ ID NO: 4978:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4978:

GTGAGGTACG TCCAGAATGG GGATTGGCTA AAAATGCATC ATTTATAATT GGACGACG 58

(2) INFORMATION FOR SEQ ID NO: 4979:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4979:

TCGCTATCTG AATCCGAGGT CGCTATCCGA ATCTGGAGTC GCTATCTGGA GTCTGGAATC 60

(2) INFORMATION FOR SEQ ID NO: 4980:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4980:

10 AAGAAGGTAA TAATCCTGTA GTCGAAAATG TTGTCTCTCT TGAGTGGATC CTGAGTAC 58

(2) INFORMATION FOR SEQ ID NO: 4981:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 75 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4981:

GTGGTGTGTT AGGGCACTCT ATACGGGTTA CAAAGTACGA CATTAGACGG ATCATCTGGA 60

AAGATGAATC AAAGT 75

25

(2) INFORMATION FOR SEQ ID NO: 4982:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4982:

GTTTTTCATT TTCATTTATA TTTATATTAG TGTTAATCCA ATCATAGATT TATCTATA 58

(2) INFORMATION FOR SEQ ID NO: 4983:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4983:

50 TGACAGCTAA CTATTGGCCA GCTTCTATGT TGGGGCCCCG CCAACTTGCA TTGTCTGTAG 60

A 61

(2) INFORMATION FOR SEQ ID NO: 4984:

55

(A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4984:

10 GGTGTTTTTA AGTCTGATGT GAAAACCCAC GGCTCAACCG GTAGAGGTCA TTGGAAACTG 60
GAAA 64

(2) INFORMATION FOR SEQ ID NO: 4985:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4985:

25 CAGCATACAA TAATGTGCAA GTTGGTCGGG GCCCCAACAT AGAGAATTTC AAAAGAAAT 59

(2) INFORMATION FOR SEQ ID NO: 4986:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4986:

TGATGAAGGT CTTCGGATCG TAAACTCTG TTATTAGGGA AGAACATATG TGTAAGT 57

(2) INFORMATION FOR SEQ ID NO: 4987:

40

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4987:

50 AAAGAATTTG CGCAAAACGC TATCGATACT GAAGGGCGTT CAATGATTAT CATGGGT 57

(2) INFORMATION FOR SEQ ID NO: 4988:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4988:

TTGTCACAAG TCAAGAAAGG TCTTTAGCGA CGATGGTAGC CAACTTACGT TCCGCTA 57

10 (2) INFORMATION FOR SEQ ID NO: 4989:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
15 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4989:

TAGGACCGTT ATAGTTACGG CCGCCGTTTA CTGGGGCTTC GATTCGTAGC TTCGCAG 57

(2) INFORMATION FOR SEQ ID NO: 4990:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4990:

AAAGTCAACG TTAATTCCAA AAAACGTAAC TATAAGTTAC TAACATTATT TAGTATTTAT 60

35

G 61

(2) INFORMATION FOR SEQ ID NO: 4991:

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4991:

TCCACGGGGT CTTTCCATCC TGTCTCGGGT AACCTGCATC TTCACAGGTA CTATGATTTC 60

50

ACCGA 65

(2) INFORMATION FOR SEQ ID NO: 4992:

55

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4992:

GTGCGGCTGG ATCACCTCCT TTCTAAGGAT ATATTCCGGAA CATCTTCTTC AGAAGAT 57

10

(2) INFORMATION FOR SEQ ID NO: 4993:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4993:

20

CCAATGCGGC TCATCGCATC CATTTTTTGC CTGGCAACGT TCTACTCTAG CGGAACG 57

(2) INFORMATION FOR SEQ ID NO: 4994:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4994:

CTGGTTTCGG GTCTACGACA AATACTAAAC GCCTATTTCAG ACTCGCTTTC GCTACGG 57

35

(2) INFORMATION FOR SEQ ID NO: 4995:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4995:

45

CAAACCTCTCG TGGTGTGACG GGCGGTGTGG TACAAGCCCC GGAACGTAT TCACCGTAGC 60

ATGCCGGTCT ACG 73

50

(2) INFORMATION FOR SEQ ID NO: 4996:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4996:

5 ACTAATTTCT ATAGGAAAAG TATTCTTTAT CGTCGTCCCA CCCCAACTCG CACATTATTG 60
TAAGC 65

(2) INFORMATION FOR SEQ ID NO: 4997:

10 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4997:

20 ATTGGATTCC CAATTTCTAC AGACAATGCA GTTGGGGTGG GACGTCGAAA TAAATTTT 58

(2) INFORMATION FOR SEQ ID NO: 4998:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4998:

30 AACTTCAACA GGTTTTGCAG GTGGCGGTGC GACTGCAGGA AGACGTTAAA TTAATG 56

(2) INFORMATION FOR SEQ ID NO: 4999:

35 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4999:

45 GGGCAGGCGT CAGCCCTATA CATCACCTTA CGGTTTAGCA GAGACCTGTG TTTTGT 56

(2) INFORMATION FOR SEQ ID NO: 5000:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5000:

TTAGGACCCG ACTAACCCAG AGCGGACGAG CCTTCCTCTG GAAACCTTAG TCAATC 56

5 (2) INFORMATION FOR SEQ ID NO: 5001:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5001:

GACGGGATTC TCACCCGTCT TTCGCTACTC ACACCGGCAT TCTCACTTCT AAGCGC 56

(2) INFORMATION FOR SEQ ID NO: 5002:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5002:

30 CCTGTGGGCC TCAGCTTAGG ACCCGACTAA CCCAGAGCGG ACGAGCCTTC CTCTGG 56

(2) INFORMATION FOR SEQ ID NO: 5003:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5003:

TTACTCATTT AGCTCTACTA AACTCGTTGC GCTCTTTTCT CGTTTCGTCA GATTCA 56

45 (2) INFORMATION FOR SEQ ID NO: 5004:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

50 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5004:

(2) INFORMATION FOR SEQ ID NO: 5005:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5005:

GACATAGATT AAGTTATTAA GGGCGCACGG TGGATGCCTT GGCAC TAGAA GCCGATG 57

(2) INFORMATION FOR SEQ ID NO: 5006:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5006:

GGAACCACTA CATAATAAAT CATTAGTGGC TCTTTATCAT TCTGTCCAC TCCCCTG 57

(2) INFORMATION FOR SEQ ID NO: 5007:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 69 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5007:

CGCTACGTTT TTCCTCAACA TTTAAGAAAA TAAAGAATGC TACAATTACG ATTGCAATCA 60
 AACCAAAGA 69

(2) INFORMATION FOR SEQ ID NO: 5008:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5008:

AAAAGCTTGT TACAAGCGCT ATTTTCGTTT AGTCAACTAC TGCCAATATA ACTTCGT 57

5 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5009:
ACATCTTAGT ACCCGGAGAA GAGAAAGAAA ATTCGATTCC CTTAGTAGCG GCGAGC 56

(2) INFORMATION FOR SEQ ID NO: 5010:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 65 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5010:
25 GTTTGGACGA GGGGCCCTCT CGGGTTACGA TTCAGACAAA CTCCGATGCA ATTAATTTAC 60
TTGGG 65

(2) INFORMATION FOR SEQ ID NO: 5011:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5011:
40 TTTACTTGTA TTGGAATAAT TTCATCTTTG AACCGACCAT CACGTTGTGC GTCATA 56

(2) INFORMATION FOR SEQ ID NO: 5012:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5012:
CCTTATACAT CACCTTTACG GTTTTAGCAG AAACCTGTGT TTTTGTATAA ACAGTCGCTT 60

55 (2) INFORMATION FOR SEQ ID NO: 5013:

(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5013:

10 GGGCCCAACA CAGAAGCTGG CGAAAAGTCA GCATACAAAA TTGTGCAAGT TGGCGGGTCC 60
ACA 63

(2) INFORMATION FOR SEQ ID NO: 5014:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5014:

25 TAGGGTAGTA TCCCACCACT GGCCTCCACG TAAGCTAGCG CTTACGTTT CAAAGGCT 58

(2) INFORMATION FOR SEQ ID NO: 5015:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 105 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5015:

CAACTCCGAT GCAATTAATT TAACTTGGGA nCAGACATGG GTGATAAGGT CGTGTTTCGAA 60
40 GGGAACAGCC AGACACAGCT AAGTCCAGAT ATATGTAAGT GGAAA 105

(2) INFORMATION FOR SEQ ID NO: 5016:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5016:

CAAACGATTT ATTTATATGC TTATTTCTTT ATTTATTATT ATTACAATTA CATTTT 56

55

(2) INFORMATION FOR SEQ ID NO: 5017:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5017:

10 TCTGTAGAAA TTGGGGAATC CAATTTCTCT TGGTTTGGGT CCCATCCCCA ACTTGCACAT 60
TATTG 65

(2) INFORMATION FOR SEQ ID NO: 5018:

15

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5018:

25 GGGGATGGGC CCCAACAAAG AGAAATTGGA TTCCCAATTT CTACAGACAA TGCAAC 56

(2) INFORMATION FOR SEQ ID NO: 5019:

30

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5019:

CGATTGGATT GCACGTCTAA GCAGTAAGGC TGAGTATTAG GCAAATCCGG TACTC 55

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(2) INFORMATION FOR SEQ ID NO: 5020:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5020:

50 TACGGCGTTT AGTATTTGGT CGTAGCCGGA AACCAGGTGA TCTACCCTTG GTCAGGTT 58

(2) INFORMATION FOR SEQ ID NO: 5021:

55

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 55 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5021:

TTGTGCGGGT CCCCGTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCCA 55

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(2) INFORMATION FOR SEQ ID NO: 5022:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5022:

20

AGAGTTCACA TCGACGGGGA GGTTGGCAC CTCGATGTCG GTCATCGCA TCCTG 55

(2) INFORMATION FOR SEQ ID NO: 5023:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 58 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5023:

CCTTAGCTGG TGGTCTGGGC TGTTCCCTT TCGAACACGG ACCTTATCAC CCATGGTC 58

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(2) INFORMATION FOR SEQ ID NO: 5024:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5024:

TAAAGGCTAA ACTACCAATG TTTTCAATGG ATTTCCAAAA TGAATCATCT GGGAT 55

(2) INFORMATION FOR SEQ ID NO: 5025:

50

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 63 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5025:

TCAAACCGGA GGGGTCATTG GAAACTGGAA AACTTGAGTG CAGAAGAGGA AAGTGAATT 60
5 CCA 63

(2) INFORMATION FOR SEQ ID NO: 5026:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5026:

GCTTGCGTAC CTAAAGAGCA CCCCTTCTCC GAATTACGGG GTCATTTTGC CGAGTTCCTT 60
20 AACG 64

(2) INFORMATION FOR SEQ ID NO: 5027:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5027:

AATACATAGC ATATCATAAG GCACACCCGG AGAACTGAAA CATCTTAGTA CCCGGA 56

(2) INFORMATION FOR SEQ ID NO: 5028:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5028:

GGGCCCCCTCT CGGGTTACCA ATTCAGACAA ACTCCGAATG CCAATTAATT TAACT 55

(2) INFORMATION FOR SEQ ID NO: 5029:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5029:
 5 CGTAACTATA ACGGTCCTAA GGTAGCCGAA ATTCCTTGTC GGGTAAGTTC CGAC 54
 (2) INFORMATION FOR SEQ ID NO: 5030:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 57 base pairs
 10 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5030:
 15 ATCCCCGGGG CCCCAACACA GAGAATTTTCG AAAAGAAATT CTACAGGCAA TGCAAGT 57
 (2) INFORMATION FOR SEQ ID NO: 5031:
 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 25 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5031:
 30 TGCTTGGTAA AATCTATATT TTA CTTACTT ATCTAGTTTT CAATGTACAA TTTC 54
 (2) INFORMATION FOR SEQ ID NO: 5032:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 35 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5032:
 40 TCCCTATCCG TCGTGGGCGT AGGAAATTTG AGAGGAGCTG TCCTTAGTAC GAGA 54
 (2) INFORMATION FOR SEQ ID NO: 5033:
 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5033:
 55

(2) INFORMATION FOR SEQ ID NO: 5034:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5034:

TATCTGAATC TGAGTCGCTG TCTGAATCTG AATCGCTATC CGAGTCTGAG TCGC 54

(2) INFORMATION FOR SEQ ID NO: 5035:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5035:

CACCAGCAAT TCAATTAGCT AAAGATTATT TAGCAACTAG ACCGGAATGA AAAA 54

(2) INFORMATION FOR SEQ ID NO: 5036:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5036:

CTACCATCGA CGCTAAGAGC TTAACCTCTG TGTTCCGCAT GCGAACAGGT GTGA 54

(2) INFORMATION FOR SEQ ID NO: 5037:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5037:

CGGCGAGTTA CGATTTGATG CAAGGTTAAG CAGTAAATGT GGAGCCGTAG CGGAAG 56

(2) INFORMATION FOR SEQ ID NO: 5038:

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5038:

10 GACCGGGATG GACATACCTC TGGTGTACCA GTTGTGCGTG CCAACGCATA AGCT 54

(2) INFORMATION FOR SEQ ID NO: 5039:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5039:

TTTCACCGAG TCTCTCGTTG AGCAGTGCCC AAATCGTTAC GCCTTTCGTG CGGG 54

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(2) INFORMATION FOR SEQ ID NO: 5040:

(i) SEQUENCE CHARACTERISTICS:

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- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5040:

35

TTATAACACG TATGCTTGGG GAGTGTAATA AGCTTGATCA GAGATTCCnA TGGGAACCAG 60

CATGAGTTAT GTCATTTATC ATATGTGATC ATAGCATATC AAAGG 105

40

(2) INFORMATION FOR SEQ ID NO: 5041:

(i) SEQUENCE CHARACTERISTICS:

45

- (A) LENGTH: 54 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5041:

50

GGCACCTATT TTCTATCTAG AGGCTTTTCT CGGCAGTGTG GAAATCAACG ACTC 54

(2) INFORMATION FOR SEQ ID NO: 5042:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 54 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5042:

ACTTATCTAG TTTTCAATGT ACAAATAATG GTGGAGACTA GCGGGATCGA ACCG

54

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(2) INFORMATION FOR SEQ ID NO: 5043:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5043:

20

CGTTCAGTCA ACTACTGCCA ATATAACATC GTAGAGCATA GAACATTGAT TTA

53

(2) INFORMATION FOR SEQ ID NO: 5044:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 59 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5044:

ACTAGAGAGT ATTTAGACTT AGGAGTGGTC CTCCAGATT CCGACGGATT TCACGTGCT

59

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(2) INFORMATION FOR SEQ ID NO: 5045:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5045:

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TTTCGTCGTC CCACCCAAC TTGCACGCTA TTGTGAGCTG ACTTTTCGCC AGCTTCTGTG

60

TT

62

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(2) INFORMATION FOR SEQ ID NO: 5046:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5046:

5 CGTCATCCCC ACCTTCCTCC GGTTCGTCAC CGGCAGTCAA CTTAGAGTGC CCA 53

(2) INFORMATION FOR SEQ ID NO: 5047:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5047:

TATTTATTAA ACCTAATAAA GATGAATTAG AAGTGATGTT TAATACAACA GTG 53

(2) INFORMATION FOR SEQ ID NO: 5048:

(i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5048:

30 CCTCGGCACC ATTTTCAATA AAAACATATG CGCCCGTAGC TCAATTGGAT AGA 53

(2) INFORMATION FOR SEQ ID NO: 5049:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5049:

AAATGGCCAA CTTAAGCCAG GATACAATTT ACAAATAGCG ACAAATTCTC AATGTGTTT 59

45 (2) INFORMATION FOR SEQ ID NO: 5050:

(i) SEQUENCE CHARACTERISTICS:

- 50 (A) LENGTH: 111 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

55

CGAAAGACAC nCACAAGATT AATAACGCGT TTGAGTCTTT TTATAAAGAC GTACTTCATG 60
 TTACGTTGAC TTTAAGATGG TGGAACATAG TTAGTTTTAG GGCCACGGGG G 111

5 (2) INFORMATION FOR SEQ ID NO: 5051:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5051:

ACGTTGACAT ATTGTCATTC AGTTTTCAAT GTTCATTAAT GTTCAATCTC TTT 53

(2) INFORMATION FOR SEQ ID NO: 5052:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5052:

30 CTGAATTCGG TAACCCGAGA GGGCCCCTCG TCCAAACAGT GCTCTACCTC CAA 53

(2) INFORMATION FOR SEQ ID NO: 5053:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5053:

TACATAGCAT ATCAGAAGGC ACACCCGGAG AACTGAAACA TCTTAGTACC CGG 53

(2) INFORMATION FOR SEQ ID NO: 5054:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 50 (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5054:

(2) INFORMATION FOR SEQ ID NO: 5055:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5055:

TAGGGCTAGC CTCAAGTGAT GATTATTGGA GGTAGAGCAC TGTTCGACG AGG 53

(2) INFORMATION FOR SEQ ID NO: 5056:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5056:

ACTGCTTTGA AATGTTGTTG TCTCAGTTAA TATTCAATTG CTTTCTTTT GCATAATTGA 60
 CAA 63

(2) INFORMATION FOR SEQ ID NO: 5057:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5057:

CTATGTTGGG GCCCCGCCAA CTTGCATTGT CTGTAGAATT CCTTTTCGAA ATTC 54

(2) INFORMATION FOR SEQ ID NO: 5058:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5058:

CTGAATCCGA GTCGCTATCC GAGTCTGAGT CGCTATCTGA GTCTGAATCG CTG 53

5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5059:
 TTTGGGCTAC ACACGTGCTA CAATGGACAA TACAAAGGGC AGCGAAACCG TGATGTCAA 59

(2) INFORMATION FOR SEQ ID NO: 5060:

15 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5060:
 AAATAACTAA TAACATTTAG AGGCTGGGAC ATAAATCCCT AAAAAACAGC AGT 53

25 (2) INFORMATION FOR SEQ ID NO: 5061:

30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 55 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5061:
 TTAAAGAGTG CGTAATAGCT CACTAATCGA GTGACAATGG CGCCGAAAAT GTACC 55

(2) INFORMATION FOR SEQ ID NO: 5062:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5062:
 TACCAGGGTA TCTAATCCTG TTTGATCCCC ACGCTTTTCGC ACATCAGCGT CA 52

50 (2) INFORMATION FOR SEQ ID NO: 5063:

55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5063:

TCGCCAAGCC ATTTTCTTT GTGTTTCTTT TTATTTTGAC GTTTTAGACA TA 52

10

(2) INFORMATION FOR SEQ ID NO: 5064:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 76 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5064:

20

CTCAAGCTCC CTTGTGCCTT TACACTCTAT GTGTGCTTTC CGACCGTTCT GGGGGGAAC 60

TTGGAGCGCC TCCGTT 76

25

(2) INFORMATION FOR SEQ ID NO: 5065:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 54 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5065:

35

CCACCGCTTG TCGGGGTCCC CGTCAATTCC TTTGAGTCGC AACCTTGCGG TCGT 54

(2) INFORMATION FOR SEQ ID NO: 5066:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5066:

45

TCCCCGGGCT AAACATATTA CCGAAGCTGT GGATTGTCCT TTGGACAATG GTAGG 55

50

(2) INFORMATION FOR SEQ ID NO: 5067:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5067:

GCTCATCGCA TCCACTTTTT GCCTGGCAAC GTTCTACTCT AGCGGAACGT AA 52

(2) INFORMATION FOR SEQ ID NO: 5068:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5068:

CGGACACCAG AAGTACCAAG CGAGCCGGAA ACACCAACAC CACCGACACC AGACGTACAA 60

GCGAGCCGGAA ACAACAACAA CG 82

(2) INFORMATION FOR SEQ ID NO: 5069:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5069:

TCCATAACGT GCTGTATCTG TAGCAATAAC TAATACTTTT TCATTCCGGTC TA 52

(2) INFORMATION FOR SEQ ID NO: 5070:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5070:

CGACTCGAAG ACTCAATGTC TTCTCCCAT CACAGCTCAG CCTTAACGAG TA 52

(2) INFORMATION FOR SEQ ID NO: 5071:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5071:

GCGATGGATA ACAGGTTGAT ATTCTGTAC CACCTATAAT CGTTTTAATC GA

52

5

(2) INFORMATION FOR SEQ ID NO: 5072:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

10

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5072:

15

CACTTCACCA CAGCCGCCAT GGCATGGGCA GTAGGAATCG AACCCACACC AAA

53

(2) INFORMATION FOR SEQ ID NO: 5073:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5073:

GTCCAGACTC CTACGGGAGG CAGCAGTAGG GAATCTTCCG CAATGGGCGA AA

52

30

(2) INFORMATION FOR SEQ ID NO: 5074:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 base pairs

(B) TYPE: nucleic acid

35

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5074:

40

TGTTGGCTTA GAATCAGCCA TCATTTAAAG AGTGCCTAAT AGCTCACTAG TCGC

54

(2) INFORMATION FOR SEQ ID NO: 5075:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5075:

55

AAACTTCCTT TTGG

74

(2) INFORMATION FOR SEQ ID NO: 5076:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 53 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5076:

TGAGCTAATC AGACATCATA ATTTTATGG AGAGTTTGAT CCTGGCTCAA GAT

53

(2) INFORMATION FOR SEQ ID NO: 5077:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5077:

GTTAAGCTCC TTAGCGTCGA TGGTAGTCGA ACTTACGTTC CGCTAGAGTA GA

52

(2) INFORMATION FOR SEQ ID NO: 5078:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5078:

GGGTAAGTTC CGACCCGCAC GAAAGGCGTA ACGATTGTTGG CACTGTCTCA AC

52

(2) INFORMATION FOR SEQ ID NO: 5079:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5079:

ATTAATCCAT TGTGCCACAA GTGCCGACC AGAAATGATG GTATTTAATA AT

52

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5080:
 AATAGCGACG AATCACACCT TCTGCGGCAC CACGGAATAA TACACCATGT GG

(2) INFORMATION FOR SEQ ID NO: 5081:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5081:
 CTTTCGCTAC TCACACCGGC ATTCTCACTT CTAAGCGCTC CACATGTCCT TA

(2) INFORMATION FOR SEQ ID NO: 5082:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 56 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5082:
 CAGACAGCGA CTCAGATCAG ATAGCGATCG GACTCAGACA ACGACTCAGA TTCAGA

(2) INFORMATION FOR SEQ ID NO: 5083:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5083:
 AGGGTATGAT CCATCCCGGG TCCTCTCGGT ACTAAGGGAC AGCTCCTCTC AAATTCCTA
 CG

(2) INFORMATION FOR SEQ ID NO: 5084:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5084:

10 GTGTACCACT TGTCGTGCCA ACGGCATAGC TGGGTAGCTA TGTGTGGACG AG 52

(2) INFORMATION FOR SEQ ID NO: 5085:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 78 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5085:

TTGCTTACGC TTGCTATAGC CAATATATAG ATGTTGGAGG GGGCAGATTC GAATGCGAAC 60

CCGAGGAGCG GATTAACA 78

25

(2) INFORMATION FOR SEQ ID NO: 5086:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 52 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5086:

ACTGACGCTG ATGTGCGAAG CGTGGGGATC ACACAGGATT AGATACCCTG GT 52

(2) INFORMATION FOR SEQ ID NO: 5087:

40

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5087:

50 AAGTTGTTCT CAGTTCGGAT TGTAGTCTGC AACTCGACTA CATGAAGCTG G 51

(2) INFORMATION FOR SEQ ID NO: 5088:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 51 base pairs

55

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5088:

AATACTTTAA AAAAATAAGA CACTTTGGCC AACTTAAGCC AGGATACAAT T

51

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(2) INFORMATION FOR SEQ ID NO: 5089:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5089:

20

AGAACGTAAA TTTAATCCTG ATTTAGCACC AGGGACAGAA AAAGTAACAA G

51

(2) INFORMATION FOR SEQ ID NO: 5090:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5090:

CCGCTACCCT CAGTTCATCC GCTCACTTTT CAACGTAAGT CGGTTCCGGTC C

51

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(2) INFORMATION FOR SEQ ID NO: 5091:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5091:

45

CATGGGTGAT AAGGTCCGTG TTCGAAAGGG AAACAGCCCA GACCACCAGC T

51

(2) INFORMATION FOR SEQ ID NO: 5092:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5092:
 TTGTGCGGAT CCCCCTCAAT TCCTTTGAGT TTCAACCTTG CGGTCGTACT CCCC
 55

5 (2) INFORMATION FOR SEQ ID NO: 5093:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 10 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5093:
 CCGCAAACCG ACACAGGTAG TCAAGATGAG AATTCTAAGG TGAGCGAGCG A
 51

(2) INFORMATION FOR SEQ ID NO: 5094:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5094:
 ACGAATACTA ATCGATCGAA GACTTAATCA AAATAAATGT TTTGCGACAA A
 51

30 (2) INFORMATION FOR SEQ ID NO: 5095:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 77 base pairs
 (B) TYPE: nucleic acid
 35 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5095:
 AATCGTTGTT ACCTTCATTA TACCACTTAC TTGTGGAGTG ATCTTCTTCA AAGTAACACT
 60
 ATTGTGCCAC CGATTGA
 77

45 (2) INFORMATION FOR SEQ ID NO: 5096:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 50 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

55

TTCGTAAGGA CATGTGGAGC GCTTAGAAGT GAGAATGCCG GTGTGAGTAG CG

52

(2) INFORMATION FOR SEQ ID NO: 5097:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5097:

15 GGGTCTGTTT TCTAATTGA GCACAATCTT CGTTCTCAAT AGAATGATTT A

51

(2) INFORMATION FOR SEQ ID NO: 5098:

- 20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5098:

CTGTAGAAAT TGGGAATCCA ATTTCTCTAT GTTGGGGCCC ACACCCCAAC T

51

(2) INFORMATION FOR SEQ ID NO: 5099:

30

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5099:

40 CTGTGGATTG TCCTTTGGCA TGAGATAGGA GAGCGTTCTA AGGGCGTTGA A

51

(2) INFORMATION FOR SEQ ID NO: 5100:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5100:

GGTTCAGAAC GTCGTGAGAC AGTTCGGTCC CTATCCGTCG TGGGCGTAGG A

51

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 64 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5101:

TGACTGATAC GATCAATGCG CTGTGAACAA GCTTTTTTCA ATTCTAGTCA GGGGCCCCAA

CACA

(2) INFORMATION FOR SEQ ID NO: 5102:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 58 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5102:

TATTTGCATT TATATTGACG TTTTAAACAT AAAAAAAGAA ACCTTGCGGT CTCAATGG

(2) INFORMATION FOR SEQ ID NO: 5103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5103:

ATTACCATTT TGGTATACCA CATCGTTATT CAACACATTA TCTTTTACTT

(2) INFORMATION FOR SEQ ID NO: 5104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5104:

GGACACTGCT CCCTCAGGAG TCTCGCCATT AATACTACGT ATTAACATGT AAT

(2) INFORMATION FOR SEQ ID NO: 5105:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5105:

10 ATTTCTTCTT TTTCTACAAT CGAGTCTCCT TTTACAGGTC CATATTTTGT 50

(2) INFORMATION FOR SEQ ID NO: 5106:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5106:

TGGTCAAGCG GTTAAGACAC CGCCCTTTCA CGGCGGTAAC ACGGGTTCGA 50

25

(2) INFORMATION FOR SEQ ID NO: 5107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5107:

35 TTTTTCAGCAG TAATTGCCAC ATCTGTGTGA CGATAATGAT ATGCGACAGT 50

(2) INFORMATION FOR SEQ ID NO: 5108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5108:

CAAGCCATTT TTCTTTGTGT TTACTTTTTA TTTTGACGTT TTAGACATAA 50

50

(2) INFORMATION FOR SEQ ID NO: 5109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5109:

AGCCGATGAA GGACGTTACT AACGACGATA TGCTTTGGGG AGCTGTAAGT

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(2) INFORMATION FOR SEQ ID NO: 5110:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5110:

ATCCATAACG TTTGGTATCT GTAGCAATAA CTAATACTTT TTCATTCGGT CTA

53

15

(2) INFORMATION FOR SEQ ID NO: 5111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 53 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5111:

CCCTTAGTAC TGCAGCTAAC GCATTAAGCA CTCGCCTGA GGAGTACGAC CTC

53

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(2) INFORMATION FOR SEQ ID NO: 5112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5112:

GGAGTCAAAG TCCGTTGCCT TACCGCTTGG CTATAGCCCA ATATATAGAT

50

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(2) INFORMATION FOR SEQ ID NO: 5113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

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AGAnTTTCTT TTCGAAATTC TTTATGTTGG GGCCCCGCCA ACTTGCATTG

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(2) INFORMATION FOR SEQ ID NO: 5114:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5114:

15

GCTGTGATGG GGAGAAGACA TTGTGTCTTC GAGTCGTTGA TTTCACACTG

50

(2) INFORMATION FOR SEQ ID NO: 5115:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 55 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5115:

CTTGATTAAC TCATTATCAA GTTATGCACG TGTAATGAA TTCGGCTTTA TCGAA

55

(2) INFORMATION FOR SEQ ID NO: 5116:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5116:

40

GTACTTAAAA AATGAATACA TGAGTAAAGC TCATGGCATA AGAAATACTA

50

(2) INFORMATION FOR SEQ ID NO: 5117:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5117:

CAGAATCAGA TAGCGACTCA GAATCAGATA GTGAGTCAGA TTCAGCAGTn

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5118:
CGAATACTAA TCGATCGAAG ACTTAATCAA AATAAATGTT TTGCGACnAA

(2) INFORMATION FOR SEQ ID NO: 5119:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5119:
AATCGTCGAA ACTTAATCAA AATAAATGTT TTGCGACAAA TCACTTTTAC TTACTATCTA

(2) INFORMATION FOR SEQ ID NO: 5120:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5120:
CCGAAGTTTA CGGGGTCATT TTGCCGAGTT CCTTAACGAG AGTTCGCTCG

(2) INFORMATION FOR SEQ ID NO: 5121:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5121:
ATAATCCTGT AGTCGAAAAT GTTGTCTCTC TTGAGTGGAT CCTTAGTACG CCGGGGCACG

T

(2) INFORMATION FOR SEQ ID NO: 5122:

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5122:

10 TAGCGACTCA GATTGAGACA GCGATTGAGA CAGCGACTCA GACTGAGATA 50

(2) INFORMATION FOR SEQ ID NO: 5123:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5123:

TATTGTGAAA TTGTATCCTG GCTTAAGTTG GCCATTTTTC ATATGGTCTT 50

(2) INFORMATION FOR SEQ ID NO: 5124:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5124:

35 CACGAGCTGA CGACAACCAT GCACCACCTG TCACTTTGTC CCCCAGAGAAG GTCTCTATCT 60

(2) INFORMATION FOR SEQ ID NO: 5125:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 64 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5125:

AGAACACATT GCAGTCTTCG AGTCGTTGAT TTCACACTGC CGTAGTAAAA GCCTCTAGAT 60

50

AGAA 64

(2) INFORMATION FOR SEQ ID NO: 5126:

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 57 base pairs

(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5126:

GGACGACATT AGACGAATCA TCTGGAAAAG ATGAGTCAAA GAAGGTAATA GTCCTGT 57

10

(2) INFORMATION FOR SEQ ID NO: 5127:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5127:

20

GTCCTTAGTA CGAGATGACC GGGATGGACA TACCTCTGGT GTACCAGTTG 50

(2) INFORMATION FOR SEQ ID NO: 5128:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5128:

GCCGATTTTA GCAGTTGTTG CTTCGTTCAA TTTTATGGGG CCATTTATGG 50

35

(2) INFORMATION FOR SEQ ID NO: 5129:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5129:

45

TCCACACATA GCTACCCAGT CTATGCCGTT TGCACTACAA CTGGTACACC A 51

(2) INFORMATION FOR SEQ ID NO: 5130:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 57 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5130:

CTCAGTTGGT TGAGCATCTG ACTTTTAATC AAAGGGTCAA GGGTCGAATC CTCTTTT

57

(2) INFORMATION FOR SEQ ID NO: 5131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5131:

TGATATTCAC TTCAATGTTA TCAATATTAG TGCCATCTAT GACATCTGCC A

51

(2) INFORMATION FOR SEQ ID NO: 5132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5132:

TCCTGTAGTC GAACGTGTTG TCTCTTTGA GTGGATCCTG AGTACGACGG A

51

(2) INFORMATION FOR SEQ ID NO: 5133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5133:

ACTCAGACAT TGGATTCAGA TTCAGACAGC GACTCAGATT CAGATAGCGA CTCAGATTC

59

(2) INFORMATION FOR SEQ ID NO: 5134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5134:

(2) INFORMATION FOR SEQ ID NO: 5135:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5135:

CAATACaAG GGCAGCGAAA CCGTGATTCA AGCAAATCCC ATAAAGTTGG

(2) INFORMATION FOR SEQ ID NO: 5136:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5136:

GAAGCTGGCG AAAAGTCAGC TTACAAAATG TGCCAGTTGG CGGGGGCCCA AC

(2) INFORMATION FOR SEQ ID NO: 5137:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5137:

TTGTAAGGAA GATGCTCTCC CAGCTGAGCT AATTCTCCAA AATAATGAnT

(2) INFORMATION FOR SEQ ID NO: 5138:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5138:

CTGTACAAGC TGTGCCGATA TTTCAATATC AnGnTACAGT AnAGCTCCAC

(2) INFORMATION FOR SEQ ID NO: 5139:

(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5139:

10 GGTTCGAATC CTGTCTTCCC GATATACTGT AATTATTATG GGGGCTTTGC TC 52

(2) INFORMATION FOR SEQ ID NO: 5140:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5140:

GCTACTGAAC CTATAAAATG TATGATGGCG GTCTCGAGGG AATCGAACCC AGATCT 56

25 (2) INFORMATION FOR SEQ ID NO: 5141:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5141:

35 AGGAGGCTCG TCCGCTCTAG GTTAGTCGGG TCCTAAGCTG AGGCCGACAG TA 52

(2) INFORMATION FOR SEQ ID NO: 5142:

(i) SEQUENCE CHARACTERISTICS:

40

(A) LENGTH: 56 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5142:

CACGCTTTTCG ACATCAGCGT CAGTTACAGA CCAGAAAGTC GCCTTCGCAC TGGTGT 56

50 (2) INFORMATION FOR SEQ ID NO: 5143:

(i) SEQUENCE CHARACTERISTICS:

55

(A) LENGTH: 75 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5143:

CTCCTAAAAC AATTACATC CAAACCTTCA TCACTCACGC GCGTTGCTC CGTCAGCTTT 60
CGCCATTGCG AAGAT 75

(2) INFORMATION FOR SEQ ID NO: 5144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5144:

GAGGAGTGGT TAGCTTCTGC GGAGTACGAA TCGAGCCCCG TAAACGGCGG CCGGT 55

(2) INFORMATION FOR SEQ ID NO: 5145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 53 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5145:

GCCTAATACT CAGCCTGACT GCTTAGACGT GCAATCCATA TCAGCACGAT TCG 53

(2) INFORMATION FOR SEQ ID NO: 5146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5146:

AGCTGTGGAT TGTCTTTTG GCATGGGTAA GGAGAACGTT CTAAGGGCGT T 51

(2) INFORMATION FOR SEQ ID NO: 5147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5147:

CTCTTTGATC CGTAGTCAAA CGCTCTATCC AATTGAGCTA CGGGCGCATA

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(2) INFORMATION FOR SEQ ID NO: 5148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5148:

GAACTAATTC TCCAAAATAA TGA CTCCTAC AGGAACTCGA ACCCGTATAA CCGCCGTAAA

60

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(2) INFORMATION FOR SEQ ID NO: 5149:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 50 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5149:

AAAGCACACC CGGAAACTG AAACATCTTA AGTACCCGGA GnaAGAGAAA

50

30

(2) INFORMATION FOR SEQ ID NO: 5150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5150:

GTAAGTTCGC ACTACCATCG ACGCTAAGGG AGCTTAACTT CTGTGGTTCG GCATGG

56

40

(2) INFORMATION FOR SEQ ID NO: 5151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

45

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5151:

55

(2) INFORMATION FOR SEQ ID NO: 5152:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 59 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5152:

CTATTCTCTG TGTCGGGCTC ACCCCAACCTT GCACACTATT GTAAGCTGAC TTTCCTCCA 59

(2) INFORMATION FOR SEQ ID NO: 5153:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 65 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5153:

TAACCACATC ATTCGGATAC TGTTCATGGA AGTAATTTCT CTATTCTTCG GACCAGGAAA 60

ATACA 65

(2) INFORMATION FOR SEQ ID NO: 5154:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 91 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5154:

CCATATGTGT CAGTCACTGT GCACATCTTG ACGGTACCTA ATCAGACAGC CACGGCTAAC 60

TCCGTGCCAG CCGCCGCGGT ACTACGTGGT G 91

(2) INFORMATION FOR SEQ ID NO: 5155:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5155:

(2) INFORMATION FOR SEQ ID NO: 5156:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 58 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5156:

GACTCTGGGA GGACCATCTC CTAAGGCTAA ACTACTCTCT CGTGACCGAT AGTGAACC 58

(2) INFORMATION FOR SEQ ID NO: 5157:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5157:

TTGTAAGTCC GGTATAGGAG TGTCTACAA CCCCAACAAG CAAGCTTGTT G 51

(2) INFORMATION FOR SEQ ID NO: 5158:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5158:

TAGTnACCGn TAGTGAACCA TTACCGTGAG GGAAAGGTGA AAAGCACCCC 50

(2) INFORMATION FOR SEQ ID NO: 5159:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5159:

TTCGCTCGCC GCTACTCAAG GGAATCGCAT TTCCTTTCTC TTCCTCCGGG T 51

(2) INFORMATION FOR SEQ ID NO: 5160:

- (A) LENGTH: 61 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5160:

10 AACTGGAGAA ACAACTTTAT GGGGTTTGCT TGAACCTCGC GGTTCGCTG CCCTTTGTAT 60

T 61

(2) INFORMATION FOR SEQ ID NO: 5161:

15

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5161:

25 AGACCTCTGC CTTACCACTT GGCTATGCGC CAATAACTGG GCTACCTGGA T 51

(2) INFORMATION FOR SEQ ID NO: 5162:

30

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5162:

CCGCTCACTT TTCAACGTAA GTCGGATCGG TCCTCCATTC AGTGTCACCT GAACT 55

40

(2) INFORMATION FOR SEQ ID NO: 5163:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5163:

50

CTTGATCTGT ATTTAAAATG ATATTTTCTA TCTTTTCITT ATTATTAAACG TCTATGACGT 60

CGTAGTATAA GATTCCGTGT A 81

(2) INFORMATION FOR SEQ ID NO: 5164:

55

(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5164:

10 GTTCGAATCC CGTCTTCTGC TCCATTATTT TGCCGGGGTG GCGGCAACTC TCACACGCAC 60

AG 62

(2) INFORMATION FOR SEQ ID NO: 5165:

15

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5165:

25 CAGGGGTCTT TCGTCCTGTG TGGGTAACTG CATCTTCACA GGTACTATGA TTTCA 55

(2) INFORMATION FOR SEQ ID NO: 5166:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

30

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5166:

AAGCTGAGGC CGACAGCGTA GCGATGGAT GACAGGTTGA TATTGCCGGT ACCACCCGAT 60

AA 62

40

(2) INFORMATION FOR SEQ ID NO: 5167:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 52 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

45

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5167:

CTTGCGTCTC CAGTTCCGCC ACCCCGGCAC TATAAAATG GAGCAGAAGA CG 52

(2) INFORMATION FOR SEQ ID NO: 5168:

55

- (A) LENGTH: 56 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5168:

10 TCGTCCGCTA TCTCCACCAT TATTTGTACA TTGAACTAG ATAAGTAGTA AATATA

56

(2) INFORMATION FOR SEQ ID NO: 5169:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 55 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5169:

CTTGGACGTC GGTGGGTAGT CGAACTTAC GTTCGCTAG AGTAGAACGT TGCCA

55

(2) INFORMATION FOR SEQ ID NO: 5170:

25

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 52 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5170:

35

CTACTGCTGC ATATGCGGGT GAAGGGAGTC GAACCCCCAC GCCGTAAGCA TA

52

(2) INFORMATION FOR SEQ ID NO: 5171:

(i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5171:

GGGCTTnGGA CATTAGTTC TnAGGCAATG TAAAAAGCT GATTCTATT

50

(2) INFORMATION FOR SEQ ID NO: 5172:

50

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5172:

AAATTACATG TTAATACGTA ATTAATGGCG AGACTCCTGA GGAACCATTG CCATTGGAAG 60

5

(2) INFORMATION FOR SEQ ID NO: 5173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5173:

GTTTTATTTT TTAAAGTAT GTAAAAGTAA AATTACATGn TAATACGTAn 50

15

(2) INFORMATION FOR SEQ ID NO: 5174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 57 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5174:

CAACTCTCGT TAAGGAACTC GGCAAAATAC CCCGTAAC TT CGGAGTAGGT CTCTTTA 57

30

(2) INFORMATION FOR SEQ ID NO: 5175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5175:

GGAAACTGGA ATAAATAAAC ATTCAATTGA GCGCATCAGT ATTAGGATTC ACTCTAAAAA 60

40

(2) INFORMATION FOR SEQ ID NO: 5176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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55

GTAACGGACG CGCTCAAAGG TTCCCTCACA ATGGTTGGAA ATCATTGATA

50

(2) INFORMATION FOR SEQ ID NO: 5177:

5

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 50 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5177:

15

AGTTACGTTT TTTTATAAAG AGGTTTGAGA CGCGTTATTA ATCTTGTGAG

50

(2) INFORMATION FOR SEQ ID NO: 5178:

20

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5178:

GTGTGGATCC TGAGTACGAC GGAGCACGTG ACAATTCCGT CGGCAATCTG GGG

53

(2) INFORMATION FOR SEQ ID NO: 5179:

30

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 83 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5179:

40

CGGTAACCTT ATACCTTTTA ACATATTTTG CATTTGATTG CGTTTACCTT TTTTACCTTT

60

ACCGCCACCA GTGAACTGTT TCA

83

(2) INFORMATION FOR SEQ ID NO: 5180:

45

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5180:

55

TTTAAA

66

(2) INFORMATION FOR SEQ ID NO: 5181:

5

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 67 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5181:

15

GTTCGGTAAC TCGAGCGGGT CTCATAACCC GTAGGTCGGG TGGTTCAAAT CCGTCCTCCC
GCAATAT

60

67

(2) INFORMATION FOR SEQ ID NO: 5182:

20

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5182:

30

TAGCGGTGAA ATGCGCAGAG ATATGGAGGA ACACCACTAG CGAAGGCAAC TTTCT

55

(2) INFORMATION FOR SEQ ID NO: 5183:

35

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5183:

GAATTCCATG TGTAGCGGTG AAATGCGCAG AGATATGnAC GAACACCAAT

50

(2) INFORMATION FOR SEQ ID NO: 5184:

45

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 62 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5184:

55

CC

62

(2) INFORMATION FOR SEQ ID NO: 5185:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 55 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5185:

GAGACCTTGT CGGTCCATAT GCGGCTCATC GCATCCATTT TTTGCCTGGC AACGT

(2) INFORMATION FOR SEQ ID NO: 5186:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5186:

CCATCATTAAGTTGGGCACT CTAAGTTGAC TGCCGGnGnC ACCnAAGAAG

(2) INFORMATION FOR SEQ ID NO: 5187:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5187:

TTAATACGTT GCAATCCAAT CGCAGCTTC GCCTATCCTA CTGCCnTCCC

(2) INFORMATION FOR SEQ ID NO: 5188:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 50 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5188:

AGTCGCTATC CGAATCTGAG TCGCTATCTG AGTCTnAGTC GCTAnnCCAG

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 54 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5189:

ATAGATGCCC TTACCGCAAA CCGACACATG TAGTCAATAT GATAATTCTA AGGT

(2) INFORMATION FOR SEQ ID NO: 5190:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 50 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5190:

CTTTAATGGG CGAACAGnAC CCTTGGACCG ACTACAGCCC AGATCGATGA

(2) INFORMATION FOR SEQ ID NO: 5191:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5191:

ACATAGCACC CAGCGAGCCG TTGGACGACA ACTGGTACAC CAGAGGATGC CATCCGGCCT

(2) INFORMATION FOR SEQ ID NO: 5192:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 320 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5192:

Met Lys Met Ile Asn Lys Leu Ile Val Pro Val Thr Ala Ser Ala Leu
 1 5 10 15

EP 0 786 519 A2

	20	25	30
5	Leu Ile Ser Ser Lys Ala Gly Asp Val Thr Val Ala Asp Thr Met Lys 35 40 45		
	Lys Ile Gly Lys Asp Gln Ile Ala Asn Ala Ser Phe Thr Glu Met Leu 50 55 60		
10	Asn Lys Ile Leu Ala Asp Lys Tyr Lys Asn Lys Val Asn Asp Lys Lys 65 70 75 80		
	Ile Asp Glu Gln Ile Glu Lys Met Gln Lys Gln Tyr Gly Gly Lys Asp 85 90 95		
15	Lys Phe Glu Lys Ala Leu Gln Gln Gln Gly Leu Thr Ala Asp Lys Tyr 100 105 110		
	Lys Glu Asn Leu Arg Thr Ala Ala Tyr His Lys Glu Leu Leu Ser Asp 115 120 125		
20	Lys Ile Lys Ile Ser Asp Ser Glu Ile Lys Glu Asp Ser Lys Lys Ala 130 135 140		
	Ser His Ile Leu Ile Lys Val Lys Ser Lys Lys Ser Asp Xaa Glu Gly 145 150 155 160		
25	Leu Asp Asp Lys Glu Ala Lys Gln Lys Ala Glu Glu Ile Gln Lys Glu 165 170 175		
	Val Ser Lys Asp Pro Ser Lys Phe Gly Glu Ile Ala Lys Lys Glu Ser 180 185 190		
30	Met Asp Thr Gly Ser Ala Lys Lys Asp Gly Glu Leu Gly Tyr Val Leu 195 200 205		
	Lys Gly Gln Thr Asp Lys Asp Phe Glu Lys Ala Leu Phe Lys Leu Lys 210 215 220		
35	Asp Gly Glu Val Ser Glu Val Val Lys Ser Ser Phe Gly Tyr His Ile 225 230 235 240		
40	Ile Lys Ala Asp Lys Pro Thr Asp Phe Asn Ser Glu Lys Gln Ser Leu 245 250 255		
	Lys Glu Lys Leu Val Asp Gln Lys Val Gln Lys Asn Pro Lys Leu Leu 260 265 270		
45	Thr Asp Ala Tyr Lys Asp Leu Leu Lys Glu Tyr Asp Val Asp Phe Lys 275 280 285		
	Asp Arg Asp Ile Lys Ser Val Val Glu Asp Lys Ile Leu Asn Pro Glu 290 295 300		
50	Lys Leu Lys Gln Gly Gly Ala Gln Gly Gly Gln Ser Gly Met Ser Gln 305 310 315 320		

55

(2) INFORMATION FOR SEQ ID NO:5193:

(A) LENGTH: 330 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5193:

Met Asn Lys Val Ile Lys Met Leu Val Val Thr Leu Ala Phe Leu Leu
 1 5 10 15
 Val Leu Ala Gly Cys Ser Gly Asn Ser Asn Lys Gln Ser Ser Asp Asn
 20 25 30
 Lys Asp Lys Glu Thr Thr Ser Ile Lys His Ala Met Gly Thr Thr Glu
 35 40 45
 Ile Lys Gly Lys Pro Lys Arg Val Val Thr Leu Tyr Gln Gly Ala Thr
 50 55 60
 Asp Val Ala Val Ser Leu Gly Val Lys Pro Val Gly Ala Val Glu Ser
 65 70 75 80
 Trp Thr Gln Lys Pro Lys Phe Glu Tyr Ile Lys Asn Asp Leu Lys Asp
 85 90 95
 Thr Lys Ile Val Gly Gln Glu Pro Ala Pro Asn Leu Glu Glu Ile Ser
 100 105 110
 Lys Leu Lys Pro Asp Leu Ile Val Ala Ser Lys Val Arg Asn Glu Lys
 115 120 125
 Val Tyr Asp Gln Leu Ser Lys Ile Ala Pro Thr Val Ser Thr Asp Thr
 130 135 140
 Val Phe Lys Phe Lys Asp Thr Thr Lys Leu Met Gly Lys Ala Leu Gly
 145 150 155 160
 Lys Glu Lys Glu Ala Glu Asp Leu Leu Lys Lys Tyr Asp Asp Lys Val
 165 170 175
 Ala Ala Phe Gln Lys Asp Ala Lys Ala Lys Tyr Lys Asp Ala Trp Pro
 180 185 190
 Leu Lys Ala Ser Val Val Asn Phe Arg Ala Asp His Thr Arg Ile Tyr
 195 200 205
 Ala Gly Gly Tyr Ala Gly Glu Ile Leu Asn Asp Leu Gly Phe Lys Arg
 210 215 220
 Asn Lys Asp Leu Gln Lys Gln Val Asp Asn Gly Lys Asp Ile Ile Gln
 225 230 235 240
 Leu Thr Ser Lys Glu Ser Ile Pro Leu Met Asn Ala Asp His Ile Phe
 245 250 255

EP 0 786 519 A2

Val Val Lys Ser Asp Pro Asn Ala Lys Asp Ala Ala Leu Val Lys Lys
260 265 270

5 Thr Glu Ser Glu Trp Thr Ser Ser Lys Glu Trp Lys Asn Leu Asp Ala
275 280 285

Val Lys Asn Asn Gln Val Ser Asp Asp Leu Asp Glu Ile Thr Trp Asn
290 295 300

10 Leu Ala Gly Gly Tyr Lys Ser Ser Leu Lys Leu Ile Asp Asp Leu Tyr
305 310 315 320

Glu Lys Leu Asn Ile Glu Lys Gln Ser Lys
325 330

(2) INFORMATION FOR SEQ ID NO:5194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5194:

30 Met Thr Arg Lys Phe Arg Thr Leu Ile Leu Ile Leu Ile Ala Thr Ile
1 5 10 15

Ala Leu Ser Gly Cys Ala Asn Asp Asp Gly Ile Tyr Ser Asp Lys Gly
20 25 30

35 Gln Val Phe Arg Lys Ile Leu Ser Ser Asp Leu Thr Ser Leu Asp Thr
35 40 45

Ser Leu Ile Thr Asp Glu Ile Ser Ser Glu Val Thr Ala Gln Thr Phe
50 55 60

40 Glu Gly Leu Tyr Thr Leu Gly Lys Gly Asp Lys Pro Val Leu Gly Val
65 70 75 80

Ala Lys Ala Phe Pro Glu Lys Ser Lys Asp Gly Lys Thr Leu Lys Val
85 90 95

45 Lys Leu Arg Ser Asp Ala Lys Trp Ser Asn Gly Asp Lys Val Thr Ala
100 105 110

50 Gln Asp Phe Val Tyr Ala Trp Arg Lys Thr Val Asp Pro Lys Thr Gly
115 120 125

Ser Glu Phe Ala Tyr Ile Met Gly Asp Ile Lys Asn Ala Ser Asp Ile
130 135 140

55 Ser Thr Gly Lys Lys Pro Val Glu Gln Leu Gly Ile Lys Ala Leu Asn
145 150 155 160

EP 0 786 519 A2

Asp Glu Thr Leu Gln Ile Glu Leu Glu Lys Pro Val Pro Tyr Ile Asn
165 170 175

Gln Leu Leu Ala Leu Asn Thr Phe Ala Pro Gln Asn Glu Lys Val Ala
5 180 185 190

Lys Lys Tyr Gly Lys Asn Tyr Gly Thr Ala Ala Asp Arg Ala Val Tyr
195 200 205

Asn Gly Pro Phe Lys Val Asp Asp Trp Lys Gln Glu Asp Lys Thr Leu
10 210 215 220

Leu Ser Lys Asn Gln Tyr Tyr Trp Asp Lys Lys Asn Val Lys Leu Asp
225 230 235 240

Lys Val Asn Tyr Lys Val Ile Lys Asp Leu Gln Ala Gly Ala Ser Leu
15 245 250 255

Tyr Asp Thr Glu Ser Val Asp Asp Ala Phe Ile Thr Ala Asp Gln Val
20 260 265 270

Asn Lys Tyr Lys Asp Asn Lys Gly Leu Asn Phe Val Leu Thr Thr Gly
275 280 285

Thr Phe Phe Val Lys Met Asn Glu Lys Gln Tyr Pro Asp Phe Lys Asn
25 290 295 300

Lys Asn Leu Arg Leu Xaa Ser His Lys Gln
305 310

(2) INFORMATION FOR SEQ ID NO:5195:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 280 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
35 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5195:

Met Lys Arg Leu Ile Gly Leu Val Ile Val Ala Leu Val Leu Leu Ala
1 5 10 15

Ala Cys Gly Gly Asn Asn Asp Lys Lys Val Thr Ile Gly Val Ala Ser
20 25 30

Asn Asp Thr Lys Ala Trp Glu Lys Val Lys Glu Leu Ala Lys Lys Asp
50 35 40 45

Asp Ile Asp Val Glu Ile Lys His Phe Ser Asp Tyr Asn Leu Pro Asn
50 55 60

Lys Ala Leu Asn Asp Gly Asp Ile Asp Met Asn Ala Phe Gln His Phe
55 65 70 75 80

EP 0 786 519 A2

Ala Phe Leu Asp Gln Tyr Lys Lys Ala His Lys Gly Thr Lys Ile Ser
85 90 95

5 Ala Leu Ser Thr Thr Val Leu Ala Pro Leu Gly Ile Tyr Ser Asp Lys
100 105 110

Ile Lys Asp Val Lys Lys Val Lys Asp Gly Ala Lys Val Val Ile Pro
115 120 125

10 Asn Asp Val Ser Asn Gln Ala Arg Ala Leu Lys Leu Leu Glu Ala Ala
130 135 140

Gly Leu Ile Lys Leu Lys Lys Asp Phe Gly Leu Ala Gly Thr Val Lys
145 150 155 160

15 Asp Ile Thr Ser Asn Pro Lys His Leu Lys Ile Thr Ala Val Asp Ala
165 170 175

Gln Gln Thr Ala Arg Ala Leu Ser Asp Val Asp Ile Ala Val Ile Asn
180 185 190

20 Asn Gly Val Ala Thr Lys Ala Gly Lys Asp Pro Lys Asn Asp Pro Ile
195 200 205

Phe Leu Glu Lys Ser Asn Ser Asp Ala Val Lys Pro Tyr Ile Asn Ile
210 215 220

25 Val Ala Val Asn Asp Lys Asp Leu Asp Asn Lys Thr Tyr Ala Lys Ile
225 230 235 240

30 Val Glu Leu Tyr His Ser Lys Glu Ala Gln Lys Ala Leu Gln Glu Asp
245 250 255

Val Lys Asp Gly Glu Lys Pro Val Asn Leu Ser Lys Asp Glu Ile Lys
260 265 270

35 Ala Ile Glu Thr Ser Leu Ala Lys
275 280

(2) INFORMATION FOR SEQ ID NO:5196:

40 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 273 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5196:

Met Lys Lys Leu Phe Gly Leu Ile Leu Val Leu Thr Phe Ala Val Val
1 5 10 15

55 Leu Ala Ala Cys Gly Asn Gly Asn Lys Ser Gly Ser Asp Asp Lys Lys
20 25 30

Ile Thr Val Ser Ala Ser Pro Ala Pro His Ala Glu Ile Leu Glu Lys
 35 40 45
 5 Ala Lys Pro Leu Leu Glu Lys Lys Gly Tyr Glu Leu Asp Ile Lys Thr
 50 55 60
 Ile Asn Asp Tyr Thr Thr Pro Asn Lys Leu Leu Asp Lys Gly Glu Ile
 65 70 75 80
 10 Asp Ala Asn Tyr Phe Gln His Thr Pro Tyr Leu Asn Thr Glu Lys Lys
 85 90 95
 Asp Lys Gly Tyr Lys Ile Val Ser Ala Gly Asp Val His Leu Glu Pro
 100 105 110
 15 Met Ala Val Tyr Ser Lys Lys Tyr Lys Ser Leu Lys Glu Leu Pro Lys
 115 120 125
 Gly Ala Thr Val Tyr Val Ser Asn Asn Pro Ala Glu Gln Gly Arg Phe
 130 135 140
 20 Leu Lys Phe Phe Val Asp Ala Gly Leu Ile Lys Ile Lys Lys Gly Val
 145 150 155 160
 Lys Ile Glu Asp Ala Lys Phe Ser Asp Ile Thr Glu Asn Lys Lys Asp
 165 170 175
 25 Ile Lys Phe Asn Asn Lys Gln Ser Ala Glu Phe Leu Pro Lys Ile Tyr
 180 185 190
 Gln Asn Glu Asp Ala Asp Ala Val Ile Ile Asn Ser Asn Phe Ala Ile
 195 200 205
 Glu Gln Lys Leu Asn Pro Lys Lys Asp Ser Ile Ala Val Glu Ser Ala
 210 215 220
 35 Lys Asp Asn Pro Tyr Ala Asn Leu Ile Ala Val Lys Glu Gly His Gln
 225 230 235 240
 Asp Asp Lys Lys Ile Lys Ala Leu Ile Glu Val Leu Gln Ser Lys Asp
 245 250 255
 40 Ile Gln Asp Phe Ile Asn Glu Lys Tyr Asn Gly Ala Val Ile Pro Ala
 260 265 270

Lys

45

(2) INFORMATION FOR SEQ ID NO:5197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: protein

55

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5197:

5	Met	Lys	Lys	Ile	Lys	Tyr	Ile	Leu	Val	Val	Phe	Val	Leu	Ser	Leu	Thr	1	5	10	15
	Val	Leu	Ser	Gly	Cys	Ser	Leu	Pro	Gly	Leu	Gly	Ser	Lys	Ser	Thr	Lys	20	25	30	
10	Asn	Asp	Val	Lys	Ile	Thr	Ala	Leu	Ser	Thr	Ser	Glu	Ser	Gln	Ile	Ile	35	40	45	
	Ser	His	Met	Leu	Arg	Leu	Leu	Ile	Glu	His	Asp	Thr	His	Gly	Lys	Ile	50	55	60	
15	Lys	Pro	Thr	Leu	Val	Asn	Asn	Leu	Gly	Ser	Ser	Thr	Ile	Gln	His	Asn	65	70	75	80
	Ala	Leu	Ile	Asn	Gly	Asp	Ala	Asn	Ile	Ser	Gly	Val	Arg	Tyr	Asn	Gly	85	90	95	
20	Thr	Asp	Leu	Thr	Gly	Ala	Leu	Lys	Glu	Ala	Pro	Ile	Lys	Asn	Pro	Lys	100	105	110	
	Lys	Ala	Met	Ile	Ala	Thr	Gln	Gln	Gly	Phe	Lys	Lys	Lys	Phe	Asp	Gln	115	120	125	
25	Thr	Phe	Phe	Asp	Ser	Tyr	Gly	Phe	Ala	Asn	Thr	Tyr	Ala	Phe	Met	Val	130	135	140	
	Thr	Lys	Glu	Thr	Ala	Lys	Lys	Tyr	His	Leu	Glu	Thr	Val	Ser	Asp	Leu	145	150	155	160
30	Ala	Lys	His	Ser	Lys	Asp	Leu	Arg	Leu	Gly	Met	Asp	Ser	Ser	Trp	Met	165	170	175	
	Asn	Arg	Lys	Gly	Asp	Gly	Tyr	Glu	Gly	Phe	Lys	Lys	Glu	Tyr	Gly	Phe	180	185	190	
35	Asp	Phe	Gly	Thr	Val	Arg	Pro	Met	Gln	Ile	Gly	Leu	Val	Tyr	Asp	Ala	195	200	205	
40	Leu	Asn	Ser	Glu	Lys	Leu	Asp	Val	Ala	Leu	Gly	Tyr	Ser	Thr	Asp	Gly	210	215	220	
	Arg	Ile	Ala	Ala	Tyr	Asp	Leu	Lys	Val	Leu	Lys	Asp	Asp	Lys	Gln	Phe	225	230	235	240
45	Phe	Pro	Pro	Tyr	Ala	Ala	Ser	Ala	Val	Ala	Thr	Asn	Glu	Leu	Leu	Arg	245	250	255	
	Gln	His	Pro	Glu	Leu	Lys	Thr	Thr	Ile	Asn	Lys	Leu	Thr	Gly	Lys	Ile	260	265	270	
50	Ser	Thr	Ser	Glu	Met	Gln	Arg	Leu	Asn	Tyr	Glu	Ala	Asp	Gly	Lys	Gly	275	280	285	
55	Lys	Glu	Pro	Ala	Val	Val	Ala	Glu	Glu	Phe	Leu	Lys	Lys	His	His	Tyr	290	295	300	

Phe Asp Lys Gln Lys Gly Gly His Lys
305 310

(2) INFORMATION FOR SEQ ID NO:5198:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 284 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5198:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala
1 5 10 15
 Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys
20 20 25 30
 Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr
25 35 40 45
 Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu
50 55 60
 Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala
30 65 70 75 80
 Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala
85 90 95
 Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp
35 100 105 110
 Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile
115 120 125
 Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys
40 130 135 140
 Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala
45 145 150 155 160
 Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp
165 170 175
 Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile
50 180 185 190
 Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala
195 200 205
 Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys
55 210 215 220

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Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
 225 230 235 240
 Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
 5 245 250 255
 Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu
 260 265 270
 Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
 10 275 280

(2) INFORMATION FOR SEQ ID NO:5199:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 284 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5199:

Met Lys Lys Leu Thr Thr Leu Leu Leu Ala Ser Thr Leu Leu Ile Ala
 1 5 10 15
 Ala Cys Gly Asn Asp Asp Ser Lys Lys Asp Asp Ser Lys Thr Ser Lys
 30 20 25 30
 Lys Asp Asp Gly Val Lys Ala Glu Leu Lys Gln Ala Thr Lys Ala Tyr
 35 35 40 45
 Asp Lys Tyr Thr Asp Glu Gln Leu Asn Glu Phe Leu Lys Gly Thr Glu
 50 55 60
 Lys Phe Val Lys Ala Ile Glu Asn Asn Asp Met Ala Gln Ala Lys Ala
 65 70 75 80
 Leu Tyr Pro Lys Val Arg Met Tyr Tyr Glu Arg Ser Glu Pro Val Ala
 40 85 90 95
 Glu Ala Phe Gly Asp Leu Asp Pro Lys Ile Asp Ala Arg Leu Ala Asp
 100 105 110
 Met Lys Glu Glu Lys Lys Glu Lys Glu Trp Ser Gly Tyr His Lys Ile
 45 115 120 125
 Glu Lys Ala Leu Tyr Glu Asp Lys Lys Ile Asp Asp Val Thr Lys Lys
 50 130 135 140
 Asp Ala Gln Gln Leu Leu Lys Asp Ala Lys Glu Leu His Ala Lys Ala
 145 150 155 160
 Asp Thr Leu Asp Ile Thr Pro Lys Leu Met Leu Gln Gly Ser Val Asp
 55 165 170 175

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Leu Leu Asn Glu Val Ala Thr Ser Lys Ile Thr Gly Glu Glu Glu Ile
180 185 190

5 Tyr Ser His Thr Asp Leu Tyr Asp Phe Lys Ala Asn Val Glu Gly Ala
195 200 205

Gln Lys Ile Tyr Asp Leu Phe Lys Pro Ile Leu Glu Lys Lys Asp Lys
210 215 220

10 Lys Leu Ser Asp Asp Ile Gln Met Asn Phe Asp Lys Val Asn Gln Leu
225 230 235 240

Leu Asp Lys Tyr Lys Asp Asn Asn Gly Gly Tyr Glu Ser Phe Glu Lys
245 250 255

15 Val Ser Lys Lys Asp Arg Lys Ala Phe Ala Asp Ala Val Asn Ala Leu
260 265 270

Gly Glu Pro Leu Ser Lys Met Ala Val Ile Thr Glu
275 280

(2) INFORMATION FOR SEQ ID NO:5200:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 208 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5200:

Met Lys Phe Lys Ala Ile Val Ala Ile Thr Leu Ser Leu Ser Leu Leu
1 5 10 15

Thr Ala Cys Gly Ala Asn Gln His Lys Glu Asn Ser Ser Lys Ser Asn
20 25 30

40 Asp Thr Asn Lys Lys Thr Gln Gln Thr Asp Asn Thr Thr Gln Ser Asn
35 40 45

Thr Glu Lys Gln Met Thr Pro Gln Glu Ala Glu Asp Ile Val Arg Asn
50 55 60

45 Asp Tyr Lys Ala Arg Gly Val Asn Glu Tyr Gln Thr Leu Asn Tyr Lys
65 70 75 80

Thr Asn Leu Glu Arg Ser Asn Glu His Glu Tyr Tyr Val Glu His Leu
85 90 95

50 Val Arg Asp Ala Val Gly Thr Pro Leu Lys Arg Cys Ala Ile Val Asn
100 105 110

Arg His Asn Gly Thr Ile Ile Asn Ile Phe Asp Asp Met Ser Glu Lys
115 120 125

55

Asp Lys Glu Glu Phe Glu Ala Phe Lys Lys Arg Ser Pro Lys Tyr Asn
 130 135 140
 5 Pro Gly Met Asn Asn His Asp Glu Thr Asp Gly Glu Ser Glu Asp Ile
 145 150 155 160
 Gln His His Asp Ile Asp Asn Asn Lys Ala Ile Gln Asn Asp Ile Pro
 165 170 175
 10 Asp Gln Lys Val Asp Asp Lys Asn Asp Lys Asn Ala Val Asn Lys Glu
 180 185 190
 Glu Lys His Asp Asn Gly Ala Asn Asn Ser Glu Glu Thr Lys Val Lys
 195 200 205

(2) INFORMATION FOR SEQ ID NO:5201:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5201:

30 Met Leu Lys Gly Cys Gly Gly Cys Leu Ile Ser Phe Ile Leu Leu Ile
 1 5 10 15
 Ile Leu Leu Ser Ala Cys Ser Met Met Phe Ser Asn Asn Asp Asn Ser
 20 25 30
 35 Thr Asn Asn Gln Ser Ser Lys Thr Gln Leu Thr Gln Lys Asp Glu Asn
 35 40 45
 Lys Asn Glu Asp Lys Pro Glu Glu Lys Ser Glu Thr Ala Thr Asp Glu
 50 55 60
 40 Asp Leu Gln Ser Thr Glu Glu Val Pro Ala Asn Glu Asn Thr Glu Asn
 65 70 75 80
 Asn Gln His Glu Ile Asp Glu Ile Thr Thr Lys Asp Gln Ser Asp Asp
 85 90 95
 45 Asp Ile Asn Thr Pro Asn Val Ala Glu Asp Lys Ser Gln Asp Asp Leu
 100 105 110
 Lys Asp Asp Leu Lys Glu Lys Gln Gln Ser Ser Asn His His Gln Ser
 115 120 125
 50 Thr Gln Pro Lys Thr Ser Pro Ser Thr Glu Thr Asn Thr Gln Gln Ser
 130 135 140
 55 Phe Ala Asn Cys Lys Gln Leu Arg Gln Val Tyr Pro Asn Gly Val Thr

Ala Asp His Pro Ala Tyr Arg Pro His Leu Asp Arg Asp Lys Asp Lys
 165 170 175

5 Arg Ala Cys Glu Pro Asp Lys Tyr
 180

(2) INFORMATION FOR SEQ ID NO:5202:

10 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 208 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5202:

Met Lys Lys Arg Leu Leu Leu Ser Thr Phe Leu Ala Ser Thr Leu Ile
 1 5 10 15

Leu Thr Gly Cys Ala Ser Asp Gln Ser Asp Asn Glu Asp His His Thr
 25 20 25 30

Ser Thr Gly Ile His Ala Pro Lys Ser Ala Lys Lys Leu Glu Thr Lys
 35 40 45

Asp Ile Phe Xaa Ser Asp Lys Lys Asn Ser Asp Ile Ser Asp Ala Glu
 30 50 55 60

Met Lys Gln Ala Ile Glu Lys Tyr Leu Ser Val Asn Ser Asp Ile Leu
 65 70 75 80

Asp Asn Lys Tyr Ile Met Gln His Lys Leu Asp Lys Gln Ile Asp Ser
 35 85 90 95

Gln Thr Lys Val Thr Glu Lys Gln Ala Glu Thr Leu Ser His Leu Ser
 100 105 110

Asn Leu Ala Val Lys Asn Asp Leu His Phe Lys Lys Phe Val Thr Glu
 40 115 120 125

Asn Asn Ile Pro Lys Glu Tyr Lys Lys Pro Val Glu Leu Met Met Asn
 45 130 135 140

Tyr Phe Lys Ala Leu Asn Ser Thr Ile Ala Asn Val Asp Glu Asp Ile
 145 150 155 160

Glu Lys Leu Ser Tyr Gln Pro Gln Asn Lys Ile Asn Val Val Asp Val
 50 165 170 175

Pro Thr Lys Tyr Ala Gly Asp Val Asn Lys Lys Gln Gln Asp Lys Ile
 180 185 190

Lys Asp Phe Leu Lys Ser Lys Gly Ile Lys Ser Asp Val Ile Asp Lys
 55

(2) INFORMATION FOR SEQ ID NO:5203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5203:

Met Lys Ser Lys Ile Tyr Ile Leu Leu Leu Xaa Leu Ile Phe Leu Ser
 1 5 10 15

Ala Cys Ala Asn Thr Arg His Ser Glu Ser Asp Lys Asn Val Leu Thr
 20 25 30

Val Tyr Ser Pro Tyr Gln Ser Asn Leu Ile Arg Pro Ile Leu Asn Glu
 35 40 45

Xaa Glu Lys Gln Glu His Val Lys Ile Glu Ile Lys His Gly Ser Thr
 50 55 60

Gln Val Leu Leu Ser Asn Leu His Asn Glu Asp Phe Ser Glu Arg Gly
 65 70 75 80

Asp Val Phe Met Gly Gly Val Leu Ser Glu Thr Ile Asp His Pro Glu
 85 90 95

Asp Phe Val Pro Tyr Gln Asp Thr Ser Val Thr Gln Gln Leu Glu Asp
 100 105 110

Tyr Arg Ser Asn Asn Lys Tyr Val Thr Ser Phe Leu Leu Met Pro Thr
 115 120 125

Val Ile Val Val Asn Ser Asp Leu Gln Gly Asp Ile Lys Ile Arg Gly
 130 135 140

Tyr Gln Asp Leu Leu Gln Pro Ile Leu Lys Gly Lys Ile Ala Tyr Ser
 145 150 155 160

Asn Pro Asn Thr Thr Thr Thr Gly Tyr Gln His Met Arg Ala Ile Tyr
 165 170 175

Ser Met His His Arg Val Ser Asp Val His Gln Phe Gln Asn His Ala
 180 185 190

Met Gln Leu Ser Lys Thr Ser Lys Val Ile Glu Asp Val Ala Lys Gly
 195 200 205

Lys Tyr Tyr Ala Gly Leu Ser Tyr Glu Gln Asp Ala Arg Thr Trp Lys
 210 215 220

	225		230		235		240
	Leu Asn Val Asp Gly Ile Ala Leu Val Lys Asn Ala His Pro His Pro						
		245			250		255
5	Lys Arg Lys Lys Leu Val Gln Tyr Leu Thr Ser Arg Ser Val Gln Gln						
		260			265		270
	Arg Leu Val Ala Glu Phe Asp Ala Lys Ser Ile						
10		275			280		

(2) INFORMATION FOR SEQ ID NO:5204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5204:

25	Met	Lys	Lys	Phe	Ile	Gly	Ser	Val	Leu	Ala	Thr	Thr	Leu	Ile	Leu	Gly	
	1				5					10					15		
	Gly	Cys	Ser	Thr	Met	Glu	Asn	Glu	Ser	Lys	Lys	Asp	Thr	Lys	Thr	Glu	
				20					25					30			
30	Thr	Lys	Ser	Val	Pro	Glu	Glu	Met	Glu	Ala	Ser	Lys	Tyr	Val	Gly	Gln	
			35					40					45				
	Gly	Phe	Gln	Pro	Pro	Ala	Glu	Lys	Asn	Ala	Ile	Glu	Phe	Ala	Lys	Lys	
		50					55					60					
35	His	Arg	Lys	Glu	Phe	Glu	Lys	Val	Gly	Glu	Gln	Phe	Phe	Lys	Asp	Asn	
	65					70					75					80	
	Phe	Gly	Leu	Lys	Val	Lys	Ala	Thr	Asn	Val	Val	Gly	Lys	Asp	Asp	Gly	
40					85					90					95		
	Val	Glu	Val	Tyr	Val	His	Cys	Glu	Asp	His	Gly	Ile	Val	Phe	Asn	Ala	
				100					105					110			
	Ser	Leu	Pro	Leu	Tyr	Lys	Asp	Ala	Ile	His	Gln	Lys	Gly	Ser	Met	Arg	
45			115					120					125				
	Ser	Asn	Asp	Asn	Gly	Asp	Asp	Met	Ser	Met	Met	Val	Gly	Thr	Val	Leu	
		130					135					140					
	Ser	Gly	Phe	Glu	Tyr	Arg	Ala	Gln	Lys	Glu	Lys	Tyr	Asp	Asn	Leu	Tyr	
50		145				150					155					160	
	Lys	Phe	Phe	Lys	Glu	Asn	Glu	Lys	Lys	Tyr	Gln	Tyr	Thr	Gly	Phe	Thr	
				165						170					175		

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	180	185	190
	Phe Tyr Ile Thr Tyr Ser Ser	Arg Ser Leu Lys Glu	Tyr Arg Lys Tyr
	195	200	205
5	Tyr Glu Pro Leu Ile Arg Lys Asn Asp Lys Glu Phe Lys Glu Gly Met		
	210	215	220
	Glu Arg Ala Arg Lys Glu Val Asn Tyr Ala Ala Asn Thr Asp Ala Val		
10	225	230	235 240
	Ala Thr Leu Phe Ser Thr Lys Lys Asn Phe Thr Lys Asp Asn Thr Val		
	245	250	255
	Asp Asp Val Ile Glu Leu Ser Asp Lys Leu Tyr Asn Leu Lys Asn Lys		
15	260	265	270
	Pro Asp Lys Ser Thr Ile Thr Ile Gln Ile Gly Lys Pro Thr Ile Asn		
	275	280	285
	Thr Lys Lys Ala Phe Tyr Asp Asp Asn Arg Pro Ile Glu Tyr Gly Val		
20	290	295	300
	His Ser Lys Asp Glu		
	305		

25 (2) INFORMATION FOR SEQ ID NO:5205:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 193 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5205:

40	Met Lys Lys Leu Val Ser Ile Val Gly Ala Thr Leu Leu Leu Ala Gly
	1 5 10 15
	Cys Gly Ser Gln Asn Leu Ala Pro Leu Glu Glu Lys Thr Thr Asp Leu
	20 25 30
45	Arg Glu Asp Asn His Gln Leu Lys Leu Asp Ile Gln Glu Leu Asn Gln
	35 40 45
	Gln Ile Ser Asp Ser Lys Ser Lys Ile Lys Gly Leu Glu Lys Asp Lys
	50 55 60
50	Glu Asn Ser Lys Lys Thr Ala Ser Asn Asn Thr Lys Ile Lys Leu Met
	65 70 75 80
	Asn Val Thr Ser Thr Tyr Tyr Asp Lys Val Ala Lys Ala Leu Lys Ser
55	85 90 95

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		100						105					110				
	Val	Gln	Ser	Lys	Leu	Asn	Gln	Ile	Ser	Asn	Asp	Ile	Gln	Ser	Ala	His	
			115					120					125				
5	Thr	Ser	Tyr	Lys	Asp	Ala	Ile	Asp	Gly	Leu	Ser	Leu	Ser	Asp	Asp	Asp	
		130					135					140					
	Lys	Lys	Thr	Ser	Lys	Asn	Ile	Asp	Lys	Leu	Asn	Ser	Asp	Leu	Asn	His	
10		145				150					155				160		
	Ala	Phe	Asp	Asp	Ile	Lys	Asn	Gly	Tyr	Gln	Asn	Lys	Asp	Lys	Lys	Gln	
					165					170					175		
	Leu	Thr	Lys	Gly	Gln	Gln	Ala	Leu	Ser	Lys	Leu	Asn	Leu	Asn	Ala	Lys	
15				180				185					190				
	Ser																

(2) INFORMATION FOR SEQ ID NO:5206:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 259 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5206:

	Met	Lys	Arg	Leu	Leu	Phe	Val	Met	Ile	Ala	Phe	Val	Phe	Ile	Leu	Ala	
35	1				5					10					15		
	Ala	Cys	Gly	Asn	Asn	Ser	Ser	Lys	Asp	Lys	Glu	Ala	Ser	Lys	Asp	Ser	
				20					25					30			
	Lys	Thr	Ile	Asn	Val	Gly	Thr	Glu	Gly	Thr	Tyr	Ala	Pro	Phe	Ser	Phe	
40			35					40					45				
	His	Asp	Lys	Asp	Gly	Lys	Leu	Thr	Gly	Tyr	Asp	Ile	Asp	Val	Ile	Lys	
		50					55					60					
	Ala	Val	Ala	Lys	Glu	Glu	Gly	Leu	Lys	Leu	Lys	Phe	Asn	Glu	Thr	Ser	
45		65				70					75				80		
	Trp	Asp	Ser	Met	Phe	Ala	Gly	Leu	Asp	Ala	Gly	Arg	Phe	Asp	Val	Ile	
				85						90					95		
	Ala	Asn	Gln	Val	Gly	Ile	Asn	Pro	Asp	Arg	Glu	Lys	Lys	Tyr	Lys	Phe	
50				100					105					110			
	Ser	Lys	Pro	Tyr	Thr	Phe	Ser	Ser	Ala	Val	Leu	Val	Ile	Arg	Glu	Asn	
55				115				120						125			

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	130	135	140
	Gln Thr Phe Thr Ser Asn Tyr Gly Lys Leu Ala Lys Asp Lys Gly Ala		
	145	150	155 160
5	Asp Ile Thr Lys Val Asp Gly Phe Asn Gln Ser Met Asp Leu Leu Leu		
		165 170	175
	Ser Lys Arg Val Asp Gly Thr Phe Asn Asp Ser Leu Ser Tyr Leu Asp		
10		180 185	190
	Tyr Lys Lys Gln Lys Pro Asn Ala Lys Ile Lys Ala Ile Lys Gly Asn		
		195 200	205
	Ala Glu Gln Ser Arg Ser Ala Phe Ala Phe Ser Lys Lys Ala Asp Asp		
15		210 215	220
	Glu Thr Val Gln Lys Phe Asn Asp Gly Leu Lys Lys Ile Glu Glu Asn		
	225	230 235	240
20	Gly Glu Leu Ala Lys Ile Gly Lys Lys Trp Phe Gly Gln Asp Val Ser		
		245 250	255
	Lys Ser Lys		

25 (2) INFORMATION FOR SEQ ID NO:5207:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 203 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5207:

40	Met Gly Val His Ser Met Lys Leu Lys Arg Leu Phe Ala Val Val Ile	
	1	5 10 15
	Ala Met Leu Leu Val Leu Ala Gly Cys Ser Asn Ser Asn Asp Asn Asn	
		20 25 30
45	Glu Ser Lys Lys Asp Asp Ala Asp Asn Gly Lys Lys Gln Glu Ile Gln	
		35 40 45
	Val Ala Ala Ala Ala Ser Leu Thr Asp Val Thr Lys Lys Leu Ala Ser	
		50 55 60
50	Glu Phe Lys Lys Glu His Lys Asn Ala Asp Ile Lys Phe Asn Tyr Gly	
		65 70 75 80
	Gly Ser Gly Ala Leu Arg Lys Gln Ile Glu Ser Gly Ala Pro Val Asp	
		85 90 95

55

100 105 110
 Asn Lys Ala His Asp Thr Tyr Lys Tyr Ala Lys Asn Ser Leu Val Leu
 115 120 125
 5
 Ile Gly Asp Lys Asp Ser Asn Tyr Thr Ser Val Lys Asp Leu Lys Asp
 130 135 140
 Asn Asp Lys Leu Ala Leu Gly Glu Val Lys Thr Val Pro Ala Gly Lys
 145 150 155 160
 10
 Tyr Ala Lys Gln Tyr Leu Asp Asn Asn Asn Leu Phe Lys Glu Val Glu
 165 170 175
 Ser Xaa Ile Val Tyr Ala Lys Asp Val Lys Gln Val Leu Asn Tyr Val
 180 185 190
 15
 Xaa Lys Gly Asn Ala Lys Gln Gly Phe Val Tyr
 195 200

(2) INFORMATION FOR SEQ ID NO:5208:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5208:

Met Lys Lys Trp Gln Phe Val Gly Thr Thr Ala Leu Gly Ala Thr Leu
 1 5 10 15
 35
 Leu Leu Gly Ala Cys Gly Gly Gly Asn Gly Gly Ser Gly Asn Ser Asp
 20 25 30
 40
 Leu Lys Gly Glu Ala Lys Gly Asp Gly Ser Ser Thr Val Ala Pro Ile
 35 40 45
 Val Glu Lys Leu Asn Glu Lys Trp Ala Gln Asp His Ser Asp Ala Lys
 50 55 60
 45
 Ile Ser Ala Gly Gln Ala Gly Thr Gly Ala Gly Phe Gln Lys Phe Ile
 65 70 75 80
 Ala Gly Asp Ile Asp Phe Ala Asp Ala Ser Arg Pro Ile Lys Asp Glu
 85 90 95
 50
 Glu Lys Gln Lys Leu Gln Asp Lys Asn Ile Lys Tyr Lys Glu Phe Lys
 100 105 110
 Ile Ala Gln Asp Gly Val Thr Val Ala Val Asn Lys Glu Asn Asp Phe
 115 120 125
 55

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	130		135		140												
	Ala	Lys	Thr	Trp	Lys	Asp	Val	Asn	Ser	Lys	Trp	Pro	Asp	Lys	Lys	Ile	
	145					150					155					160	
5	Asn	Ala	Val	Ser	Pro	Asn	Ser	Ser	His	Gly	Thr	Tyr	Asp	Phe	Phe	Glu	
					165					170					175		
	Asn	Glu	Val	Met	Asn	Lys	Glu	Asp	Ile	Lys	Ala	Glu	Lys	Asn	Ala	Asp	
10				180					185					190			
	Thr	Asn	Ala	Ile	Val	Ser	Ser	Val	Thr	Lys	Asn	Lys	Glu	Gly	Ile	Gly	
		195						200					205				
	Tyr	Phe	Gly	Tyr	Asn	Phe	Tyr	Val	Gln	Asn	Lys	Asp	Lys	Leu	Lys	Glu	
15		210					215					220					
	Val	Lys	Ile	Lys	Asp	Glu	Asn	Gly	Lys	Ala	Thr	Glu	Pro	Thr	Lys	Lys	
	225				230						235					240	
	Thr	Ile	Gln	Asp	Asn	Ser	Tyr	Ala	Leu	Ser	Arg	Pro	Leu	Phe	Ile	Tyr	
20					245					250					255		
	Val	Asn	Glu	Lys	Ala	Leu	Lys	Asp	Asn	Lys	Val	Met	Ser	Glu	Phe	Ile	
				260					265					270			
25	Lys	Phe	Val	Leu	Glu	Asp	Lys	Gly	Lys	Ala	Ala	Glu	Glu	Ala	Gly	Tyr	
		275						280					285				
	Val	Ala	Ala	Pro	Glu	Lys	Thr	Tyr	Lys	Ser	Gln	Leu	Asp	Asp	Leu	Lys	
		290					295					300					
30	Ala	Phe	Ile	Asp	Lys	Asn	Gln	Lys	Ser	Asp	Asp	Lys	Lys	Ser	Asp	Asp	
	305					310				315						320	
	Lys	Lys	Ser	Glu	Asp	Lys	Lys										
35					325												

(2) INFORMATION FOR SEQ ID NO:5209:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 324 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5209:

Met	Lys	Arg	Leu	Ser	Ile	Ile	Val	Ile	Ile	Gly	Ile	Phe	Ile	Ile	Thr
1				5					10					15	
Gly	Cys	Asp	Trp	Gln	Arg	Thr	Ser	Lys	Glu	Arg	Ser	Lys	Asn	Ala	Gln
			20					25					30		

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	35	40	45
5	Asn Leu Met Met Thr Lys Lys Leu Leu Ser Gln Tyr Asn His Pro Lys 50 55 60		
	Tyr Lys Leu Glu Leu Val Lys Phe Asn Asn Trp Pro Asp Leu Met Asp 65 70 75 80		
10	Ala Leu Asn Ser Gly Arg Ile Asp Gly Ala Ser Thr Leu Ile Glu Leu 85 90 95		
	Ala Met Lys Ser Lys Gln Lys Gly Ser Asn Ile Lys Ala Val Ala Leu 100 105 110		
15	Gly His His Glu Gly Asn Val Ile Met Gly Gln Lys Gly Met His Leu 115 120 125		
	Asn Glu Phe Asn Asn Asn Gly Asp Asp Tyr His Phe Gly Ile Pro His 130 135 140		
20	Arg Tyr Ser Thr His Tyr Leu Leu Leu Glu Glu Leu Arg Lys Gln Leu 145 150 155 160		
	Lys Ile Lys Pro Gly His Phe Ser Tyr His Glu Met Ser Pro Ala Glu 165 170 175		
25	Met Pro Ala Ala Leu Ser Glu His Arg Ile Thr Gly Tyr Ser Val Ala 180 185 190		
	Glu Pro Phe Gly Ala Leu Gly Glu Lys Leu Gly Lys Gly Lys Thr Leu 195 200 205		
30	Lys His Gly Asp Asp Val Ile Pro Asp Ala Tyr Cys Cys Val Leu Val 210 215 220		
	Leu Arg Gly Glu Leu Leu Asp Gln His Lys Asp Val Ala Gln Ala Phe 225 230 235 240		
35	Val Gln Asp Tyr Lys Lys Ser Gly Phe Lys Met Asn Asp Arg Lys Gln 245 250 255		
	Ser Val Asp Ile Met Thr His His Phe Lys Gln Ser Arg Asp Val Leu 260 265 270		
40	Thr Gln Ser Ala Ala Trp Thr Ser Tyr Gly Asp Leu Thr Ile Lys Pro 275 280 285		
	Ser Gly Tyr Gln Glu Ile Thr Thr Leu Val Lys Gln His His Leu Phe 290 295 300		
45	Asn Pro Pro Ala Tyr Asp Asp Phe Val Glu Pro Ser Leu Tyr Lys Glu 305 310 315 320		
50	Ala Ser Arg Ser		

(2) INFORMATION FOR SEQ ID NO:5210:

55 (i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5210:

Met Lys Lys Thr Leu Gly Cys Leu Leu Leu Ile Met Leu Leu Val Val
 1 5 10 15
 Ala Gly Cys Ser Phe Gly Gly Asn His Lys Leu Ser Ser Lys Lys Ser
 15 20 25 30
 Glu Glu Ser Lys Gln Glu Thr Val Lys Lys Glu Ser Glu Glu Glu Lys
 35 40 45
 Asp Pro Asp Leu Glu Lys Tyr Glu Glu Ile Glu Lys Lys Met Lys Gly
 20 50 55 60
 Ile Lys Asp Ala Pro Ser Leu Asp Lys Leu Asp Pro Leu Met Thr Glu
 65 70 75 80
 Lys Ser Phe Thr Asn Ser Lys Gly Ile Gln Gly Trp Lys Asp Tyr Lys
 25 85 90 95
 Glu Leu Met Gly Lys Val Glu Leu Ala Asp Tyr Arg Phe Thr Lys Asp
 100 105 110
 Ser Lys Gly Ser Ser Ile Lys Asp Val Asp Ala Phe Phe Lys Gly Lys
 30 115 120 125
 Lys Gly Ile Lys Arg Lys Val Ile Glu Thr His Asp Asp Val Lys Gln
 35 130 135 140
 Val Asp Tyr Trp
 145

(2) INFORMATION FOR SEQ ID NO:5211:

40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 45 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5211:

Trp Pro Cys Ala Thr Xaa Gln Glx Glu Trp Trp Ser Arg His Xaa Trp
 1 5 10 15
 55

20

25

30

His

5

(2) INFORMATION FOR SEQ ID NO:5212:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 490 amino acids

10

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5212:

20

Met Ser Ile Ile Met Glu Val Ala Thr Met Gln Ala Lys Leu Thr Lys
1 5 10 15Asn Glu Phe Ile Glu Trp Leu Lys Thr Ser Glu Gly Lys Gln Phe Asn
20 25 30

25

Val Asp Leu Trp Tyr Gly Phe Gln Cys Phe Asp Tyr Ala Asn Ala Gly
35 40 45Trp Lys Val Leu Phe Gly Leu Leu Leu Lys Gly Leu Gly Ala Lys Asp
50 55 60

30

Ile Pro Phe Ala Asn Asn Phe Asp Gly Leu Ala Thr Val Tyr Gln Asn
65 70 75 80Thr Pro Asp Phe Leu Ala Gln Pro Gly Asp Met Val Val Phe Gly Ser
85 90 95

35

Asn Tyr Gly Ala Gly Tyr Gly His Val Ala Trp Val Ile Glu Ala Thr
100 105 110Leu Asp Tyr Ile Ile Val Tyr Glu Gln Asn Trp Leu Gly Gly Gly Trp
115 120 125

40

Thr Asp Gly Ile Glu Gln Pro Gly Trp Gly Trp Glu Lys Val Thr Arg
130 135 140Arg Gln His Ala Tyr Asp Phe Pro Met Trp Phe Ile Arg Pro Asn Phe
145 150 155 160

45

Lys Ser Glu Thr Ala Pro Arg Ser Val Gln Ser Pro Thr Gln Ala Pro
165 170 175Lys Lys Glu Thr Ala Lys Pro Gln Pro Lys Ala Val Glu Leu Lys Ile
180 185 190

50

Ile Lys Asp Val Val Lys Gly Tyr Asp Leu Pro Lys Arg Gly Ser Asn
195 200 205

55

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	210	215	220
	Ala Glu Ala Tyr Arg Asn Gly Leu Val Asn Ala Pro Leu Ser Arg Leu		
	225	230	235 240
5	Glu Ala Gly Ile Ala His Ser Tyr Val Ser Gly Asn Thr Val Trp Gln		
		245	250 255
	Ala Leu Asp Glu Ser Gln Val Gly Trp His Thr Ala Asn Gln Ile Gly		
10		260	265 270
	Asn Lys Tyr Tyr Tyr Gly Ile Glu Val Cys Gln Ser Met Gly Ala Asp		
		275	280 285
15	Asn Ala Thr Phe Leu Lys Asn Glu Gln Ala Thr Phe Gln Glu Cys Ala		
		290	295 300
	Arg Leu Leu Lys Lys Trp Gly Leu Pro Ala Asn Arg Asn Thr Ile Arg		
		305	310 315 320
20	Leu His Asn Glu Phe Thr Ser Thr Ser Cys Pro His Arg Ser Ser Val		
		325	330 335
	Leu His Thr Gly Phe Asp Pro Val Thr Arg Gly Leu Leu Pro Glu Asp		
		340	345 350
25	Lys Arg Leu Gln Leu Lys Asp Tyr Phe Ile Lys Gln Ile Arg Ala Tyr		
		355	360 365
	Met Asp Gly Lys Ile Pro Val Ala Thr Val Ser Asn Glu Ser Ser Ala		
		370	375 380
30	Ser Ser Asn Thr Val Lys Pro Val Ala Ser Ala Trp Lys Arg Asn Lys		
		385	390 395 400
	Tyr Gly Thr Tyr Tyr Met Glu Glu Ser Ala Arg Phe Thr Asn Gly Asn		
		405	410 415
35	Gln Pro Ile Thr Val Arg Lys Val Gly Pro Phe Leu Ser Cys Pro Val		
		420	425 430
	Gly Tyr Gln Phe Gln Pro Gly Gly Tyr Cys Asp Tyr Thr Glu Val Met		
40		435	440 445
	Leu Gln Asp Gly His Val Trp Val Gly Tyr Thr Trp Glu Gly Gln Arg		
		450	455 460
45	Tyr Tyr Leu Pro Ile Arg Thr Trp Asn Gly Ser Ala Pro Pro Asn Gln		
		465	470 475 480
	Ile Leu Gly Asp Leu Trp Gly Glu Ile Ser		
		485	490

50 (2) INFORMATION FOR SEQ ID NO:5213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

55

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5213:

Gly Asp Lys Met Asn Lys Ile Ser Lys Tyr Ile Ala Ile Ala Ser Leu
 1 5 10 15
 Ser Val Ala Val Thr Val Ser Ala Pro Gln Thr Thr Asn Ser Thr Ala
 20 25 30
 Phe Ala Lys Ser Ser Ala Glu Val Gln Gln Thr Gln Gln Ala Ser Ile
 35 40 45
 Pro Ala Ser Gln Lys Ala Asn Leu Gly Asn Gln Asn Ile Met Ala Val
 50 55 60
 Ala Trp Tyr Gln Asn Ser Ala Glu Ala Lys Ala Leu Tyr Leu Gln Gly
 65 70 75 80
 Tyr Asn Ser Ala Lys Thr Gln Leu Asp Lys Glu Ile Lys Lys Asn Lys
 85 90 95
 Gly Lys His Lys Leu Ala Ile Ala Leu Asp Leu Asp Glu Thr Val Leu
 100 105 110
 Asp Asn Ser Pro Tyr Gln Gly Tyr Ala Ser Ile His Asn Lys Pro Phe
 115 120 125
 Pro Glu Gly Trp His Glu Trp Val Gln Ala Ala Lys Ala Lys Pro Val
 130 135 140
 Tyr Gly Ala Lys Glu Phe Leu Lys Tyr Ala Asp Lys Lys Gly Val Asp
 145 150 155 160
 Ile Tyr Tyr Ile Ser Asp Arg Asp Lys Glu Lys Asp Leu Lys Ala Thr
 165 170 175
 Gln Lys Asn Leu Lys Gln Gln Gly Ile Pro Gln Ala Lys Lys Ser His
 180 185 190
 Ile Leu Leu Lys Gly Lys Asp Asp Lys Ser Lys Glu Ser Arg Arg Gln
 195 200 205
 Met Val Gln Lys Asp His Lys Leu Val Met Leu Phe Gly Asp Asn Leu
 210 215 220
 Leu Asp Phe Thr Asp Pro Lys Glu Ala Thr Ala Glu Ser Arg Glu Ala
 225 230 235 240
 Leu Ile Glu Lys His Lys Asp Asp Phe Gly Lys Lys Tyr Ile Ile Phe
 245 250 255
 Pro Asn Pro Met Tyr Gly Ser Trp Glu Ala Thr Ile Tyr Asn Asn Asn
 260 265 270

275

280

285

Lys Gln Phe Asp Pro Lys Thr Gly Glu Val Lys
290 295

(2) INFORMATION FOR SEQ ID NO:5214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5214:

Leu Asn Lys Cys Lys Ile Ile Ile Trp Arg Ile Ile Asn Met Lys Asn
1 5 10 15
Lys Leu Ile Ala Lys Ser Leu Leu Thr Leu Ala Ala Ile Gly Ile Thr
20 25 30
Thr Thr Thr Ile Ala Ser Thr Ala Asp Ala Ser Glu Gly Tyr Gly Pro
35 40 45
Arg Glu Lys Lys Pro Val Ser Ile Asn His Asn Ile Val Glu Tyr Asn
50 55 60
Asp Gly Thr Phe Lys Tyr Gln Ser Arg Pro Lys Phe Asn Ser Thr Pro
65 70 75 80
Lys Tyr Ile Lys Phe Lys His Asp Tyr Asn Ile Leu Glu Phe Asn Asp
85 90 95
Gly Thr Phe Glu Tyr Gly Ala Arg Pro Gln Phe Asn Lys Pro Ala Ala
100 105 110
Lys Thr Asp Ala Thr Ile Lys Lys Glu Gln Lys Leu Ile Gln Ala Gln
115 120 125
Asn Leu Val Arg Glu Phe Glu Lys Thr His Thr Val Ser Ala His Arg
130 135 140
Lys Ala Gln Lys Ala Val Asn Leu Val Ser Phe Glu Tyr Lys Val Lys
145 150 155 160
Lys Met Val Leu Gln Glu Arg Ile Asp Asn Val Leu Lys Gln Gly Leu
165 170 175
Val Lys

(2) INFORMATION FOR SEQ ID NO:5215:

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: protein

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5215:

Lys	Glu	Arg	Val	Leu	Met	Lys	Lys	Leu	Leu	Thr	Ala	Ser	Ile	Ile	Ala	1	5	10	15
Cys	Ser	Val	Val	Met	Gly	Val	Gly	Leu	Val	Asn	Thr	Ser	Ala	Glu	Ala	20	25	30	
Ala	Ser	Gly	Asn	Ser	Ile	Asp	Thr	Val	Lys	Gln	Leu	Ile	Lys	Gly	Asp	35	40	45	
Gln	Ser	Leu	Glu	Asn	Val	Lys	Ile	Gly	Glu	Ser	Ile	Lys	Asp	Val	Leu	50	55	60	
Thr	Lys	Tyr	Lys	Asn	Pro	Met	Tyr	Ser	Tyr	Asn	Glu	Asp	Gly	Thr	Glu	65	70	75	80
His	Tyr	Tyr	Glu	Phe	His	Thr	Lys	Lys	Gly	Met	Leu	Leu	Val	Thr	Thr	85	90	95	
Asp	Gly	Lys	Lys	Asn	Asn	Gly	Lys	Val	Thr	His	Ile	Ser	Met	Met	Tyr	100	105	110	
Asn	Asp	Ala	Asn	Gly	Pro	Thr	Tyr	Gln	Ala	Val	Lys	Asn	Tyr	Val	Gly	115	120	125	
Lys	Ala	Val	Thr	His	Thr	Glu	Tyr	Ser	Lys	Val	Ala	Gly	Asn	Phe	Gly	130	135	140	
Tyr	Ile	Glu	Lys	Gly	Lys	Thr	Thr	Tyr	Gln	Phe	Ala	Ser	Ala	Pro	Lys	145	150	155	160
Asp	Lys	Asn	Ile	Lys	Leu	Tyr	Arg	Ile	Asp	Leu	Glu	Lys	165	170					

(2) INFORMATION FOR SEQ ID NO:5216:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5216:

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1 5 10 15
 Asn Glu Asp Gly Ser Lys Lys Lys Met Ser Thr Thr Ala Lys Val Val
 20 25 30
 5 Ser Ile Ala Thr Val Leu Leu Leu Leu Gly Gly Leu Val Phe Ala Ile
 35 40 45
 10 Phe Ala Tyr Val Asp His Ser Asn Lys Ala Lys Glu Arg Met Leu Asn
 50 55 60
 Glu Gln Lys Gln Glu Gln Lys Glu Lys Arg Gln Lys Glu Asn Ala Glu
 65 70 75 80
 15 Lys Glu Arg Lys Lys Lys Gln Gln Glu Glu Lys Glu Gln Asn Glu Leu
 85 90 95
 Asp Ser Gln Ala Asn Gln Tyr Gln Gln Leu Pro Gln Gln Asn Gln Tyr
 100 105 110
 20 Gln Tyr Val Pro Pro Gln Gln Gln Ala Pro Thr Lys Gln Arg Pro Ala
 115 120 125
 Lys Glu Glu Asn Asp Asp Lys Ala Ser Lys Asp Glu Ser Lys Asp Lys
 130 135 140
 25 Asp Asp Lys Ala Ser Gln Asp Lys Ser Asp Asp Asn Gln Lys Lys Thr
 145 150 155 160
 30 Asp Asp Asn Lys Gln Pro Ala
 165

(2) INFORMATION FOR SEQ ID NO:5217:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5217:

45 Met Lys Arg Asn Phe Pro Lys Leu Ile Ala Leu Ser Leu Ile Phe Ser
 1 5 10 15
 50 Leu Ser Val Thr Pro Ile Ala Asn Ala Glu Ser Asn Ser Asn Ile Lys
 20 25 30
 Ala Lys Asp Lys Lys His Val Gln Val Asn Val Glu Asp Lys Ser Val
 35 40 45
 55 Pro Thr Asp Val Arg Asn Leu Ala Gln Lys Asp Tyr Leu Ser Tyr Val
 50 55 60

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```

5      65      70      75      80
      Gly Glu Pro Phe Lys Ile Tyr Lys Phe Asn Lys Lys Ser Asp Gly Asn
          85          90          95
      Tyr Tyr Phe Pro Val Leu Asn Thr Glu Gly Asn Ile Asp Tyr Ile Val
          100          105          110
      Thr Ile Ser
          115
10

```

(2) INFORMATION FOR SEQ ID NO:5218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5218:

	Asn	Phe	Lys	Met	Gln	Glu	Val	Lys	Tyr	Met	Thr	Glu	Ile	Thr	Phe	Lys
	1				5					10						15
30	Gly	Gly	Pro	Ile	His	Leu	Lys	Gly	Gln	Gln	Ile	Asn	Glu	Gly	Asp	Phe
				20					25					30		
	Ala	Pro	Asp	Phe	Thr	Val	Leu	Asp	Asn	Asp	Leu	Asn	Gln	Val	Thr	Leu
			35					40					45			
35	Ala	Asp	Tyr	Ala	Gly	Lys	Lys	Lys	Leu	Ile	Ser	Val	Val	Pro	Ser	Ile
		50					55					60				
	Asp	Thr	Gly	Val	Cys	Asp	Gln	Gln	Thr	Arg	Lys	Phe	Asn	Ser	Asp	Ala
	65					70					75					80
40	Ser	Lys	Glu	Glu	Gly	Ile	Val	Leu	Thr	Ile	Ser	Ala	Asp	Leu	Pro	Phe
					85					90					95	
	Ala	Gln	Lys	Arg	Trp	Cys	Ala	Ser	Ala	Gly	Leu	Asp	Asn	Val	Ile	Thr
				100					105					110		
45	Leu	Ser	Asp	His	Arg	Asp	Leu	Ser	Phe	Gly	Glu	Asn	Tyr	Gly	Val	Val
			115					120					125			
	Met	Glu	Glu	Leu	Arg	Leu	Leu	Ala	Arg	Ala	Val	Phe	Val	Leu	Asp	Ala
50		130					135					140				
	Asp	Asn	Lys	Val	Val	Tyr	Lys	Glu	Ile	Val	Ser	Glu	Gly	Thr	Asp	Phe
	145					150					155					160
55	Pro	Asp	Phe	Asp	Ala	Ala	Leu	Ala	Ala	Tyr	Lys	Asn	Ile			
					165					170						

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5219:

Ile Glu Ser Arg Phe Ile Met Ala Lys Ile Asn Phe Asp Ala Ala Thr
 1 5 10 15
 Lys Gly Asn Pro Gly Ile Ser Thr Cys Ala Ile Val Ile Lys Glu Asp
 20 25 30
 Glu Gln His Tyr Thr Tyr Thr His Glu Leu Gly Glu Met Asp Asn His
 35 40 45
 Thr Ala Glu Trp Ala Ala Cys Ile Tyr Ala Leu Glu His Ala Arg Glu
 50 55 60
 Leu Asn Val Gln Asn Ala Leu Leu Tyr Thr Asp Ser Lys Leu Ile Ala
 65 70 75 80
 Asp Ser Ile Glu Ala Gly Tyr Val Lys Asn Ala Asn Phe Lys Pro Tyr
 85 90 95
 Phe Asp Gln Ile Glu Ile Phe Glu Lys Asp Phe Asp Leu Leu Phe Val
 100 105 110
 Lys Trp Ile Pro Arg Glu Gln Asn Lys Glu Ala Asn Gln His Ala Gln
 115 120 125
 Gln Ala Leu Tyr Lys Leu Ile Lys Lys Asn Lys
 130 135

(2) INFORMATION FOR SEQ ID NO:5220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5220:

Met Pro Gly Thr Val Leu Asp Pro Gln Met Ile Lys Asn Glu Asp Val
 1 5 10 15

	20	25	30
5	Gly Val Asn Thr Ser Met Asp Trp Asp Arg Lys Tyr Pro Tyr Gly Asp 35 40 45		
	Thr Leu Arg Gly Ile Phe Gly Asp Val Ser Thr Pro Ala Glu Gly Ile 50 55 60		
10	Pro Lys Glu Leu Thr Glu His Tyr Leu Ser Lys Gly Tyr Ser Arg Asn 65 70 75 80		
	Asp Arg Val Gly Lys Ser Tyr Leu Glu Tyr Gln Tyr Glu Asp Val Leu 85 90 95		
15	Arg Gly Lys Lys Lys Glu Met Lys Tyr Thr Thr Asp Lys Ser Gly Lys 100 105 110		
	Val Thr Ser Ser Glu Val Leu Xaa Pro Gly Ala Arg Gly Gln Asp Leu 115 120 125		
20	Lys Leu Thr Ile Asp Ile Asp Leu Gln Lys Glu Val Glu Ala Leu Leu 130 135 140		
	Asp Lys Gln Ile Lys Lys Leu Ala Val Lys Val Pro Lys Ile Trp Ile 145 150 155 160		
25	Met Gln		

(2) INFORMATION FOR SEQ ID NO:5221:

30	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 311 amino acids
	(B) TYPE: amino acid
	(C) STRANDEDNESS: single
35	(D) TOPOLOGY: linear
	(ii) MOLECULE TYPE: protein
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5221:
	Ile Met Ala Tyr Asp Gly Leu Phe Thr Lys Lys Met Val Glu Ser Leu 1 5 10 15
45	Gln Phe Leu Thr Thr Gly Arg Val His Lys Ile Asn Gln Pro Asp Asn 20 25 30
	Asp Thr Ile Leu Met Val Val Arg Gln Asn Arg Gln Asn His Gln Leu 35 40 45
50	Leu Leu Ser Ile His Pro Asn Phe Ser Arg Leu Gln Leu Thr Thr Lys 50 55 60
	Lys Tyr Asp Asn Pro Phe Asn Pro Pro Met Phe Ala Arg Val Phe Arg 65 70 75 80

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	85	90	95
	Asp Arg Arg Ile Glu Ile Asp Ile Lys Ser Lys Asp Glu Ile Gly Asp		
	100	105	110
5	Thr Ile Tyr Arg Thr Val Ile Leu Glu Ile Met Gly Lys His Ser Asn		
	115	120	125
	Leu Ile Leu Val Asp Glu Asn Arg Lys Ile Ile Glu Gly Phe Lys His		
10	130	135	140
	Leu Thr Pro Asn Thr Asn His Tyr Arg Thr Val Met Pro Gly Phe Asn		
	145	150	155
	Tyr Glu Ala Pro Pro Thr Gln His Lys Ile Asn Pro Tyr Asp Ile Thr		
15	165	170	175
	Gly Ala Glu Val Leu Lys Tyr Ile Asp Phe Asn Ala Gly Asn Ile Ala		
	180	185	190
	Lys Gln Leu Leu Asn Gln Phe Glu Gly Phe Ser Pro Leu Ile Thr Asn		
20	195	200	205
	Glu Ile Val Ser Arg Arg Gln Phe Met Thr Ser Ser Thr Leu Pro Glu		
	210	215	220
25	Ala Phe Asp Glu Val Met Ala Glu Thr Lys Leu Pro Pro Thr Pro Ile		
	225	230	235
	Phe His Lys Asn His Glu Thr Gly Lys Glu Asp Phe Tyr Phe Ile Lys		
30	245	250	255
	Leu Asn Gln Phe Asn Asp Asp Thr Val Thr Tyr Asp Ser Leu Asn Asp		
	260	265	270
	Leu Leu Asp Arg Phe Tyr Asp Ala Arg Gly Glu Arg Glu Arg Val Lys		
35	275	280	285
	Gln Arg Ala Asn Asp Leu Val Arg Phe Val Gln Gln Gln Leu His Lys		
	290	295	300
40	Tyr Gln Asn Lys Leu Ala Ser		
	305	310	

(2) INFORMATION FOR SEQ ID NO:5222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5222:

	1		5		10		15
	Glu	Gln	Leu	Tyr	Gly	Glu	Leu
			20				25
	Thr	Ala	Asn	Ile	Tyr	Arg	Ile
5						30	Lys
	Gln	Gly	Asp	Lys	Glu	Val	Thr
			35			40	
	Ala	Leu	Asn	Tyr	Tyr	Thr	Asn
						45	Glu
	Val	Val	Ile	Pro	Leu	Asn	Pro
					55		
10	Thr	Lys	Ser	Pro	Ser	Ala	Asn
					60		Ala
	Gln	Tyr	Tyr	Lys	Gln	Tyr	Xaa
					70		
	Arg	Met	Lys	Thr	Arg	Xaa	Arg
					75		Glu
	Leu						80
15	Gln	His	Gln	Ile	Gln	Leu	Thr
					85		
	Lys	Asp	Asn	Ile	Asp	Tyr	Phe
					90		Ser
	Thr						95
	Ile	Glu	Gln	Gln	Leu	His	His
					100		
	Ile	Ser	Val	His	Asp	Ile	Asp
					105		Glu
20							110
	Arg	Asp	Glu	Leu	Ala	Glu	Gln
					115		
	Gly	Phe	Met	Lys	Gln	Arg	Lys
					120		Asn
	Gln						Gln
25	Thr	Lys	Lys	Lys	Lys	Ala	Gln
							130
	Ile	Gln	Leu	Gln	His	Tyr	Val
					135		Ser
	Thr						140
	Asp	Gly	Asp	Asp	Ile	Tyr	Val
					145		
	Gly	Lys	Asn	Asn	Lys	Gln	Asn
					150		Asp
	Tyr						155
30							160
	Leu	Thr	Asn	Lys	Lys	Ala	Lys
					165		
	Lys	Lys	Thr	His	Thr	Trp	Leu
					170		His
	Thr						175
	Asp	Ile	Pro	Gly	Ser	His	Val
					180		
	Val	Val	Ile	Phe	Asn	Asp	Ala
					185		Pro
	Ser						190
35							
	Thr	Thr	Ile	Lys	Glu	Ala	Ala
					195		
	Met	Leu	Ala	Gly	Tyr	Phe	Ser
					200		Lys
	Ala						205
	Gly	Asn	Ser	Gly	Gln	Ile	Pro
					210		
	Val	Asp	Tyr	Thr	Leu	Ile	Lys
					215		Asn
40							220
	His	Lys	Pro	Ser	Gly	Ala	Lys
					225		
	Pro	Gly	Phe	Val	Thr	Tyr	Asp
					230		Asn
	Gln						235
							240
45	Lys	Thr	Leu	Tyr	Ala		
					245		

(2) INFORMATION FOR SEQ ID NO:5223:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 99 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5223:

Tyr Ile Thr Asn Pro Gln Asn Pro Lys Ile Lys Ile Thr Gly Ile Ser
 1 5 10 15
 Leu Ser Ser Gly Val Gly Asn Phe Phe Ile Ile Thr Asn Gly Lys Arg
 20 25 30
 Ile Ile Val Ala Lys Ile Lys Arg Asn Ala Asp Asn Asp Ser Ala Leu
 35 40 45
 Lys Ser Phe Asn Ala Ile Phe Ile Ile Gly Asn Ala Asp Pro His Asn
 50 55 60
 Met Ile Val Asn Lys Tyr Asp Arg Lys Val Val Ser Arg Ser Leu Phe
 65 70 75 80
 Ile Asn Ile Ile Thr Pro Leu Ile Met Cys Phe Tyr Ile Lys Lys Tyr
 85 90 95
 Asp Leu Lys

(2) INFORMATION FOR SEQ ID NO:5224:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 131 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5224:

Glu Asn Val Leu Ala Lys Glu Tyr Ala Val Lys Tyr Asn Ala Val Glu
 1 5 10 15
 Ala Ile Gln His Arg Gly Glu Thr Val Thr Glu Gly Ser Ser Ser Asn
 20 25 30
 Ala Tyr Ala Ile Lys Asp Gly Val Ile Tyr Thr His Pro Ile Asn Asn
 35 40 45
 Tyr Ile Leu Asn Gly Ile Thr Arg Ile Val Ile Lys Lys Ile Ala Glu
 50 55 60
 Asp Tyr Asn Ile Pro Phe Lys Glu Glu Thr Phe Thr Val Asp Phe Leu
 65 70 75 80
 Lys Asn Ala Asp Glu Val Ile Val Ser Ser Thr Ser Ala Glu Val Thr
 85 90 95
 Pro Val Ile Lys Leu Asp Gly Glu Pro Val Asn Asp Gly Lys Val Gly
 100 105 110

115

120

125

His Ser Ile
130

5

(2) INFORMATION FOR SEQ ID NO:5225:

(i) SEQUENCE CHARACTERISTICS:

10

- (A) LENGTH: 540 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5225:

20

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn
1 5 10 15

25

Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile
20 25 30

Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr
35 40 45

30

Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala
50 55 60

Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln
65 70 75 80

35

Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro
85 90 95

Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly
100 105 110

40

Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp
115 120 125

Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala
130 135 140

45

Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala
145 150 155 160

50

Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln
165 170 175

Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala
180 185 190

55

Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp
195 200 205

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	210	215	220
5	Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly 225 230 235 240		
	Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn 245 250 255		
10	Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val 260 265 270		
	Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys 275 280 285		
15	Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr 290 295 300		
	Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp 305 310 315 320		
20	Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly 325 330 335		
	Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu 340 345 350		
25	Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr 355 360 365		
	Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly 370 375 380		
30	Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro 385 390 395 400		
	Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn 405 410 415		
	Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu 420 425 430		
40	Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr 435 440 445		
	Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr 450 455 460		
45	Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly 465 470 475 480		
	Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp 485 490 495		
50	Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr 500 505 510		
55	Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser 515 520 525		

530

535

540

(2) INFORMATION FOR SEQ ID NO:5226:

5

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 177 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5226:

20

Tyr Lys Glu Leu Ser His Gly Arg Leu Ile Gly Gly Thr Lys Met His
 1 5 10 15

Lys Lys Tyr Phe Ile Gly Thr Ser Ile Leu Ile Ala Val Phe Val Val
 20 25 30

Ile Phe Asp Gln Val Thr Lys Tyr Ile Ile Ala Thr Thr Met Lys Ile
 35 40 45

25

Gly Asp Ser Phe Glu Val Ile Pro His Phe Leu Asn Ile Thr Ser His
 50 55 60

30

Arg Asn Asn Gly Ala Ala Trp Gly Ile Leu Ser Gly Lys Met Thr Phe
 65 70 75 80

Phe Phe Ile Ile Thr Ile Ile Ile Leu Ile Ala Leu Val Tyr Phe Phe
 85 90 95

35

Ile Lys Asp Ala Gln Tyr Asn Leu Phe Met Gln Val Ala Ile Ser Leu
 100 105 110

Leu Phe Ala Gly Ala Leu Gly Asn Phe Ile Asp Arg Ile Leu Thr Gly
 115 120 125

40

Glu Val Val Asp Phe Ile Asp Thr Asn Ile Phe Gly Tyr Asp Phe Pro
 130 135 140

Ile Phe Asn Ile Ala Asp Ser Ser Leu Thr Ile Gly Val Ile Leu Ile
 145 150 155 160

45

Ile Ile Ala Leu Leu Lys Asp Thr Ser Asn Lys Lys Glu Lys Glu Val
 165 170 175

Lys

50

(2) INFORMATION FOR SEQ ID NO:5227:

55

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 209 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5227:

Ala Gly Lys Ser Ser Leu Ile Lys Ser Leu Ile Gly Glu Phe Asn Ala
1 5 10 15
Thr Gly Thr Lys Leu Leu Tyr Asn Lys Pro Ile Gln Gln Gln Leu Gln
20 25 30
His Ile Thr Tyr Ile Pro Gln Lys Ala His Ile Asp Leu Asp Phe Pro
35 40 45
Ile Ser Val Glu Gln Val Ile Leu Ser Gly Cys Tyr Lys Glu Ile Gly
50 55 60
Trp Phe Arg Arg Pro Asn Lys Ser Ala Arg Asp Lys Leu Lys Gln Leu
65 70 75 80
Leu Ser Asp Leu Glu Leu Glu Ser Leu Arg His Arg Gln Ile Ser Glu
85 90 95
Leu Ser Gly Gly Gln Leu Gln Arg Val Leu Val Ala Arg Ala Leu Met
100 105 110
Ser Xaa Ser Glu Val Tyr Phe Leu Asp Glu Pro Phe Val Gly Ile Asp
115 120 125
Phe Ser Ser Glu Lys Leu Ile Met Thr Lys Ile Glu Asn Leu Lys Gln
130 135 140
Gln Gly Lys Leu Ile Leu Ile Ile His His Asp Leu Ser Lys Ala Lys
145 150 155 160
Gln Tyr Phe Asp Arg Ile Ile Leu Leu Asn Gln Thr Leu Arg Tyr Phe
165 170 175
Gly Asp Ser Glu Glu Ala Met Ser Val Thr Arg Leu Asn Glu Thr Phe
180 185 190
Met Ser Ser Thr Asp Cys Ser Asp Pro Ser Gln Arg Ser Asn Ile Thr
195 200 205
Cys

45

(2) INFORMATION FOR SEQ ID NO:5228:

50

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 256 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5228:

5 Thr Phe Arg Ile Ile Phe Leu Leu Ser Ile Arg Lys Arg Ser Asn Arg
 1 5 10 15
 Thr His Val Ser Ile His Trp Ser Thr Val Asn Lys Glu Glu Ile Cys
 20 25 30
 10 Leu Arg Val Lys Asp Asn Leu Gln Gln Ile Ser Thr Gln Ile Asn Asp
 35 40 45
 Lys Ser Glu Lys Asn Asn Phe Ser Thr Lys Pro Asn Val Ile Ala Val
 50 55 60
 15 Thr Lys Tyr Val Thr Ile Glu Arg Ala Lys Glu Ala Tyr Glu Ala Gly
 65 70 75 80
 Ile Arg His Phe Gly Glu Asn Arg Leu Glu Gly Phe Phe Gln Lys Lys
 85 90 95
 20 Glu Ala Leu Pro Ser Asp Ala Val Ile His Phe Ile Gly Ser Leu Gln
 100 105 110
 Ser Arg Lys Val Lys Asp Val Ile Asn Asp Val Asp Tyr Phe His Ala
 115 120 125
 25 Leu Asp Arg Leu Ser Leu Ala Lys Glu Ile Asn Lys Arg Ala Glu His
 130 135 140
 Lys Ile Lys Cys Phe Leu Gln Val Asn Val Ser Gly Glu Ala Ser Lys
 145 150 155 160
 His Gly Ile Ala Leu Glu Asp Val Asp Gln Phe Ile Asp Asp Leu Lys
 165 170 175
 35 Lys Tyr Asp Lys Ile Glu Ile Val Gly Leu Met Thr Met Ala Pro Leu
 180 185 190
 Thr Asp Asp Glu Ala Tyr Ile Arg Ser Leu Phe Lys Gln Leu Arg Leu
 195 200 205
 40 Lys Lys Glu Glu Ile Gln Arg Leu Asn Leu Glu Tyr Ala Pro Cys Asp
 210 215 220
 Glu Leu Ser Met Gly Met Ser Asn Asp Tyr Leu Ile Ala Val Glu Glu
 225 230 235 240
 45 Gly Ala Thr Phe Val Arg Ile Gly Thr Lys Leu Val Gly Glu Glu Glu
 245 250 255
 50

(2) INFORMATION FOR SEQ ID NO:5229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 246 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5229:

10 Lys His Lys Leu Thr Ile Ile Thr Gly Gly Phe Phe Thr Met Lys Lys
 1 5 10 15
 Thr Ile Met Ala Ser Ser Leu Ala Val Ala Leu Gly Val Thr Gly Tyr
 20 25 30
 15 Ala Ala Gly Thr Gly His Gln Ala His Ala Ala Glu Val Asn Val Asp
 35 40 45
 Gln Ala His Leu Val Asp Leu Ala His Asn His Gln Asp Gln Leu Asn
 50 55 60
 20 Ala Ala Pro Ile Lys Asp Gly Ala Tyr Asp Ile His Phe Val Lys Asp
 65 70 75 80
 Gly Phe Gln Tyr Asn Phe Thr Ser Asn Gly Thr Thr Trp Ser Trp Ser
 85 90 95
 25 Tyr Glu Ala Ala Asn Gly Gln Thr Ala Gly Phe Ser Asn Val Ala Gly
 100 105 110
 Ala Asp Tyr Thr Thr Ser Tyr Asn Gln Gly Ser Asn Val Gln Ser Val
 115 120 125
 Ser Tyr Asn Ala Gln Ser Ser Asn Ser Asn Val Glu Ala Val Ser Ala
 130 135 140
 35 Pro Thr Tyr His Asn Tyr Ser Thr Ser Thr Thr Ser Ser Ser Val Arg
 145 150 155 160
 Leu Ser Asn Gly Asn Thr Ala Gly Ala Thr Gly Ser Ser Ala Ala Gln
 165 170 175
 40 Ile Met Ala Gln Arg Thr Gly Val Ser Ala Ser Thr Trp Ala Ala Ile
 180 185 190
 Ile Ala Arg Glu Ser Asn Gly Gln Val Asn Ala Tyr Asn Pro Ser Gly
 195 200 205
 45 Ala Ser Gly Leu Phe Gln Thr Met Pro Gly Trp Gly Pro Thr Asn Thr
 210 215 220
 Val Asp Gln Gln Ile Asn Ala Ala Val Lys Ala Tyr Lys Ala Gln Gly
 225 230 235 240
 Leu Gly Ala Trp Gly Phe
 245

55

(2) INFORMATION FOR SEQ ID NO:5230:

(A) LENGTH: 519 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: protein

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5230:

Lys Glu Pro His Lys Met Lys Lys Ile Tyr Lys Ser Leu Thr Val Ser
 1 5 10 15
 Ala Ile Val Ala Thr Val Ser Leu Ser Ala Leu Pro Gln Ser Leu Ala
 20 25 30
 Ile Thr His Glu Ser Gln Pro Thr Lys Gln Gln Arg Thr Val Leu Phe
 35 40 45
 Asp Arg Ser His Gly Gln Thr Ala Gly Ala Ala Asp Trp Val Ser Asp
 50 55 60
 Gly Ala Phe Ser Asp Tyr Ala Asp Ser Ile Gln Lys Gln Gly Tyr Asp
 65 70 75 80
 Val Lys Ala Ile Asp Gly His Ser Asn Ile Thr Glu Ala Ser Leu Lys
 85 90 95
 Ser Ser Lys Ile Phe Val Ile Pro Glu Ala Asn Ile Pro Phe Lys Glu
 100 105 110
 Ser Glu Gln Ala Ala Ile Val Lys Tyr Val Lys Gln Gly Gly Asn Val
 115 120 125
 Val Phe Ile Ser Asp His Tyr Asn Ala Asp Arg Asn Leu Asn Arg Ile
 130 135 140
 Asp Ser Ser Glu Ala Met Asn Gly Tyr Arg Arg Gly Ala Tyr Glu Asp
 145 150 155 160
 Met Ser Lys Gly Met Asn Ala Glu Glu Lys Ser Ser Thr Ala Met Gln
 165 170 175
 Gly Val Lys Ser Ser Asp Trp Leu Ser Thr Asn Phe Gly Val Arg Phe
 180 185 190
 Arg Tyr Asn Ala Leu Gly Asp Leu Asn Thr Ser Asn Ile Val Ser Ser
 195 200 205
 Lys Glu Ser Phe Gly Ile Thr Glu Gly Val Lys Ser Val Ser Met His
 210 215 220
 Ala Gly Ser Thr Leu Ala Ile Thr Asn Pro Glu Lys Ala Lys Gly Ile
 225 230 235 240
 Val Tyr Thr Pro Glu Gln Leu Pro Ala Lys Ser Lys Trp Ser His Ala
 245 250 255

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Val Asp Gln Gly Ile Tyr Asn Gly Gly Gly Lys Ala Glu Gly Pro Tyr
260 265 270

5 Val Ala Ile Ser Lys Val Gly Lys Gly Lys Ala Ala Phe Ile Gly Asp
275 280 285

Ser Ser Leu Val Glu Asp Ser Ser Pro Lys Tyr Val Arg Glu Asp Asn
290 295 300

10 Gly Glu Lys Lys Lys Thr Tyr Asp Gly Phe Lys Glu Gln Asp Asn Gly
305 310 315 320

Lys Leu Leu Asn Asn Ile Thr Ala Trp Met Ser Lys Asp Asn Asp Gly
325 330 335

15 Lys Ser Leu Lys Ala Ser Ser Leu Thr Leu Asp Thr Lys Thr Lys Leu
340 345 350

Leu Asp Phe Glu Arg Pro Glu Arg Ser Thr Glu Pro Glu Lys Glu Pro
355 360 365

20 Trp Ser Gln Pro Pro Ser Gly Tyr Lys Trp Tyr Asp Pro Thr Thr Phe
370 375 380

Lys Ala Gly Ser Tyr Gly Ser Glu Lys Gly Ala Asp Pro Gln Pro Asn
385 390 395 400

25 Thr Pro Asp Asp His Thr Pro Pro Asn Gln Asn Glu Lys Val Thr Phe
405 410 415

30 Asp Ile Pro Gln Asn Val Ser Val Asn Glu Pro Phe Glu Met Thr Ile
420 425 430

His Leu Lys Gly Phe Glu Ala Asn Gln Thr Leu Glu Asn Leu Arg Val
435 440 445

35 Gly Ile Tyr Lys Glu Gly Gly Arg Gln Ile Gly Gln Phe Ser Ser Lys
450 455 460

Asp Asn Asp Tyr Asn Pro Pro Gly Tyr Ser Thr Leu Pro Thr Val Lys
465 470 475 480

40 Ala Asp Glu Asn Gly Asn Val Thr Ile Lys Val Asn Ala Lys Val Leu
485 490 495

Glu Ser Met Glu Gly Ser Lys Ile Arg Leu Lys Leu Gly Asp Lys Thr
500 505 510

45 Leu Ile Thr Thr Asp Phe Lys
515

50 (2) INFORMATION FOR SEQ ID NO:5231:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 316 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5231:

5	Arg	Asp	Glu	Arg	Ile	Lys	Thr	Met	Thr	Asn	Ser	Ser	Lys	Ser	Phe	Thr	1	5	10	15
	Lys	Phe	Met	Ala	Ala	Ser	Ala	Val	Phe	Thr	Met	Gly	Phe	Leu	Ser	Val	20	25	30	
10	Pro	Thr	Ala	Gly	Ala	Glu	Gln	Thr	Asn	Gln	Ile	Ala	Asn	Lys	Pro	Gln	35	40	45	
	Ala	Ile	Gln	Trp	His	Thr	Asn	Leu	Thr	Asn	Glu	Arg	Phe	Thr	Thr	Ile	50	55	60	
15	Ala	His	Arg	Gly	Ala	Ser	Gly	Tyr	Ala	Pro	Glu	His	Thr	Phe	Gln	Ala	65	70	75	80
	Tyr	Asp	Lys	Ser	His	Asn	Glu	Leu	Lys	Ala	Ser	Tyr	Ile	Glu	Ile	Asp	85	90	95	
20	Leu	Gln	Arg	Thr	Lys	Asp	Gly	His	Leu	Val	Ala	Met	His	Asp	Glu	Thr	100	105	110	
	Val	Asn	Arg	Thr	Thr	Asn	Gly	His	Gly	Lys	Val	Glu	Asp	Tyr	Thr	Leu	115	120	125	
25	Asp	Glu	Leu	Lys	Gln	Leu	Asp	Ala	Gly	Ser	Trp	Phe	Asn	Lys	Lys	Tyr	130	135	140	
30	Pro	Lys	Tyr	Ala	Arg	Ala	Ser	Tyr	Lys	Asn	Ala	Lys	Val	Pro	Thr	Leu	145	150	155	160
	Asp	Glu	Ile	Leu	Glu	Arg	Tyr	Gly	Pro	Asn	Ala	Asn	Tyr	Tyr	Ile	Glu	165	170	175	
35	Thr	Lys	Ser	Pro	Asp	Val	Tyr	Pro	Gly	Met	Glu	Glu	Gln	Leu	Leu	Ala	180	185	190	
	Ser	Leu	Lys	Lys	His	His	Leu	Leu	Asn	Asn	Asn	Lys	Leu	Lys	Asn	Gly	195	200	205	
40	His	Val	Met	Ile	Gln	Ser	Phe	Ser	Asp	Glu	Ser	Leu	Lys	Lys	Ile	His	210	215	220	
45	Arg	Gln	Asn	Lys	His	Val	Pro	Leu	Val	Lys	Leu	Val	Asp	Lys	Gly	Glu	225	230	235	240
	Leu	Gln	Gln	Phe	Asn	Asp	Gln	Arg	Leu	Lys	Glu	Ile	Arg	Ser	Tyr	Ala	245	250	255	
50	Ile	Gly	Leu	Gly	Pro	Asp	Tyr	Thr	Asp	Leu	Thr	Glu	Gln	Asn	Thr	His	260	265	270	
55	His	Leu	Lys	Asp	Leu	Gly	Phe	Ile	Val	His	Pro	Tyr	Thr	Val	Asn	Glu	275	280	285	

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Lys Ala Asp Met Leu Arg Leu Asn Lys Tyr Gly Val Asp Gly Val Phe
290 295 300

5 Thr Asn Phe Ala Asp Lys Tyr Lys Glu Val Ile Lys
305 310 315

(2) INFORMATION FOR SEQ ID NO:5232:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 433 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5232:

20 Arg Phe Met Lys Asn Leu Ile Ser Ile Ile Ile Ile Leu Cys Leu Thr
1 5 10 15
Leu Ser Ile Met Thr Pro Tyr Ala Gln Ala Thr Asn Ser Asp Val Thr
25 20 25 30
Pro Val Gln Ala Ala Asn Gln Tyr Gly Tyr Ala Gly Leu Ser Ala Ala
35 35 40 45
Tyr Glu Pro Thr Ser Ala Val Asn Val Ser Gln Thr Gly Gln Leu Leu
30 50 55 60
Tyr Gln Tyr Asn Ile Asp Thr Lys Trp Asn Pro Ala Ser Met Thr Lys
65 70 75 80
35 Leu Met Thr Met Tyr Leu Thr Leu Glu Ala Val Asn Lys Gly Gln Leu
85 90 95
Ser Leu Asp Asp Thr Val Thr Met Thr Asn Lys Glu Tyr Ile Met Ser
100 105 110
40 Thr Leu Pro Glu Leu Ser Asn Thr Lys Leu Tyr Pro Gly Gln Val Trp
115 120 125
Thr Ile Ala Asp Leu Leu Gln Ile Thr Val Ser Asn Ser Ser Asn Ala
45 130 135 140
Ala Ala Leu Ile Leu Ala Lys Lys Val Ser Lys Asn Thr Ser Asp Phe
145 150 155 160
Val Asp Leu Met Asn Asn Lys Ala Lys Ala Ile Gly Met Lys Asn Thr
50 165 170 175
His Phe Val Asn Pro Thr Gly Ala Glu Asn Ser Arg Leu Arg Thr Phe
180 185 190
55 Ala Pro Thr Lys Tyr Lys Asp Gln Glu Arg Thr Val Thr Thr Ala Arg
195 200 205

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Asp Tyr Ala Ile Leu Asp Leu His Val Ile Lys Glu Thr Pro Lys Ile
 210 215 220
 5 Leu Asp Phe Thr Lys Gln Leu Ala Pro Thr Thr His Ala Val Thr Tyr
 225 230 235 240
 Tyr Thr Phe Asn Phe Ser Leu Glu Gly Ala Lys Met Ser Leu Pro Gly
 245 250 255
 10 Thr Asp Gly Leu Lys Thr Gly Ser Ser Asp Thr Ala Asn Tyr Asn His
 260 265 270
 Thr Ile Thr Thr Lys Arg Gly Lys Phe Arg Ile Asn Gln Val Ile Met
 275 280 285
 15 Gly Ala Gly Asp Tyr Lys Asn Leu Gly Gly Glu Lys Gln Arg Asn Met
 290 295 300
 Met Gly Asn Ala Leu Met Glu Arg Ser Phe Asp Gln Tyr Lys Tyr Val
 305 310 315 320
 20 Lys Ile Leu Ser Lys Gly Glu Gln Arg Ile Asn Gly Lys Lys Tyr Tyr
 325 330 335
 Val Glu Asn Asp Leu Tyr Asp Val Leu Pro Ser Asp Phe Ser Lys Lys
 340 345 350
 25 Asp Tyr Lys Leu Val Val Glu Asp Gly Lys Val His Ala Asp Tyr Pro
 355 360 365
 Arg Glu Phe Ile Asn Lys Asp Tyr Gly Pro Pro Thr Val Glu Val His
 370 375 380
 30 Gln Pro Ile Ile Gln Lys Ala Asn Thr Val Ala Lys Ser Met Trp Glu
 385 390 395 400
 35 Glu His Pro Leu Phe Thr Ile Ile Gly Gly Thr Cys Leu Val Ala Gly
 405 410 415
 Leu Ala Leu Ile Val His Met Ile Ile Asn Arg Leu Phe Arg Lys Arg
 420 425 430
 40 Lys

(2) INFORMATION FOR SEQ ID NO:5233:

45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 151 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5233:

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Leu Thr Lys Glu Arg Glu Tyr Met Lys Leu Lys Ser Phe Ile Thr Val
1 5 10 15

Thr Leu Ala Leu Gly Met Ile Ala Thr Thr Gly Ala Thr Val Ala Gly
5 20 25 30

Asn Glu Val Ser Ala Ala Glu Lys Asp Lys Leu Pro Ala Thr Gln Lys
35 40 45

Ala Lys Glu Met Gln Asn Val Pro Tyr Thr Ile Ala Val Asp Gly Ile
10 50 55 60

Met Ala Phe Asn Gln Ser Tyr Leu Asn Leu Pro Lys Asp Ser Gln Leu
65 70 75 80

Ser Tyr Leu Asp Leu Gly Asn Lys Val Lys Ala Leu Leu Tyr Asp Glu
15 85 90 95

Arg Gly Val Thr Pro Glu Lys Ile Arg Asn Ala Lys Ser Ala Val Tyr
100 105 110

Thr Ile Thr Trp Lys Asp Gly Ser Lys Lys Glu Val Asp Leu Lys Lys
20 115 120 125

Asp Ser Tyr Thr Ala Asn Leu Phe Asp Ser Asn Ser Ile Lys Gln Ile
25 130 135 140

Asp Ile Asn Val Lys Thr Lys
145 150

(2) INFORMATION FOR SEQ ID NO:5234:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 497 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5234:

Asn His Cys Asn Arg Ile Glu Arg Lys Met Ala Met Ser Asn Asn Phe
1 5 10 15

Lys Asp Asp Phe Glu Lys Asn Arg Gln Ser Ile Asp Thr Asn Ser His
20 25 30

Gln Asp His Thr Glu Asp Val Glu Lys Asp Gln Ser Glu Leu Glu His
35 40 45

Gln Asp Thr Ile Glu Asn Thr Glu Gln Gln Phe Pro Pro Arg Asn Ala
50 55 60

Gln Arg Arg Lys Arg Arg Arg Asp Leu Ala Thr Asn His Asn Lys Gln
55 65 70 75 80

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	Val	His	Asn	Glu	Ser	Gln	Thr	Ser	Glu	Asp	Asn	Val	Gln	Asn	Glu	Ala	
					85					90					95		
5	Gly	Thr	Ile	Asp	Asp	Arg	Gln	Val	Glu	Ser	Ser	His	Ser	Thr	Glu	Ser	
				100					105					110			
	Gln	Glu	Pro	Ser	His	Gln	Asp	Ser	Thr	Pro	Gln	His	Glu	Glu	Glu	Tyr	
			115					120					125				
10	Tyr	Asn	Lys	Asn	Ala	Phe	Ala	Met	Asp	Lys	Ser	His	Pro	Glu	Pro	Ile	
		130					135					140					
	Glu	Asp	Asn	Asp	Lys	His	Asp	Thr	Ile	Lys	Asn	Ala	Glu	Asn	Asn	Thr	
	145					150					155					160	
15	Glu	His	Ser	Thr	Val	Ser	Asp	Lys	Ser	Glu	Ala	Glu	Gln	Ser	Gln	Gln	
					165					170					175		
	Pro	Lys	Pro	Tyr	Phe	Thr	Thr	Gly	Ala	Asn	Gln	Ser	Glu	Thr	Ser	Lys	
				180					185						190		
20	Asn	Glu	His	Asp	Asn	Asp	Ser	Val	Lys	Gln	Asp	Gln	Asp	Glu	Pro	Lys	
			195					200					205				
	Glu	His	His	Asn	Gly	Lys	Lys	Ala	Ala	Ala	Ile	Gly	Ala	Gly	Thr	Ala	
25		210				215						220					
	Gly	Val	Ala	Gly	Ala	Ala	Gly	Ala	Met	Ala	Ala	Ser	Lys	Ala	Lys	Lys	
	225				230					235						240	
	His	Ser	Asn	Asp	Ala	Gln	Asn	Lys	Ser	Asn	Ser	Gly	Lys	Ala	Asn	Asn	
30					245					250					255		
	Ser	Thr	Glu	Asp	Lys	Ala	Ser	Gln	Asp	Lys	Ser	Lys	Asp	His	His	Asn	
				260					265					270			
35	Gly	Lys	Lys	Gly	Ala	Ala	Ile	Gly	Ala	Gly	Thr	Ala	Gly	Leu	Ala	Gly	
		275						280					285				
	Gly	Ala	Ala	Ser	Lys	Ser	Ala	Ser	Ala	Ala	Ser	Lys	Pro	His	Ala	Ser	
		290					295					300					
40	Asn	Asn	Ala	Ser	Gln	Asn	His	Asp	Glu	His	Asp	Asn	His	Asp	Arg	Asp	
	305					310					315					320	
	Lys	Glu	Arg	Lys	Lys	Gly	Gly	Met	Ala	Lys	Val	Leu	Leu	Pro	Leu	Ile	
				325						330					335		
45	Ala	Ala	Val	Leu	Ile	Ile	Gly	Ala	Leu	Ala	Ile	Phe	Gly	Gly	Met	Ala	
				340					345					350			
	Leu	Asn	Asn	His	Asn	Asn	Gly	Thr	Lys	Glu	Asn	Lys	Ile	Ala	Asn	Thr	
50		355					360						365				
	Asn	Lys	Asn	Asn	Ala	Asp	Glu	Ser	Lys	Asp	Lys	Asp	Thr	Ser	Lys	Asp	
		370					375					380					
55	Ala	Ser	Lys	Asp	Lys	Ser	Lys	Ser	Thr	Asp	Ser	Asp	Lys	Ser	Lys	Glu	
	385				390						395					400	

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Asp Gln Asp Lys Ala Thr Lys Asp Glu Ser Asp Asn Asp Gln Asn Asn
405 410 415

Ala Asn Gln Ala Asn Asn Gln Ala Gln Asn Asn Gln Asn Gln Gln Gln
5 420 425 430

Ala Asn Gln Asn Gln Gln Gln Gln Gln Gln Arg Gln Gly Gly Gly Gln
435 440 445

Arg His Thr Val Asn Gly Gln Glu Asn Leu Tyr Arg Ile Ala Ile Gln
10 450 455 460

Tyr Tyr Gly Ser Gly Ser Pro Glu Asn Val Glu Lys Ile Arg Arg Ala
465 470 475 480

Asn Gly Leu Ser Gly Asn Asn Ile Arg Asn Gly Gln Gln Ile Val Ile
15 485 490 495

Pro

20

(2) INFORMATION FOR SEQ ID NO:5235:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 886 amino acids
25 (B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5235:

Leu Leu Ser Ile Lys Tyr Asn Leu Ile Gly Val Val Asn Asn Met Asn
35 1 5 10 15

Lys His His Pro Lys Leu Arg Ser Phe Tyr Ser Ile Arg Lys Ser Thr
20 25 30

Leu Gly Val Ala Ser Val Ile Val Ser Thr Leu Phe Leu Ile Thr Ser
40 35 40 45

Gln His Gln Ala Gln Ala Ala Glu Asn Thr Asn Thr Ser Asp Lys Ile
50 55 60

Ser Glu Asn Gln Asn Asn Asn Ala Thr Thr Thr Gln Pro Pro Lys Asp
65 70 75 80

Thr Asn Gln Thr Gln Pro Ala Thr Gln Pro Ala Asn Thr Ala Lys Asn
50 85 90 95

Tyr Pro Ala Ala Asp Glu Ser Leu Lys Asp Ala Ile Lys Asp Pro Ala
100 105 110

Leu Glu Asn Lys Glu His Asp Ile Gly Pro Arg Glu Gln Val Asn Phe
55 115 120 125

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	Gln	Leu	Leu	Asp	Lys	Asn	Asn	Glu	Thr	Gln	Tyr	Tyr	His	Phe	Phe	Ser
	130						135					140				
5	Ile	Lys	Asp	Pro	Ala	Asp	Val	Tyr	Tyr	Thr	Lys	Lys	Lys	Ala	Glu	Val
	145					150					155					160
	Glu	Leu	Asp	Ile	Asn	Thr	Ala	Ser	Thr	Trp	Lys	Lys	Phe	Glu	Val	Tyr
					165					170					175	
10	Glu	Asn	Asn	Gln	Lys	Leu	Pro	Val	Arg	Leu	Val	Ser	Tyr	Ser	Pro	Val
				180					185					190		
	Pro	Glu	Asp	His	Ala	Tyr	Ile	Arg	Phe	Pro	Val	Ser	Asp	Gly	Thr	Gln
			195					200					205			
15	Glu	Leu	Lys	Ile	Val	Ser	Ser	Thr	Gln	Ile	Asp	Asp	Gly	Glu	Glu	Thr
	210						215					220				
	Asn	Tyr	Asp	Tyr	Thr	Lys	Leu	Val	Phe	Ala	Lys	Pro	Ile	Tyr	Asn	Asp
	225					230					235					240
20	Pro	Ser	Leu	Val	Lys	Ser	Asp	Thr	Asn	Asp	Ala	Val	Val	Thr	Asn	Asp
					245					250						255
	Gln	Ser	Ser	Ser	Val	Ala	Ser	Asn	Gln	Thr	Asn	Thr	Asn	Thr	Ser	Asn
25					260				265					270		
	Gln	Asn	Ile	Ser	Thr	Ile	Asn	Asn	Ala	Asn	Asn	Gln	Pro	Gln	Ala	Thr
			275					280					285			
30	Thr	Asn	Met	Ser	Gln	Pro	Ala	Gln	Pro	Lys	Ser	Ser	Thr	Asn	Ala	Asp
	290						295						300			
	Gln	Ala	Ser	Ser	Gln	Pro	Ala	His	Glu	Thr	Asn	Ser	Asn	Gly	Asn	Thr
	305					310					315					320
35	Asn	Asp	Lys	Thr	Asn	Glu	Ser	Ser	Asn	Gln	Ser	Asp	Val	Asn	Gln	Gln
					325					330					335	
	Tyr	Pro	Pro	Ala	Asp	Glu	Ser	Leu	Gln	Asp	Ala	Ile	Lys	Asn	Pro	Ala
				340					345					350		
40	Ile	Ile	Asp	Lys	Glu	His	Thr	Ala	Asp	Asn	Trp	Arg	Pro	Ile	Asp	Phe
			355					360					365			
	Gln	Met	Lys	Asn	Asp	Lys	Gly	Glu	Arg	Gln	Phe	Tyr	His	Tyr	Ala	Ser
45		370					375					380				
	Thr	Val	Glu	Pro	Ala	Thr	Val	Ile	Phe	Thr	Lys	Thr	Gly	Pro	Ile	Ile
	385					390					395					400
50	Glu	Leu	Gly	Leu	Lys	Thr	Ala	Ser	Thr	Trp	Lys	Lys	Phe	Glu	Val	Tyr
					405					410					415	
	Glu	Gly	Asp	Lys	Lys	Leu	Pro	Val	Glu	Leu	Val	Ser	Tyr	Asp	Ser	Asp
				420					425					430		
55	Lys	Asp	Tyr	Ala	Tyr	Ile	Arg	Phe	Pro	Val	Ser	Asn	Gly	Thr	Arg	Glu
		435						440					445			

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	Val	Lys	Ile	Val	Ser	Ser	Ile	Glu	Tyr	Gly	Glu	Asn	Ile	His	Glu	Asp	
	450						455					460					
5	Tyr	Asp	Tyr	Thr	Leu	Met	Val	Phe	Ala	Gln	Pro	Ile	Thr	Asn	Asn	Pro	
	465					470					475					480	
	Asp	Asp	Tyr	Val	Asp	Glu	Glu	Thr	Tyr	Asn	Leu	Gln	Lys	Leu	Leu	Ala	
					485					490						495	
10	Pro	Tyr	His	Lys	Ala	Lys	Thr	Leu	Glu	Arg	Gln	Val	Tyr	Glu	Leu	Glu	
				500					505					510			
	Lys	Leu	Gln	Glu	Lys	Leu	Pro	Glu	Lys	Tyr	Lys	Ala	Glu	Tyr	Lys	Lys	
			515					520					525				
15	Lys	Leu	Asp	Gln	Thr	Arg	Val	Glu	Leu	Ala	Asp	Gln	Val	Lys	Ser	Ala	
		530					535					540					
	Val	Thr	Glu	Phe	Glu	Asn	Val	Thr	Pro	Thr	Asn	Asp	Gln	Leu	Thr	Asp	
	545					550					555					560	
20	Leu	Gln	Glu	Ala	His	Phe	Val	Val	Phe	Glu	Ser	Glu	Glu	Asn	Ser	Glu	
					565					570						575	
	Ser	Val	Met	Asp	Gly	Phe	Val	Glu	His	Pro	Phe	Tyr	Thr	Ala	Thr	Leu	
25				580					585					590			
	Asn	Gly	Gln	Lys	Tyr	Val	Val	Met	Lys	Thr	Lys	Asp	Asp	Ser	Tyr	Trp	
			595					600					605				
30	Lys	Asp	Leu	Ile	Val	Glu	Gly	Lys	Arg	Val	Thr	Thr	Val	Ser	Lys	Asp	
		610					615						620				
	Pro	Lys	Asn	Asn	Ser	Arg	Thr	Leu	Ile	Phe	Pro	Tyr	Ile	Pro	Asp	Lys	
						630					635					640	
35	Ala	Val	Tyr	Asn	Ala	Ile	Val	Lys	Val	Val	Val	Ala	Asn	Ile	Gly	Tyr	
					645						650					655	
	Glu	Gly	Gln	Tyr	His	Val	Arg	Ile	Ile	Asn	Gln	Asp	Ile	Asn	Thr	Lys	
				660					665					670			
40	Asp	Asp	Asp	Thr	Ser	Gln	Asn	Asn	Thr	Ser	Glu	Pro	Leu	Asn	Val	Gln	
			675					680						685			
	Thr	Gly	Gln	Glu	Gly	Lys	Val	Ala	Asp	Thr	Asp	Val	Ala	Glu	Asn	Ser	
45			690				695					700					
	Ser	Thr	Ala	Thr	Asn	Pro	Lys	Asp	Ala	Ser	Asp	Lys	Ala	Asp	Val	Ile	
						710					715					720	
	Glu	Pro	Glu	Ser	Asp	Val	Val	Lys	Asp	Ala	Asp	Asn	Asn	Ile	Asp	Lys	
50					725					730					735		
	Asp	Val	Gln	His	Asp	Val	Asp	His	Leu	Ser	Asp	Met	Ser	Asp	Asn	Asn	
				740					745					750			
55	His	Phe	Asp	Lys	Tyr	Asp	Leu	Lys	Glu	Met	Asp	Thr	Gln	Ile	Ala	Lys	
			755					760						765			

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Asp Thr Asp Arg Asn Val Asp Lys Asp Ala Asp Asn Ser Val Gly Met
770 775 780

5 Ser Ser Asn Val Asp Thr Asp Lys Asp Ser Asn Lys Asn Lys Asp Lys
785 790 795 800

Val Ile Gln Leu Asn His Ile Ala Asp Lys Asn Asn His Thr Gly Lys
805 810 815

10 Ala Ala Lys Leu Asp Val Val Lys Gln Asn Tyr Asn Asn Thr Asp Lys
820 825 830

Val Thr Asp Lys Lys Thr Thr Glu His Leu Pro Ser Asp Ile His Lys
835 840 845

15 Thr Val Asp Lys Thr Val Lys Thr Lys Glu Lys Ala Gly Thr Pro Ser
850 855 860

Lys Glu Asn Lys Leu Ser Gln Ser Lys Met Leu Thr Lys Asn Trp Arg
865 870 875 880

20 Asn Asn Xaa Gln Ala Asn
885

(2) INFORMATION FOR SEQ ID NO:5236:

25 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 236 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5236:

Asn Met Asn Lys Asn Val Met Val Lys Gly Leu Thr Ala Leu Thr Ile
1 5 10 15

40 Leu Thr Ser Leu Gly Phe Ala Glu Asn Ile Ser Asn Gln Xaa His Ser
20 25 30

Ile Ala Lys Ala Glu Lys Asn Val Lys Glu Ile Thr Asp Ala Thr Lys
35 40 45

45 Glu Pro Tyr Asn Ser Val Val Ala Phe Val Gly Gly Thr Gly Val Val
50 55 60

50 Val Gly Lys Asn Thr Ile Val Thr Asn Lys His Ile Ala Lys Ser Asn
65 70 75 80

Asp Ile Phe Lys Asn Arg Val Ser Ala His His Ser Ser Lys Gly Lys
85 90 95

55 Gly Gly Gly Asn Tyr Asp Val Lys Asp Ile Val Glu Tyr Pro Gly Lys
100 105 110

Glu Asp Leu Ala Ile Val His Val His Glu Thr Ser Thr Glu Gly Leu
 115 120 125
 Asn Phe Asn Lys Asn Val Ser Tyr Thr Lys Phe Ala Asp Gly Ala Lys
 130 135 140
 Val Lys Asp Arg Ile Ser Val Ile Gly Tyr Pro Lys Gly Ala Gln Thr
 145 150 155 160
 Lys Tyr Lys Met Phe Glu Ser Thr Gly Thr Ile Asn His Ile Ser Gly
 165 170 175
 Thr Phe Met Glu Phe Asp Ala Tyr Ala Gln Pro Gly Asn Ser Gly Ser
 180 185 190
 Pro Val Leu Asn Ser Lys His Xaa Leu Ile Gly Ile Leu Tyr Ala Gly
 195 200 205
 Ser Gly Lys Asp Glu Ser Glu Lys Asn Phe Gly Val Tyr Phe Thr Pro
 210 215 220
 Gln Leu Xaa Xaa Phe Ile Pro Asn Asn Ile Glu Lys
 225 230 235

(2) INFORMATION FOR SEQ ID NO:5237:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5237:

Tyr Arg Leu Glu His Thr Ile Met Lys Met Arg Thr Ile Ala Lys Thr
 1 5 10 15
 Ser Leu Ala Leu Gly Leu Leu Thr Thr Gly Ala Ile Thr Val Thr Thr
 20 25 30
 Gln Ser Val Lys Ala Glu Lys Ile Gln Ser Thr Lys Val Asp Lys Val
 35 40 45
 Pro Thr Leu Lys Ala Glu Arg Leu Ala Met Ile Asn Ile Thr Ala Gly
 50 55 60
 Ala Asn Ser Ala Thr Thr Gln Ala Ala Asn Thr Arg Gln Glu Arg Thr
 65 70 75 80
 Pro Lys Leu Glu Lys Ala Pro Asn Thr Asn Glu Glu Lys Thr Ser Ala
 85 90 95
 Ser Lys Ile Glu Lys Ile Ser Gln Pro Lys Gln Glu Glu Gln Lys Thr
 100 105 110

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	Leu	Asn	Ile	Ser	Ala	Thr	Pro	Ala	Pro	Lys	Gln	Glu	Gln	Ser	Gln	Thr	
			115					120					125				
5	Thr	Thr	Glu	Ser	Thr	Thr	Pro	Lys	Thr	Lys	Val	Thr	Thr	Pro	Pro	Ser	
			130					135					140				
	Thr	Asn	Thr	Pro	Gln	Pro	Met	Gln	Ser	Thr	Lys	Ser	Asp	Thr	Pro	Gln	
						150					155					160	
10	Ser	Pro	Thr	Ile	Lys	Gln	Ala	Gln	Thr	Asp	Met	Thr	Pro	Lys	Tyr	Glu	
					165					170					175		
	Asp	Leu	Arg	Ala	Tyr	Tyr	Thr	Lys	Pro	Ser	Phe	Glu	Phe	Glu	Lys	Gln	
15				180					185					190			
	Phe	Gly	Phe	Met	Leu	Lys	Pro	Trp	Thr	Thr	Val	Arg	Phe	Met	Asn	Val	
				195				200					205				
	Ile	Pro	Asn	Arg	Phe	Ile	Tyr	Lys	Ile	Ala	Leu	Val	Gly	Lys	Asp	Glu	
20			210				215					220					
	Lys	Lys	Tyr	Lys	Asp	Gly	Pro	Tyr	Asp	Asn	Ile	Asp	Val	Phe	Ile	Val	
					230						235					240	
25	Leu	Glu	Asp	Asn	Lys	Tyr	Gln	Leu	Lys	Lys	Tyr	Ser	Val	Gly	Gly	Ile	
					245					250					255		
	Thr	Lys	Thr	Asn	Ser	Lys	Lys	Val	Asn	His	Lys	Val	Glu	Leu	Ser	Ile	
				260					265					270			
30	Thr	Lys	Lys	Asp	Asn	Gln	Gly	Met	Ile	Ser	Arg	Asp	Val	Ser	Glu	Tyr	
				275				280					285				
	Met	Ile	Thr	Lys	Glu	Glu	Ile	Ser	Leu	Lys	Glu	Leu	Asp	Phe	Lys	Leu	
35				290			295					300					
	Arg	Lys	Gln	Leu	Ile	Glu	Lys	His	Asn	Leu	Tyr	Gly	Asn	Met	Gly	Ser	
					310						315					320	
40	Gly	Thr	Ile	Val	Ile	Lys	Met	Lys	Asn	Gly	Gly	Lys	Tyr	Thr	Phe	Glu	
					325					330					335		
	Leu	His	Lys	Lys	Leu	Gln	Glu	His	Arg	Met	Ala	Asp	Val	Ile	Asp	Gly	
				340					345					350			
45	Thr	Asn	Ile	Asp	Asn	Ile	Glu	Val	Asn	Ile	Lys						
				355				360									

(2) INFORMATION FOR SEQ ID NO:5238:

- 50 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 150 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- 55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5238:

5 Phe Met Lys Phe Lys Ser Leu Ile Thr Thr Thr Leu Ala Leu Gly Val
 1 5 10 15
 Leu Ala Ser Thr Gly Ala Asn Phe Asn Asn Asn Glu Ala Ser Ala Ala
 20 25 30
 10 Ala Lys Pro Leu Asp Lys Ser Ser Ser Ser Leu His His Gly Tyr Ser
 35 40 45
 Lys Val His Val Pro Tyr Ala Ile Thr Val Asn Gly Thr Ser Gln Asn
 50 55 60
 15 Ile Leu Ser Ser Leu Thr Phe Asn Lys Asn Gln Asn Ile Ser Tyr Lys
 65 70 75 80
 Asp Leu Glu Asp Arg Val Lys Ser Val Leu Lys Ser Asp Arg Gly Ile
 85 90 95
 20 Ser Asp Ile Asp Leu Arg Leu Ser Lys Gln Ala Lys Tyr Thr Val Tyr
 100 105 110
 Phe Lys Asn Gly Thr Lys Lys Val Ile Asp Leu Lys Ala Gly Ile Tyr
 115 120 125
 25 Thr Ala Asp Leu Ile Asn Thr Ser Glu Ile Lys Ala Ile Asn Ile Asn
 130 135 140
 Val Asp Thr Lys Lys Gln
 145 150
 30

(2) INFORMATION FOR SEQ ID NO:5239:

35 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5239:

45 Glu Lys Arg Phe Met Gln Met Ala Arg Lys Val Val Val Val Asp Asp
 1 5 10 15
 Glu Lys Pro Ile Ala Asp Ile Leu Glu Phe Asn Leu Lys Lys Glu Gly
 20 25 30
 50 Tyr Asp Val Tyr Cys Ala Tyr Asp Gly Asn Asp Ala Val Asp Leu Ile
 35 40 45
 Tyr Glu Glu Glu Pro Asp Ile Val Leu Leu Asp Ile Met Leu Pro Gly
 50 55 60
 55

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Arg Asp Gly Met Glu Val Cys Arg Glu Val Arg Lys Lys Tyr Glu Met
65 70 75 80

5 Pro Ile Ile Met Leu Thr Ala Lys Asp Ser Glu Ile Asp Lys Val Leu
85 90 95

Gly Leu Glu Leu Gly Ala Asp Asp Tyr Val Thr Lys Pro Phe Ser Thr
100 105 110

10 Arg Glu Leu Ile Ala Arg Val Lys Ala Asn Leu Arg Arg His Tyr Ser
115 120 125

Gln Pro Ala Gln Asp Thr Gly Asn Val Thr Asn Glu Ile Thr Ile Lys
130 135 140

15 Asp Ile Val Ile Tyr Pro Asp Ala Tyr Ser Ile Lys Lys Arg Gly Glu
145 150 155 160

Asp Ile Glu Leu Thr His Arg Glu Phe Glu Leu Phe His Tyr Leu Ser
165 170 175

20 Lys His Met Gly Gln Val Met Thr Arg Glu His Leu Leu Gln Thr Val
180 185 190

Trp Gly Tyr Asp Tyr Phe Gly Asp Val Arg Thr Val Asp Val Thr Ile
195 200 205

25 Arg Arg Leu Arg Glu Lys Ile Glu Asp Asp Pro Ser His Pro Glu Tyr
210 215 220

Ile Val Thr Arg Arg Gly Val Gly Tyr Phe Leu Gln Gln His Glu
225 230 235

30

(2) INFORMATION FOR SEQ ID NO:5240:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 133 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5240:

45 Xaa Leu Ser Thr Val Ile Gly Ala Xaa Leu Phe Phe Lys Ser Ser Val
1 5 10 15

Ser Leu Val Phe Lys Met Val Lys Lys Phe Arg Xaa Gly Val Ile Ser
20 25 30

50 Val Asn Asp Val Met Phe Ser Ser Ser Ile Met Tyr Arg Ile Lys Lys
35 40 45

55 Asn Ala Phe Ser Leu Thr Val Met Ala Ile Ile Ser Ala Ile Thr Val
50 55 60

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Ser Val Leu Cys Phe Ala Ala Ile Ser Arg Ala Ser Leu Ser Ser Glu
65 70 75 80

Ile Lys Tyr Thr Ala Pro His Asp Val Thr Ile Lys Asp Gln Gln Lys
5 85 90 95

Ala Asn Gln Leu Ala Ser Glu Leu Asn Asn Gln Lys Ile Pro His Phe
100 105 110

Tyr Asn Tyr Lys Glu Val Ile His Thr Lys Leu Tyr Lys Asp Asn Leu
10 115 120 125

Phe Asp Val Lys Ala
130

(2) INFORMATION FOR SEQ ID NO:5241:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 508 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5241:

Glu Ile Tyr Ile Ile Ala Asn Lys Gln Arg Arg Asp Asn Met Ala Val
1 5 10 15

Asn Val Arg Asp Tyr Ile Ala Glu Asn Tyr Gly Leu Phe Ile Asn Gly
20 25 30

Glu Phe Val Lys Gly Ser Ser Asp Glu Thr Ile Glu Val Thr Asn Pro
35 40 45

Ala Thr Gly Glu Thr Leu Ser His Ile Thr Arg Ala Lys Asp Lys Asp
50 55 60

Val Asp His Ala Val Lys Val Ala Gln Glu Ala Phe Glu Ser Trp Ser
65 70 75 80

Leu Thr Ser Lys Ser Glu Arg Ala Gln Met Leu Arg Asp Ile Gly Asp
85 90 95

Lys Leu Met Ala Gln Lys Asp Lys Ile Ala Met Ile Glu Thr Leu Asn
100 105 110

Asn Gly Lys Pro Ile Arg Glu Thr Thr Ala Ile Asp Ile Pro Phe Ala
115 120 125

Ala Arg His Phe His Tyr Phe Ala Ser Val Ile Glu Thr Glu Glu Gly
130 135 140

Thr Val Asn Asp Ile Asp Lys Asp Thr Met Ser Ile Val Arg His Glu
145 150 155 160

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	Pro	Ile	Gly	Val	Val	Gly	Ala	Val	Val	Ala	Trp	Asn	Phe	Pro	Met	Leu	
					165					170					175		
5	Leu	Ala	Ala	Trp	Lys	Ile	Ala	Pro	Ala	Ile	Ala	Ala	Gly	Asn	Thr	Ile	
				180				185						190			
	Val	Ile	Gln	Pro	Ser	Ser	Ser	Thr	Pro	Leu	Ser	Leu	Leu	Glu	Val	Ala	
			195					200					205				
10	Lys	Ile	Phe	Gln	Glu	Val	Leu	Pro	Lys	Gly	Val	Val	Asn	Ile	Leu	Thr	
		210					215					220					
	Gly	Lys	Gly	Ser	Glu	Ser	Gly	Asn	Ala	Ile	Phe	Asn	His	Asp	Gly	Val	
	225					230					235					240	
15	Asp	Lys	Leu	Ser	Phe	Thr	Gly	Ser	Thr	Asp	Val	Gly	Tyr	Gln	Val	Ala	
					245					250					255		
	Glu	Ala	Ala	Ala	Lys	His	Leu	Val	Pro	Ala	Thr	Leu	Glu	Leu	Gly	Gly	
					260				265					270			
20	Lys	Ser	Ala	Asn	Ile	Ile	Leu	Asp	Asp	Ala	Asn	Leu	Asp	Leu	Ala	Val	
			275					280					285				
	Glu	Gly	Ile	Gln	Leu	Gly	Ile	Leu	Phe	Asn	Gln	Gly	Glu	Val	Cys	Ser	
25		290					295					300					
	Ala	Gly	Ser	Arg	Leu	Leu	Val	His	Glu	Lys	Ile	Tyr	Asp	Gln	Leu	Val	
	305					310					315					320	
	Pro	Arg	Leu	Gln	Glu	Ala	Phe	Ser	Asn	Ile	Lys	Val	Gly	Asn	Pro	Gln	
30					325					330					335		
	Asp	Glu	Ala	Thr	Gln	Met	Gly	Ser	Gln	Thr	Gly	Lys	Asp	Gln	Leu	Asp	
				340					345					350			
35	Lys	Ile	Gln	Ser	Tyr	Ile	Asp	Ala	Ala	Lys	Glu	Ser	Asp	Ala	Gln	Ile	
			355				360						365				
	Leu	Ala	Gly	Gly	His	Arg	Leu	Thr	Glu	Asn	Gly	Leu	Asp	Lys	Gly	Phe	
		370					375					380					
40	Phe	Phe	Glu	Pro	Thr	Leu	Ile	Ala	Val	Pro	Asp	Asn	His	His	Lys	Leu	
	385					390					395					400	
	Ala	Gln	Glu	Glu	Ile	Phe	Gly	Pro	Val	Leu	Thr	Val	Ile	Lys	Val	Lys	
					405					410					415		
45	Asp	Asp	Gln	Glu	Ala	Ile	Asp	Ile	Ala	Asn	Asp	Ser	Glu	Tyr	Gly	Leu	
				420					425					430			
	Ala	Gly	Gly	Val	Phe	Ser	Gln	Asn	Ile	Thr	Arg	Ala	Leu	Asn	Ile	Ala	
			435					440					445				
50	Lys	Ala	Val	Arg	Thr	Gly	Arg	Ile	Trp	Ile	Asn	Thr	Tyr	Asn	Gln	Val	
		450					455					460					
	Pro	Glu	Gly	Ala	Pro	Phe	Gly	Gly	Tyr	Lys	Lys	Ser	Gly	Ile	Gly	Arg	
55	465					470					475					480	

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Glu Thr Tyr Lys Gly Ala Leu Ser Asn Tyr Gln Gln Val Lys Asn Ile
485 490 495

Tyr Ile Asp Thr Ser Asn Ala Leu Lys Gly Leu Tyr
500 505

(2) INFORMATION FOR SEQ ID NO:5242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 540 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5242:

Asn His Leu Thr Ala Arg Ile Ile Asn Gln Glu Asp Asp Leu Met Asn
1 5 10 15

Leu Phe Arg Gln Gln Lys Phe Ser Ile Arg Lys Phe Asn Val Gly Ile
20 25 30

Phe Ser Ala Leu Ile Ala Thr Val Thr Phe Ile Ser Thr Asn Pro Thr
35 40 45

Thr Ala Ser Ala Ala Glu Gln Asn Gln Pro Ala Gln Asn Gln Pro Ala
50 55 60

Gln Pro Ala Asp Ala Asn Thr Gln Pro Asn Ala Asn Ala Gly Ala Gln
65 70 75 80

Ala Asn Pro Thr Ala Gln Pro Ala Ala Pro Ala Asn Gln Gly Gln Pro
85 90 95

Ala Val Gln Pro Ala Asn Gln Gly Gly Gln Ala Asn Pro Ala Gly Gly
100 105 110

Ala Ala Gln Pro Asn Thr Gln Pro Ala Gly Gln Gly Asp Gln Ala Asp
115 120 125

Pro Asn Asn Ala Ala Gln Ala Gln Pro Gly Asn Gln Ala Thr Pro Ala
130 135 140

Asn Gln Ala Gly Gln Gly Asn Asn Gln Ala Thr Pro Asn Asn Asn Ala
145 150 155 160

Thr Pro Ala Asn Gln Thr Gln Pro Ala Asn Ala Pro Ala Ala Ala Gln
165 170 175

Pro Ala Ala Pro Val Ala Ala Asn Ala Gln Thr Gln Asp Pro Asn Ala
180 185 190

Ser Asn Thr Gly Glu Gly Ser Ile Asn Thr Thr Leu Thr Phe Asp Asp
195 200 205

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Pro Ala Ile Ser Thr Asp Glu Asn Arg Gln Asp Pro Thr Val Thr Val
210 215 220

5 Thr Asp Lys Val Asn Gly Tyr Ser Leu Ile Asn Asn Gly Lys Ile Gly
225 230 235 240

Phe Val Asn Ser Glu Leu Arg Arg Ser Asp Met Phe Asp Lys Asn Asn
245 250 255

10 Pro Gln Asn Tyr Gln Ala Lys Gly Asn Val Ala Ala Leu Gly Arg Val
260 265 270

Asn Ala Asn Asp Ser Thr Asp His Gly Asn Phe Asn Gly Ile Ser Lys
275 280 285

15 Thr Val Asn Val Lys Pro Asp Ser Glu Leu Ile Ile Asn Phe Thr Thr
290 295 300

Met Gln Thr Asn Ser Lys Gln Gly Ala Thr Asn Leu Val Ile Lys Asp
305 310 315 320

20 Ala Lys Lys Asn Thr Glu Leu Ala Thr Val Asn Val Ala Lys Thr Gly
325 330 335

Thr Ala His Leu Phe Lys Val Pro Thr Asp Ala Asp Arg Leu Asp Leu
340 345 350

25 Gln Phe Ile Pro Asp Asn Thr Ala Val Ala Asp Ala Ser Arg Ile Thr
355 360 365

Thr Asn Lys Asp Gly Tyr Lys Tyr Tyr Ser Phe Ile Asp Asn Val Gly
370 375 380

30 Leu Phe Ser Gly Ser His Leu Tyr Val Lys Asn Arg Asp Leu Ala Pro
385 390 395 400

Lys Ala Thr Asn Asn Lys Glu Tyr Thr Ile Asn Thr Glu Ile Gly Asn
405 410 415

35 Asn Gly Asn Phe Gly Ala Ser Leu Lys Ala Asp Gln Phe Lys Tyr Glu
420 425 430

40 Val Thr Leu Pro Gln Gly Val Thr Tyr Val Asn Asn Ser Leu Thr Thr
435 440 445

Thr Phe Pro Asn Gly Asn Glu Asp Ser Thr Val Leu Lys Asn Met Thr
450 455 460

45 Val Asn Tyr Asp Gln Asn Ala Asn Lys Val Thr Phe Thr Ser Gln Gly
465 470 475 480

Val Thr Thr Ala Arg Gly Thr His Thr Lys Glu Val Leu Phe Pro Asp
485 490 495

50 Lys Ser Leu Lys Leu Ser Tyr Lys Val Asn Val Ala Asn Ile Asp Thr
500 505 510

55 Pro Lys Asn Ile Asp Phe Asn Glu Lys Leu Thr Tyr Arg Thr Ala Ser
515 520 525

Asp Val Val Ile Asn Asn Ala Gln Pro Glu Val His
 530 535 540

(2) INFORMATION FOR SEQ ID NO:5243:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 274 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5243:

Ile Thr Leu Lys Thr Val Ser Gln Leu Ile Asp Met Lys Gln Lys Gln
 1 5 10 15
 Thr Lys Ile Ser Met Val Thr Ala Tyr Asp Phe Pro Ser Ala Lys Gln
 20 25 30
 Val Glu Ala Ala Gly Ile Asp Met Ile Leu Val Gly Asp Ser Leu Gly
 25 35 40 45
 Met Thr Val Leu Gly Tyr Glu Ser Thr Val Gln Val Thr Leu Ala Asp
 50 55 60
 Met Ile His His Gly Arg Ala Val Arg Arg Gly Ala Pro Asn Thr Phe
 30 65 70 75 80
 Val Val Val Asp Met Pro Ile Gly Ala Val Gly Ile Ser Met Thr Gln
 85 90 95
 Asp Leu Asn His Ala Leu Lys Leu Tyr Gln Glu Thr Asn Ala Asn Ala
 35 100 105 110
 Ile Lys Ala Glu Gly Ala His Ile Thr Pro Phe Ile Glu Lys Ala Thr
 115 120 125
 Ala Ile Gly Ile Pro Val Val Ala His Leu Gly Leu Thr Pro Gln Ser
 40 130 135 140
 Val Gly Val Met Gly Tyr Lys Leu Gln Gly Ala Thr Lys Glu Ala Ala
 145 150 155 160
 Glu Gln Leu Ile Leu Asp Ala Lys Asn Val Glu Gln Ala Gly Ala Val
 45 165 170 175
 Ala Leu Val Leu Glu Ala Ile Pro Asn Asp Leu Ala Glu Glu Ile Ser
 180 185 190
 Lys His Leu Thr Ile Pro Val Ile Gly Ile Gly Ala Gly Lys Gly Thr
 50 195 200 205
 Asp Gly Gln Val Leu Val Tyr His Asp Met Leu Asn Tyr Gly Val Glu
 55 210 215 220

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His Lys Ala Lys Phe Val Lys Gln Phe Ala Asp Phe Ser Val Gly Val
 225 230 235 240
 Asp Gly Leu Lys Gln Tyr Asp Gln Glu Val Lys Ser Gly Ala Phe Pro
 5 245 250 255
 Ser Glu Glu Tyr Thr Tyr Lys Lys Lys Ile Met Asn Glu Val Asn Asn
 260 265 270
 10 Asn Asp

(2) INFORMATION FOR SEQ ID NO:5244:

(i) SEQUENCE CHARACTERISTICS:
 15 (A) LENGTH: 430 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: protein

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5244:

Ser Asp Asp Trp Pro Lys Ser Ile Thr Ser Leu Ser Ile Arg Gly Val
 1 5 10 15
 Arg Met Lys His Gln Glu Thr Thr Ser Gln Gln Tyr Asn Phe Ser Ile
 30 20 25 30
 Ile Lys His Gly Asp Ile Ser Thr Pro Gln Gly Phe Thr Ala Gly Gly
 35 35 40 45
 Met His Ile Gly Leu Arg Ala Asn Lys Lys Asp Phe Gly Trp Ile Tyr
 50 55 60
 Ser Ser Ser Leu Ala Ser Ala Ala Ala Val Tyr Thr Leu Asn Gln Phe
 65 70 75 80
 Lys Ala Ala Pro Leu Ile Val Thr Glu Asp Thr Leu Gln Lys Ser Lys
 40 85 90 95
 Gly Lys Leu Gln Ala Leu Val Val Asn Ser Ala Asn Ala Asn Ser Cys
 100 105 110
 Thr Gly Gln Gln Gly Ile Asp Asp Ala Arg Gln Thr Gln Thr Trp Val
 45 115 120 125
 Ala Gln Gln Leu Gln Ile Pro Ser Glu His Val Ala Val Ala Ser Thr
 130 135 140
 Gly Val Ile Gly Glu Tyr Leu Pro Met Asp Lys Ile Lys Thr Gly Thr
 50 145 150 155 160
 Glu His Ile Lys Asp Ala Asn Phe Ala Thr Pro Gly Ala Phe Asn Glu
 55 165 170 175

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	Ala	Ile	Leu	Thr	Thr	Asp	Thr	Cys	Thr	Lys	His	Ile	Ala	Val	Ser	Leu	
				180					185					190			
5	Lys	Ile	Asp	Gly	Lys	Thr	Val	Thr	Ile	Gly	Gly	Ser	Thr	Lys	Gly	Ser	
			195					200					205				
	Gly	Met	Ile	His	Pro	Asn	Met	Ala	Thr	Met	Leu	Ala	Phe	Ile	Thr	Thr	
		210					215					220					
10	Asp	Ala	Ser	Ile	Glu	Ser	Asn	Thr	Leu	His	Gln	Leu	Leu	Lys	Ser	Ser	
		225				230					235					240	
	Thr	Asp	His	Thr	Phe	Asn	Met	Ile	Thr	Val	Asp	Gly	Asp	Thr	Ser	Thr	
				245						250					255		
15	Asn	Asp	Met	Val	Leu	Val	Met	Ala	Asn	His	Gln	Val	Glu	His	Gln	Ile	
			260						265					270			
	Leu	Ser	Gln	Asp	His	Pro	Gln	Trp	Glu	Thr	Phe	Val	Asp	Ala	Phe	Asn	
20			275					280					285				
	Phe	Val	Cys	Thr	Phe	Leu	Ala	Lys	Ala	Ile	Ala	Arg	Asp	Gly	Glu	Gly	
		290					295					300					
25	Ala	Thr	Lys	Leu	Ile	Ser	Val	Asn	Val	Ser	Gly	Ala	Lys	Ser	Ile	Ser	
		305				310					315					320	
	Asp	Ala	Arg	Lys	Ile	Gly	Lys	Thr	Ile	Val	Ser	Ser	Asn	Leu	Val	Lys	
				325						330					335		
30	Ser	Ala	Ile	Phe	Gly	Glu	Asp	Ala	Asn	Phe	Gly	Arg	Ile	Ile	Thr	Ala	
			340						345					350			
	Ile	Gly	Tyr	Ser	Gly	Cys	Glu	Ile	Asp	Pro	Asn	Cys	Thr	Tyr	Val	Gln	
			355					360					365				
35	Leu	Asn	Gln	Ile	Pro	Val	Val	Asp	Lys	Gly	Met	Ala	Val	Leu	Phe	Asp	
		370					375					380					
	Glu	Gln	Ala	Met	Ser	Asn	Thr	Leu	Thr	His	Glu	Asn	Val	Thr	Ile	Asp	
40		385				390					395					400	
	Val	Gln	Leu	Gly	Leu	Gly	Asn	Ala	Ala	Ala	Thr	Ala	Tyr	Gly	Cys	Asp	
				405					410					415			
45	Leu	Ser	Tyr	Asp	Tyr	Val	Arg	Ile	Asn	Ala	Ser	Tyr	Arg	Thr			
			420					425					430				

(2) INFORMATION FOR SEQ ID NO:5245:

- | | |
|----|-------------------------------|
| 50 | (i) SEQUENCE CHARACTERISTICS: |
| | (A) LENGTH: 469 amino acids |
| | (B) TYPE: amino acid |
| | (C) STRANDEDNESS: single |
| | (D) TOPOLOGY: linear |
| 55 | (ii) MOLECULE TYPE: protein |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5245:

5	Asn	Pro	Ala	Leu	Thr	Val	Phe	Ala	Phe	Ile	Met	Ile	Ile	Ser	Ile	Leu	1	5	10	15
	Leu	Ala	Tyr	Val	Phe	Lys	Trp	Leu	Gly	Leu	Val	Asp	Asp	Val	Leu	Leu	20	25	30	
10	Met	Val	Ile	Ile	Ile	Ser	Thr	Ile	Ser	Leu	Gly	Val	Val	Val	Pro	Thr	35	40	45	
	Leu	Lys	Glu	Met	Asn	Ile	Met	Arg	Thr	Thr	Ile	Gly	Gln	Phe	Ile	Leu	50	55	60	
15	Leu	Val	Ala	Val	Leu	Ala	Asp	Leu	Val	Thr	Met	Ile	Leu	Leu	Thr	Val	65	70	75	80
	Tyr	Gly	Ala	Ile	Asn	Gly	Gln	Gly	Gly	Ser	Thr	Ile	Trp	Leu	Ile	Gly	85	90	95	
20	Ile	Leu	Val	Val	Phe	Thr	Ala	Ile	Ser	Tyr	Ile	Leu	Gly	Val	Gln	Phe	100	105	110	
	Lys	Arg	Met	Ser	Phe	Leu	Gln	Lys	Leu	Met	Asp	Gly	Thr	Thr	Gln	Ile	115	120	125	
25	Gly	Ile	Arg	Ala	Val	Phe	Ala	Leu	Ile	Ile	Leu	Leu	Val	Ala	Leu	Ala	130	135	140	
	Glu	Gly	Val	Gly	Ala	Glu	Asn	Ile	Leu	Gly	Ala	Phe	Leu	Ala	Gly	Val	145	150	155	160
30	Val	Val	Ser	Leu	Leu	Asn	Pro	Asp	Glu	Glu	Met	Val	Glu	Lys	Leu	Asp	165	170	175	
	Ser	Phe	Gly	Tyr	Gly	Phe	Phe	Ile	Pro	Ile	Phe	Phe	Ile	Met	Xaa	Gly	180	185	190	
35	Val	Asp	Leu	Asn	Ile	Pro	Ser	Leu	Ile	Lys	Glu	Pro	Lys	Leu	Leu	Ile	195	200	205	
40	Ile	Ile	Pro	Ile	Leu	Ile	Val	Ala	Phe	Ile	Ile	Ser	Lys	Leu	Ile	Pro	210	215	220	
	Val	Met	Phe	Ile	Arg	Arg	Trp	Phe	Asp	Met	Lys	Thr	Thr	Ile	Ala	Ser	225	230	235	240
45	Ala	Phe	Leu	Leu	Thr	Ser	Thr	Leu	Ser	Leu	Val	Ile	Ala	Ala	Ala	Lys	245	250	255	
	Ile	Ser	Glu	Arg	Leu	Asn	Ala	Ile	Ser	Ala	Glu	Thr	Ser	Gly	Ile	Leu	260	265	270	
50	Ile	Leu	Ser	Ala	Val	Ile	Thr	Cys	Val	Phe	Val	Pro	Ile	Ile	Phe	Lys	275	280	285	
55	Lys	Leu	Phe	Pro	Val	Pro	Asp	Glu	Phe	Asn	Arg	Lys	Ile	Glu	Val	Ser	290	295	300	

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Leu Ile Gly Lys Asn Gln Leu Thr Ile Pro Ile Ala Gln Asn Leu Thr
305 310 315 320

5 Ser Gln Leu Tyr Asp Val Thr Leu Tyr Tyr Arg Lys Asp Leu Ser Asp
325 330 335

Arg Arg Gln Leu Ser Asp Asp Ile Thr Met Ile Glu Ile Ala Asp Tyr
340 345 350

10 Glu Gln Asp Val Leu Glu Arg Leu Gly Leu Phe Asp Arg Asp Ile Val
355 360 365

Val Cys Ala Thr Asn Asp Asp Asp Ile Asn Arg Lys Val Ala Lys Leu
370 375 380

15 Ala Lys Ala His Gln Val Glu Arg Val Ile Cys Arg Leu Glu Ser Thr
385 390 395 400

Thr Asp Asp Thr Glu Leu Val Asp Ser Gly Ile Glu Ile Phe Ser Ser
405 410 415

20 Tyr Leu Ser Asn Lys Ile Leu Leu Lys Gly Leu Ile Glu Thr Pro Asn
420 425 430

Met Leu Asn Leu Leu Ser Asn Val Glu Thr Ser Leu Tyr Glu Ile Gln
435 440 445

25 Met Leu Asn Tyr Lys Tyr Glu Asn Ile Gln Leu Arg Asn Phe Pro Phe
450 455 460

30 Gly Gly Asp Ile Ile
465

(2) INFORMATION FOR SEQ ID NO:5246:

(i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 414 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40 (ii) MOLECULE TYPE: protein

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5246:

Ala Ile Ile Val Ile Leu Leu Phe Leu Arg Asn Ile Arg Thr Thr Ala
1 5 10 15

Ile Ser Ile Ile Ser Ile Pro Leu Ser Leu Leu Met Ala Leu Ile Ala
50 20 25 30

Leu Lys Leu Ser Asp Val Ser Leu Asn Ile Leu Thr Leu Gly Ala Leu
35 40 45

55 Thr Val Ala Ile Gly Arg Val Ile Asp Asp Ser Ile Val Val Val Glu
50 55 60

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	Asn	Ile	Tyr	Arg	Arg	Leu	Thr	Asp	Ser	Glu	Glu	Gln	Leu	Lys	Gly	Glu	65	70	75	80
5	Asn	Leu	Ile	Ile	Ser	Ala	Thr	Thr	Glu	Val	Phe	Lys	Pro	Ile	Met	Ser	85	90	95	
	Ser	Thr	Leu	Val	Thr	Ile	Ile	Val	Phe	Leu	Pro	Leu	Val	Phe	Val	Ser	100	105	110	
10	Gly	Ser	Val	Gly	Glu	Met	Phe	Arg	Pro	Phe	Ala	Leu	Ala	Ile	Ala	Phe	115	120	125	
	Ser	Leu	Leu	Ala	Ser	Leu	Leu	Val	Ser	Ile	Thr	Leu	Val	Pro	Ala	Leu	130	135	140	
15	Ala	Ala	Thr	Leu	Phe	Lys	Lys	Gly	Val	Lys	Arg	Arg	Asn	Lys	Gln	His	145	150	155	160
	Gln	Glu	Gly	Leu	Gly	Val	Val	Ser	Thr	Thr	Tyr	Lys	Lys	Val	Leu	His	165	170	175	
20	Trp	Ser	Leu	Asn	His	Lys	Trp	Ile	Val	Ile	Ile	Leu	Ser	Thr	Leu	Ile	180	185	190	
25	Leu	Val	Ala	Thr	Ile	Val	Phe	Gly	Gly	Pro	Arg	Leu	Gly	Thr	Ser	Phe	195	200	205	
	Ile	Ser	Ala	Gly	Asp	Asp	Lys	Phe	Leu	Ala	Ile	Thr	Tyr	Thr	Pro	Lys	210	215	220	
30	Pro	Gly	Glu	Thr	Glu	Gln	Ala	Val	Leu	Asn	His	Ala	Lys	Asp	Val	Glu	225	230	235	240
	Lys	Tyr	Leu	Lys	Gln	Lys	Lys	His	Val	Lys	Thr	Ile	Gln	Tyr	Ser	Val	245	250	255	
35	Gly	Gly	Ser	Ser	Pro	Val	Asp	Pro	Thr	Gly	Ser	Thr	Asn	Ser	Met	Ala	260	265	270	
	Ile	Met	Val	Glu	Tyr	Asp	Asn	Asp	Thr	Pro	Asn	Phe	Asp	Val	Glu	Ala	275	280	285	
40	Asp	Lys	Val	Ile	Lys	His	Ala	Asp	Gly	Phe	Lys	His	Pro	Gly	Glu	Trp	290	295	300	
45	Lys	Asn	Gln	Asp	Leu	Gly	Thr	Gly	Ala	Gly	Asn	Lys	Ser	Val	Glu	Val	305	310	315	320
	Thr	Val	Lys	Gly	Pro	Ser	Met	Asp	Ala	Ile	Lys	Ser	Thr	Val	Lys	Asp	325	330	335	
50	Ile	Glu	Gln	Lys	Met	Lys	Gln	Val	Lys	Gly	Leu	Ala	Asn	Val	Lys	Ser	340	345	350	
	Asp	Leu	Ser	Gln	Thr	Tyr	Asp	Gln	Tyr	Glu	Ile	Lys	Val	Asp	Gln	Asn	355	360	365	
55	Lys	Ala	Ala	Glu	Asn	Gly	Ile	Ser	Ala	Ser	Gln	Leu	Ala	Met	His	Leu	370	375	380	

Asn Glu Asn Leu Pro Glu Lys Thr Val Thr Thr Val Lys Glu Asn Gly
385 390 395 400

Lys Thr Val Asp Val Lys Val Lys Gln Asn Lys Gln Thr Ala
405 410

(2) INFORMATION FOR SEQ ID NO:5247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 555 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5247:

Gly Lys Pro Phe Ile Ile Gly Leu Gly Asp Ile Ile Val Lys Lys Leu
1 5 10 15
Thr Thr Ile Leu Phe Gln Tyr Lys Ile Phe Pro Val Leu Met Phe Leu
20 25 30
Val Ser Thr Gly Leu Gly Ile Ile Val Ile Thr Gln Asn Ile Leu Ile
35 40 45
Ala Asp Phe Leu Ala Lys Ile Ile Arg His Gln Phe Gln Gly Leu Trp
50 55 60
Ile Val Leu Phe Ile Leu Leu Gly Val Leu Leu Leu Arg Ala Thr Val
65 70 75 80
Gln Phe Leu Asn Gln Trp Leu Gly Asp Thr Leu Ala Phe Lys Val Lys
85 90 95
His Met Leu Arg Gln Arg Val Ile Tyr Lys Asn Asn Gly His Pro Ile
100 105 110
Gly Glu Gln Met Thr Ile Leu Thr Glu Asn Ile Asp Gly Leu Ala Pro
115 120 125
Phe Tyr Lys Ser Tyr Leu Pro Gln Val Phe Lys Ser Met Met Val Pro
130 135 140
Leu Ile Ile Ile Ile Ala Met Phe Phe Ile His Phe Asn Thr Ala Leu
145 150 155 160
Ile Met Leu Ile Thr Ala Pro Phe Ile Pro Leu Phe Tyr Ile Ile Phe
165 170 175
Gly Leu Lys Thr Arg Asp Glu Ser Lys Asp Gln Met Thr Tyr Leu Asn
180 185 190
Gln Phe Ser Gln Arg Phe Leu Asn Ile Ala Lys Gly Leu Val Thr Leu
195 200 205

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	Lys	Leu	Phe	Asn	Arg	Thr	Glu	Gln	Thr	Glu	Lys	His	Ile	Tyr	Asp	Asp	
	210						215					220					
5	Ser	Thr	Gln	Phe	Arg	Thr	Leu	Thr	Met	Arg	Ile	Leu	Arg	Ser	Ala	Phe	
	225					230					235					240	
	Leu	Ser	Gly	Leu	Met	Leu	Glu	Phe	Ile	Ser	Met	Leu	Gly	Ile	Gly	Leu	
				245						250					255		
10	Val	Ala	Leu	Glu	Ala	Thr	Leu	Ser	Leu	Val	Val	Phe	His	Asn	Ile	Asp	
			260						265					270			
	Phe	Lys	Thr	Ala	Ala	Ile	Ala	Ile	Ile	Leu	Ala	Pro	Glu	Phe	Tyr	Asn	
			275					280					285				
15	Ala	Ile	Lys	Asp	Leu	Gly	Gln	Ala	Phe	His	Thr	Gly	Lys	Gln	Ser	Glu	
	290						295					300					
	Gly	Ala	Ser	Asp	Val	Val	Phe	Glu	Phe	Leu	Glu	Gln	Pro	Asn	Tyr	Asn	
	305				310						315					320	
20	Asn	Glu	Phe	Leu	Leu	Lys	Tyr	Glu	Glu	Asn	Gln	Lys	Pro	Phe	Ile	Gln	
				325						330					335		
	Leu	Thr	Asp	Ile	Ser	Phe	Arg	Tyr	Asp	Asp	Ser	Asp	Arg	Leu	Val	Leu	
25				340					345					350			
	Asn	Asp	Leu	Asn	Leu	Glu	Ile	Phe	Lys	Gly	Asp	Gln	Ile	Ala	Leu	Val	
			355					360					365				
	Gly	Pro	Ser	Gly	Ala	Gly	Lys	Ser	Thr	Leu	Thr	His	Leu	Ile	Ala	Gly	
30			370			375						380					
	Val	Tyr	Gln	Pro	Thr	Ile	Gly	Thr	Ile	Ser	Thr	Asn	Gln	Arg	Asp	Leu	
	385					390					395					400	
	Asn	Ile	Gly	Ile	Leu	Ser	Gln	Gln	Pro	Tyr	Ile	Phe	Ser	Ala	Ser	Ile	
35				405						410					415		
	Lys	Glu	Asn	Ile	Thr	Met	Phe	Lys	Asp	Ile	Glu	Asn	Asn	Thr	Ile	Glu	
			420					425						430			
40	Glu	Val	Leu	Asp	Glu	Val	Gly	Leu	Leu	Asp	Lys	Val	Gln	Ser	Phe	Thr	
			435				440						445				
	Lys	Gly	Ile	Asn	Thr	Ile	Ile	Gly	Glu	Gly	Gly	Glu	Met	Leu	Ser	Gly	
		450				455						460					
45	Gly	Gln	Met	Arg	Arg	Ile	Glu	Leu	Cys	Arg	Leu	Leu	Val	Met	Lys	Pro	
	465					470					475					480	
	Asp	Leu	Val	Ile	Phe	Asp	Glu	Pro	Ala	Thr	Gly	Leu	Asp	Ile	Gln	Thr	
				485					490						495		
50	Glu	His	Met	Ile	Gln	Asn	Val	Leu	Phe	Gln	His	Phe	Lys	Asp	Thr	Thr	
			500					505						510			
	Met	Ile	Val	Ile	Ala	His	Arg	Asp	Asn	Thr	Ile	Arg	His	Leu	Gln	Arg	
55			515				520						525				

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Arg Leu Tyr Ile Glu Asn Gly Arg Leu Ile Ala Asp Asp Arg Asn Ile
530 535 540

5 Ser Val Asn Ile Thr Glu Asn Gly Asp Asp Leu
545 550 555

(2) INFORMATION FOR SEQ ID NO:5248:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 393 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5248:

20 Val Trp Lys Leu Lys Met Arg Trp Ile Lys Arg Lys Lys Lys Asn Phe
1 5 10 15
Leu Asn Ser Lys Phe Asn Phe Asn Asn Gly Lys Ile Ala Thr Tyr Leu
25 20 25 30
Tyr Lys Glu Arg Thr Ala Met Trp Asn Lys Asn Arg Leu Thr Gln Met
35 35 40 45
Leu Ser Ile Glu Tyr Pro Ile Ile Gln Ala Gly Met Ala Gly Ser Thr
30 50 55 60
Thr Pro Lys Leu Val Ala Ser Val Ser Asn Ser Gly Gly Leu Gly Thr
65 70 75 80
Ile Gly Ala Gly Tyr Phe Asn Thr Gln Gln Leu Glu Asp Glu Ile Asp
35 85 90 95
Tyr Val Arg Gln Leu Thr Ser Asn Ser Phe Gly Val Asn Val Phe Val
100 105 110
40 Pro Ser Gln Gln Ser Tyr Thr Ser Ser Gln Ile Glu Asn Met Asn Ala
115 120 125
Trp Leu Lys Pro Tyr Arg Arg Ala Leu His Leu Glu Glu Pro Val Val
45 130 135 140
Lys Ile Thr Glu Glu Gln Gln Phe Lys Cys His Ile Asp Thr Ile Ile
145 150 155 160
Lys Lys Gln Val Pro Val Cys Cys Phe Thr Phe Gly Ile Pro Ser Glu
50 165 170 175
Gln Ile Ile Ser Arg Leu Lys Ala Ala Asn Val Lys Leu Ile Gly Thr
180 185 190
55 Ala Thr Ser Val Asp Glu Ala Ile Ala Asn Glu Lys Ala Gly Met Asp
195 200 205

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Ala Ile Val Ala Gln Gly Ser Glu Ala Gly Gly His Arg Gly Ser Phe
 210 215 220

5 Leu Lys Pro Lys Asn Gln Leu Pro Met Val Gly Thr Ile Ser Leu Val
 225 230 235 240

Pro Gln Ile Val Asp Val Val Ser Ile Pro Val Ile Ala Ala Gly Gly
 245 250 255

10 Ile Met Asp Gly Arg Gly Val Leu Ala Ser Ile Val Leu Gly Ala Glu
 260 265 270

Gly Val Gln Met Gly Thr Ala Phe Leu Thr Ser Gln Asp Ser Asn Ala
 275 280 285

15 Ser Glu Leu Leu Arg Asp Ala Ile Ile Asn Ser Lys Glu Thr Asp Thr
 290 295 300

Val Ile Thr Lys Ala Phe Ser Gly Lys Leu Ala Arg Gly Ile Asn Asn
 305 310 315 320

20 Arg Phe Ile Glu Glu Met Ser Gln Tyr Glu Gly Asp Ile Pro Asp Tyr
 325 330 335

Pro Ile Gln Asn Glu Leu Thr Ser Ser Ile Arg Lys Ala Ala Ala Asn
 340 345 350

25 Ile Gly Asp Lys Glu Leu Ile His Met Trp Ser Gly Gln Ser Pro Arg
 355 360 365

Leu Ala Thr Thr His Pro Ala Asn Thr Ile Met Ser Asn Ile Ile Asn
 370 375 380

Gln Ile Asn Gln Ile Met Gln Tyr Lys
 385 390

35 (2) INFORMATION FOR SEQ ID NO:5249:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 936 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

40

(ii) MOLECULE TYPE: protein

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5249:

Asn Asp Phe Leu Lys Arg Gly Asn Lys Met Asn Met Lys Lys Lys Glu
 1 5 10 15

50 Lys His Ala Ile Arg Lys Lys Ser Ile Gly Val Ala Ser Val Leu Val
 20 25 30

Gly Thr Leu Ile Gly Phe Gly Leu Leu Ser Ser Lys Glu Ala Asp Ala
 35 40 45

55

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	Ser	Glu	Asn	Ser	Val	Thr	Gln	Ser	Asp	Ser	Ala	Ser	Asn	Glu	Ser	Lys	
	50						55					60					
5	Ser	Asn	Asp	Ser	Ser	Ser	Val	Ser	Ala	Ala	Pro	Lys	Thr	Asp	Asp	Thr	
	65						70				75					80	
	Asn	Val	Ser	Asp	Thr	Lys	Thr	Ser	Ser	Asn	Thr	Asn	Asn	Gly	Glu	Thr	
					85					90					95		
10	Ser	Val	Ala	Gln	Asn	Pro	Ala	Gln	Gln	Glu	Thr	Thr	Gln	Ser	Ser	Ser	
				100					105					110			
	Thr	Asn	Ala	Thr	Thr	Glu	Glu	Thr	Pro	Val	Thr	Gly	Glu	Ala	Thr	Thr	
			115					120					125				
15	Thr	Thr	Thr	Asn	Gln	Ala	Asn	Thr	Pro	Ala	Thr	Thr	Gln	Ser	Ser	Asn	
		130					135					140					
	Thr	Asn	Ala	Glu	Glu	Leu	Val	Asn	Gln	Thr	Ser	Asn	Glu	Thr	Thr	Ser	
	145					150					155					160	
20	Asn	Asp	Thr	Asn	Thr	Val	Ser	Ser	Val	Asn	Ser	Pro	Gln	Asn	Ser	Thr	
					165					170					175		
	Asn	Ala	Glu	Asn	Val	Ser	Thr	Thr	Gln	Asp	Thr	Ser	Thr	Glu	Ala	Thr	
25				180					185					190			
	Pro	Ser	Asn	Asn	Glu	Ser	Ala	Pro	Gln	Ser	Thr	Asp	Ala	Ser	Asn	Lys	
			195					200					205				
30	Asp	Val	Val	Asn	Gln	Ala	Val	Asn	Thr	Ser	Ala	Pro	Arg	Met	Arg	Ala	
		210					215					220					
	Phe	Ser	Leu	Ala	Ala	Val	Ala	Ala	Asp	Ala	Pro	Val	Ala	Gly	Thr	Asp	
	225					230					235					240	
35	Ile	Thr	Asn	Gln	Leu	Thr	Asn	Val	Thr	Val	Gly	Ile	Asp	Ser	Gly	Thr	
					245					250					255		
	Thr	Val	Tyr	Pro	His	Gln	Ala	Gly	Tyr	Val	Lys	Leu	Asn	Tyr	Gly	Phe	
				260					265					270			
40	Ser	Val	Pro	Asn	Ser	Ala	Val	Lys	Gly	Asp	Thr	Phe	Lys	Ile	Thr	Val	
			275					280					285				
	Pro	Lys	Glu	Leu	Asn	Leu	Asn	Gly	Val	Thr	Ser	Thr	Ala	Lys	Val	Pro	
		290					295					300					
45	Pro	Ile	Met	Ala	Gly	Asp	Gln	Val	Leu	Ala	Asn	Gly	Val	Ile	Asp	Ser	
		305				310					315				320		
	Asp	Gly	Asn	Val	Ile	Tyr	Thr	Phe	Thr	Asp	Tyr	Val	Asn	Thr	Lys	Asp	
				325						330				335			
50	Asp	Val	Lys	Ala	Thr	Leu	Thr	Met	Pro	Ala	Tyr	Ile	Asp	Pro	Glu	Asn	
				340					345					350			
	Val	Lys	Lys	Thr	Gly	Asn	Val	Thr	Leu	Ala	Thr	Gly	Ile	Gly	Ser	Thr	
55			355					360					365				

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	Thr	Ala	Asn	Lys	Thr	Val	Leu	Val	Asp	Tyr	Glu	Lys	Tyr	Gly	Lys	Phe
	370						375					380				
5	Tyr	Asn	Leu	Ser	Ile	Lys	Gly	Thr	Ile	Asp	Gln	Ile	Asp	Lys	Thr	Asn
	385					390					395					400
	Asn	Thr	Tyr	Arg	Gln	Thr	Ile	Tyr	Val	Asn	Pro	Ser	Gly	Asp	Asn	Val
					405					410					415	
10	Ile	Ala	Pro	Val	Leu	Thr	Gly	Asn	Leu	Lys	Pro	Asn	Thr	Asp	Ser	Asn
				420					425					430		
	Ala	Leu	Ile	Asp	Gln	Gln	Asn	Thr	Ser	Ile	Lys	Val	Tyr	Lys	Val	Asp
				435				440						445		
15	Asn	Ala	Ala	Asp	Leu	Ser	Glu	Ser	Tyr	Phe	Val	Asn	Pro	Glu	Asn	Phe
	450						455					460				
	Glu	Asp	Val	Thr	Asn	Ser	Val	Asn	Ile	Thr	Phe	Pro	Asn	Pro	Asn	Gln
	465					470					475					480
20	Tyr	Lys	Val	Glu	Phe	Asn	Thr	Pro	Asp	Asp	Gln	Ile	Thr	Thr	Pro	Tyr
					485					490					495	
	Ile	Val	Val	Val	Asn	Gly	His	Ile	Asp	Pro	Asn	Ser	Lys	Gly	Asp	Leu
25					500				505					510		
	Ala	Leu	Arg	Ser	Thr	Leu	Tyr	Gly	Tyr	Asn	Ser	Asn	Ile	Ile	Trp	Arg
			515					520						525		
30	Ser	Met	Ser	Trp	Asp	Asn	Glu	Val	Ala	Phe	Asn	Asn	Gly	Ser	Gly	Ser
	530						535					540				
	Gly	Asp	Gly	Ile	Asp	Lys	Pro	Val	Val	Pro	Glu	Gln	Pro	Asp	Glu	Pro
	545					550					555					560
35	Gly	Glu	Ile	Glu	Pro	Ile	Pro	Glu	Asp	Ser	Asp	Ser	Asp	Pro	Gly	Ser
					565					570					575	
	Asp	Ser	Gly	Ser	Asp	Ser	Asn	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Gly	Ser
				580					585						590	
40	Asp	Ser	Thr	Ser	Asp	Ser	Gly	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser
			595					600						605		
	Ala	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Ala	Ser	Asp	Ser
			610				615						620			
45	Asp	Ser	Ala	Ser	Asp	Ser	Asp	Ser	Asp	Asn	Asp	Ser	Asp	Ser	Asp	Ser
	625					630					635					640
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
					645					650					655	
50	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
				660				665						670		
	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser	Asp	Ser
55				675			680						685			

Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 690 695 700
 5 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 705 710 715 720
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 725 730 735
 10 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 740 745 750
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 755 760 765
 15 Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Asp Ser Asp Ser
 770 775 780
 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 785 790 795 800
 20 Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 805 810 815
 25 Glu Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser Asp Ser
 820 825 830
 Asp Ser Asp Ser Asp Ser Asp Ser Ala Ser Asp Ser Asp Ser Gly Ser
 835 840 845
 30 Asp Ser Asp Ser Ser Ser Asp Ser Asp Ser Glu Ser Asp Ser Asn Ser
 850 855 860
 Asp Ser Glu Ser Val Ser Asn Asn Asn Val Val Pro Pro Asn Ser Pro
 865 870 875 880
 35 Lys Asn Gly Thr Asn Ala Ser Asn Lys Asn Glu Ala Lys Asp Ser Lys
 885 890 895
 40 Glu Pro Leu Pro Asp Thr Gly Ser Glu Asp Glu Ala Asn Thr Ser Leu
 900 905 910
 Ile Trp Gly Leu Leu Ala Ser Ile Gly Ser Leu Leu Leu Phe Arg Arg
 915 920 925
 45 Lys Lys Glu Asn Lys Asp Lys Lys
 930 935

(2) INFORMATION FOR SEQ ID NO:5250:

- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 194 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5250:

5 Val Ser Lys Leu Lys Lys Glu Ile Leu Glu Trp Ile Ile Ser Ile Ala
1 5 10 15

Val Ala Phe Val Ile Leu Phe Ile Val Gly Lys Phe Ile Val Thr Pro
20 25 30

10 Tyr Thr Ile Lys Gly Glu Ser Met Asp Pro Thr Leu Lys Asp Gly Glu
35 40 45

Arg Val Ala Val Asn Ile Val Gly Tyr Lys Thr Gly Gly Leu Glu Lys
50 55 60

15 Gly Asn Val Val Val Phe His Ala Asn Lys Asn Asp Asp Tyr Val Lys
65 70 75 80

Arg Val Ile Gly Val Pro Gly Asp Lys Val Glu Tyr Lys Asn Asp Thr
85 90 95

20 Leu Tyr Val Asn Gly Lys Lys Gln Asp Glu Pro Tyr Leu Asn Tyr Asn
100 105 110

Leu Lys His Lys Lys Gln Gly Asp Tyr Ile Thr Gly Thr Phe Gln Val Lys
115 120 125

25 Asp Leu Pro Asn Ala Asn Pro Lys Ser Asn Val Ile Pro Lys Gly Lys
130 135 140

Tyr Leu Val Leu Gly Asp Asn Arg Glu Val Ser Lys Asp Ser Arg Ala
145 150 155 160

Phe Gly Leu Ile Asp Glu Asp Gln Ile Val Gly Lys Val Ser Phe Gln
165 170 175

35 Val Leu Ala His Phe Ser Glu Phe Gln Thr Ser Ile Ser Xaa Leu Lys
180 185 190

Ile Leu

40 (2) INFORMATION FOR SEQ ID NO:5251:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 559 amino acids
 (B) TYPE: amino acid
 45 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5251:

55 Leu Lys Ala Xaa Tyr Ala Lys Leu Asp Asp Val Ser Lys Phe Glu Asp
1 5 10 15

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	Val	Thr	Asp	Asn	Met	Ser	Leu	Asp	Phe	Asp	Thr	Asn	Gly	Gly	Tyr	Ser	
				20					25					30			
5	Leu	Asn	Phe	Asn	Asn	Leu	Asp	Gln	Ser	Lys	Asn	Tyr	Val	Ile	Lys	Tyr	
			35					40					45				
	Glu	Gly	Tyr	Tyr	Asp	Ser	Asn	Ala	Ser	Asn	Leu	Glu	Phe	Gln	Thr	His	
		50					55					60					
10	Leu	Phe	Gly	Tyr	Tyr	Asn	Tyr	Tyr	Tyr	Thr	Ser	Asn	Leu	Thr	Trp	Lys	
	65					70					75					80	
	Asn	Gly	Val	Ala	Phe	Tyr	Ser	Asn	Asn	Ala	Gln	Gly	Asp	Gly	Lys	Asp	
					85					90					95		
15	Lys	Leu	Lys	Glu	Pro	Ile	Ile	Glu	His	Ser	Thr	Pro	Ile	Glu	Leu	Glu	
				100					105					110			
	Phe	Lys	Ser	Glu	Pro	Pro	Val	Glu	Lys	His	Glu	Leu	Thr	Gly	Thr	Ile	
20			115					120					125				
	Glu	Glu	Ser	Asn	Asp	Ser	Lys	Pro	Ile	Asp	Phe	Glu	Tyr	His	Thr	Ala	
		130					135					140					
25	Val	Glu	Gly	Ala	Glu	Gly	His	Ala	Glu	Gly	Thr	Ile	Glu	Thr	Glu	Glu	
	145					150					155					160	
	Asp	Ser	Ile	His	Val	Asp	Phe	Glu	Glu	Ser	Thr	His	Glu	Asn	Ser	Lys	
					165					170					175		
30	His	His	Ala	Asp	Val	Val	Glu	Tyr	Glu	Glu	Asp	Thr	Asn	Pro	Gly	Gly	
				180					185					190			
	Gly	Gln	Val	Thr	Thr	Glu	Ser	Asn	Leu	Val	Glu	Phe	Asp	Glu	Asp	Ser	
			195					200					205				
35	Thr	Lys	Gly	Ile	Val	Thr	Gly	Ala	Val	Ser	Asp	His	Thr	Thr	Ile	Glu	
		210					215					220					
	Asp	Thr	Lys	Glu	Tyr	Thr	Thr	Glu	Ser	Asn	Leu	Ile	Glu	Leu	Val	Asp	
40		225				230					235					240	
	Glu	Leu	Pro	Glu	Glu	His	Gly	Gln	Ala	Gln	Gly	Pro	Ile	Glu	Glu	Ile	
					245					250					255		
	Thr	Glu	Asn	Asn	His	His	Ile	Ser	His	Ser	Gly	Leu	Gly	Thr	Glu	Asn	
45					260				265					270			
	Gly	His	Gly	Asn	Tyr	Gly	Val	Ile	Glu	Glu	Ile	Glu	Glu	Asn	Ser	His	
			275					280					285				
50	Val	Asp	Ile	Lys	Ser	Glu	Leu	Gly	Tyr	Glu	Gly	Gly	Gln	Asn	Ser	Gly	
		290					295					300					
	Asn	Gln	Ser	Phe	Glu	Glu	Asp	Thr	Glu	Glu	Asp	Lys	Pro	Lys	Tyr	Glu	
		305				310					315					320	
55	Gln	Gly	Gly	Asn	Ile	Val	Asp	Ile	Asp	Phe	Asp	Ser	Val	Pro	Gln	Ile	
					325					330					335		

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His Gly Gln Asn Asn Gly Asn Gln Ser Phe Glu Glu Asp Thr Glu Lys
340 345 350

5 Asp Lys Pro Lys Tyr Glu Gln Gly Gly Asn Ile Ile Asp Ile Asp Phe
355 360 365

Asp Ser Val Pro His Ile His Gly Phe Asn Lys His Thr Glu Ile Ile
370 375 380

10 Glu Glu Asp Thr Asn Lys Asp Lys Pro Asn Tyr Gln Phe Gly Gly His
385 390 395 400

Asn Ser Val Asp Phe Glu Glu Asp Thr Leu Pro Gln Val Ser Gly His
405 410 415

15 Asn Glu Gly Gln Gln Thr Ile Glu Glu Asp Thr Thr Pro Pro Ile Val
420 425 430

Pro Pro Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro
435 440 445

20 Thr Pro Pro Thr Pro Glu Val Pro Ser Glu Pro Glu Thr Pro Thr Pro
450 455 460

Pro Thr Pro Glu Val Pro Thr Glu Pro Gly Lys Pro Ile Pro Pro Ala
465 470 475 480

25 Lys Glu Glu Pro Lys Lys Pro Ser Lys Pro Val Glu Gln Gly Lys Val
485 490 495

Val Thr Pro Val Ile Glu Ile Asn Glu Lys Val Lys Ala Val Val Pro
500 505 510

Thr Lys Lys Ala Gln Ser Lys Lys Ser Glu Leu Pro Glu Thr Gly Gly
515 520 525

35 Glu Glu Ser Thr Asn Asn Gly Met Leu Phe Gly Gly Leu Phe Ser Ile
530 535 540

Leu Gly Leu Ala Leu Leu Arg Arg Asn Lys Lys Asn His Lys Ala
545 550 555

(2) INFORMATION FOR SEQ ID NO:5252:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 251 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5252:

Thr Lys Asn Glu Lys Ile Asn Asp Val Thr Ala Val Ala Glu Lys Glu
1 5 10 15

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Val Val Glu Glu Thr Lys Ala Thr Gly Thr Asp Val Thr Asn Lys Val
20 25 30

5 Glu Val Glu Glu Gly Ser Glu Ile Val Gly His Lys Gln Asp Thr Asn
35 40 45

Val Val Asn Pro His Asn Ala Glu Arg Val Thr Leu Lys Tyr Lys Trp
50 55 60

10 Lys Phe Gly Glu Gly Ile Lys Ala Gly Asp Tyr Phe Asp Phe Thr Leu
65 70 75 80

Ser Asp Asn Val Glu Thr His Gly Ile Ser Thr Leu Arg Lys Val Pro
85 90 95

15 Glu Ile Lys Ser Thr Asp Gly Gln Val Met Ala Thr Gly Glu Ile Ile
100 105 110

Gly Glu Arg Lys Val Arg Tyr Thr Phe Lys Glu Tyr Val Gln Glu Lys
115 120 125

20 Lys Asp Leu Thr Ala Glu Leu Ser Leu Asn Leu Phe Ile Asp Pro Thr
130 135 140

Thr Val Thr Gln Lys Gly Asn Gln Asn Val Glu Val Lys Leu Gly Glu
145 150 155 160

25 Thr Thr Val Ser Lys Ile Phe Asn Ile Gln Tyr Leu Gly Gly Val Arg
165 170 175

30 Asp Asn Trp Gly Val Thr Ala Asn Gly Arg Ile Asp Thr Leu Asn Lys
180 185 190

Val Asp Gly Lys Phe Ser His Phe Ala Tyr Met Lys Pro Asn Asn Gln
195 200 205

35 Ser Leu Ser Ser Val Thr Val Thr Gly Gln Val Thr Lys Gly Asn Lys
210 215 220

Pro Gly Val Asn Asn Pro Thr Val Lys Val Tyr Lys His Ile Gly Ser
225 230 235 240

40 Asp Asp Leu Ala Glu Ser Xaa Xaa Cys Lys Ala
245 250

(2) INFORMATION FOR SEQ ID NO:5253:

- 45 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 163 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 50 (ii) MOLECULE TYPE: protein

- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5253:

Ile Leu His Leu Arg Glu Asn Ile Ile Val Lys Ser Asn Leu Arg Tyr
 1 5 10 15
 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr
 5 20 25 30
 Met Ile Val Val Gly Met Gly Gln Glu Lys Glu Ala Ala Ala Ser Glu
 35 40 45
 Gln Asn Asn Thr Thr Val Glu Ser Gly Ser Ser Ala Thr Glu Ser
 10 50 55 60
 Lys Ala Ser Glu Thr Gln Thr Thr Thr Asn Asn Val Asn Thr Ile Asp
 65 70 75 80
 Glu Thr Gln Ser Tyr Ser Ala Thr Ser Thr Glu Gln Pro Ser Gln Ser
 15 85 90 95
 Thr Gln Val Thr Thr Glu Glu Ala Pro Lys Thr Val Gln Ala Pro Lys
 100 105 110
 Val Glu Thr Ser Arg Val Asp Leu Pro Ser Glu Lys Val Ala Asp Lys
 115 120 125
 Glu Thr Thr Gly Thr Gln Val Asp Ile Ala Gln Pro Ser Asn Val Ser
 130 135 140
 Glu Ile Lys Pro Arg Met Lys Arg Ser Met Thr Leu Gln Gln Leu Gln
 145 150 155 160
 Arg Lys Lys

(2) INFORMATION FOR SEQ ID NO:5254:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1027 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5254:

Ile Leu His Leu Lys Gly Asp Ile Ile Val Lys Asn Asn Leu Arg Tyr
 1 5 10 15
 Gly Ile Arg Lys His Lys Leu Gly Ala Ala Ser Val Phe Leu Gly Thr
 20 25 30
 Met Ile Val Val Gly Met Gly Gln Asp Lys Glu Ala Ala Ala Ser Glu
 35 40 45
 Gln Lys Thr Thr Thr Val Glu Glu Asn Gly Asn Ser Ala Thr Asp Asn
 50 55 60

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	Lys	Thr	Ser	Glu	Thr	Gln	Thr	Thr	Ala	Thr	Asn	Val	Asn	His	Ile	Glu	65	70	75	80
5	Glu	Thr	Gln	Ser	Tyr	Asn	Ala	Thr	Val	Thr	Glu	Gln	Pro	Ser	Asn	Ala	85	90	95	
	Thr	Gln	Val	Thr	Thr	Glu	Glu	Ala	Pro	Lys	Ala	Val	Gln	Ala	Pro	Gln	100	105	110	
10	Thr	Ala	Gln	Pro	Ala	Asn	Ile	Glu	Thr	Val	Lys	Glu	Glu	Val	Val	Lys	115	120	125	
	Glu	Glu	Ala	Lys	Pro	Gln	Val	Lys	Glu	Thr	Thr	Gln	Ser	Gln	Asp	Asn	130	135	140	
15	Ser	Gly	Asp	Gln	Arg	Gln	Val	Asp	Leu	Thr	Pro	Lys	Lys	Ala	Thr	Gln	145	150	155	160
	Asn	Gln	Val	Ala	Glu	Thr	Gln	Val	Glu	Val	Ala	Gln	Pro	Arg	Thr	Ala	165	170	175	
20	Ser	Glu	Ser	Lys	Pro	Arg	Val	Thr	Arg	Ser	Ala	Asp	Val	Ala	Glu	Ala	180	185	190	
	Lys	Glu	Ala	Ser	Asn	Ala	Lys	Val	Glu	Thr	Gly	Thr	Asp	Val	Thr	Ser	195	200	205	
25	Lys	Val	Thr	Val	Glu	Ile	Gly	Ser	Ile	Glu	Gly	His	Asn	Asn	Thr	Asn	210	215	220	
	Lys	Val	Glu	Pro	His	Ala	Gly	Gln	Arg	Ala	Val	Leu	Lys	Tyr	Lys	Leu	225	230	235	240
	Lys	Phe	Glu	Asn	Gly	Leu	His	Gln	Gly	Asp	Tyr	Phe	Asp	Phe	Thr	Leu	245	250	255	
35	Ser	Asn	Asn	Val	Asn	Thr	His	Gly	Val	Ser	Thr	Ala	Arg	Lys	Val	Pro	260	265	270	
	Glu	Ile	Lys	Asn	Gly	Ser	Val	Val	Met	Ala	Thr	Gly	Glu	Val	Leu	Glu	275	280	285	
40	Gly	Gly	Lys	Ile	Arg	Tyr	Thr	Phe	Thr	Asn	Asp	Ile	Glu	Asp	Lys	Val	290	295	300	
	Asp	Val	Thr	Ala	Glu	Leu	Glu	Ile	Asn	Leu	Phe	Ile	Asp	Pro	Lys	Thr	305	310	315	320
45	Val	Gln	Thr	Asn	Gly	Asn	Gln	Thr	Ile	Thr	Ser	Thr	Leu	Asn	Glu	Glu	325	330	335	
	Gln	Thr	Ser	Lys	Glu	Leu	Asp	Val	Lys	Tyr	Lys	Asp	Gly	Ile	Gly	Asn	340	345	350	
50	Tyr	Tyr	Ala	Asn	Leu	Asn	Gly	Ser	Ile	Glu	Thr	Phe	Asn	Lys	Ala	Asn	355	360	365	
55	Asn	Arg	Phe	Ser	His	Val	Ala	Phe	Ile	Lys	Pro	Asn	Asn	Gly	Lys	Thr	370	375	380	

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	Thr	Ser	Val	Thr	Val	Thr	Gly	Thr	Leu	Met	Lys	Gly	Ser	Asn	Gln	Asn	385		390		395		400
5	Gly	Asn	Gln	Pro	Lys	Val	Arg	Ile	Phe	Glu	Tyr	Leu	Gly	Asn	Asn	Glu			405		410		415
	Asp	Ile	Ala	Lys	Ser	Val	Tyr	Ala	Asn	Thr	Thr	Asp	Thr	Ser	Lys	Phe			420		425		430
10	Lys	Glu	Val	Thr	Ser	Asn	Met	Ser	Gly	Asn	Leu	Asn	Leu	Gln	Asn	Asn			435		440		445
	Gly	Ser	Tyr	Ser	Leu	Asn	Ile	Glu	Asn	Leu	Asp	Lys	Thr	Tyr	Val	Val			450		455		460
15	His	Tyr	Asp	Gly	Glu	Tyr	Leu	Asn	Gly	Thr	Asp	Glu	Val	Asp	Phe	Arg			465		470		475
	Thr	Gln	Met	Val	Gly	His	Pro	Glu	Gln	Leu	Tyr	Lys	Tyr	Tyr	Tyr	Asp			485		490		495
20	Arg	Gly	Tyr	Thr	Leu	Thr	Trp	Asp	Asn	Gly	Leu	Val	Leu	Tyr	Ser	Asn			500		505		510
	Lys	Ala	Asn	Gly	Asn	Glu	Lys	Asn	Gly	Pro	Ile	Ile	Gln	Asn	Asn	Lys			515		520		525
25	Phe	Glu	Tyr	Lys	Glu	Asp	Thr	Ile	Lys	Glu	Thr	Leu	Thr	Gly	Gln	Tyr			530		535		540
	Asp	Lys	Asn	Leu	Val	Thr	Thr	Val	Glu	Glu	Glu	Tyr	Asp	Ser	Ser	Thr			545		550		555
30	Leu	Asp	Ile	Asp	Tyr	His	Thr	Ala	Ile	Asp	Gly	Gly	Gly	Gly	Tyr	Val			565		570		575
	Asp	Gly	Tyr	Ile	Glu	Thr	Ile	Glu	Glu	Thr	Asp	Ser	Ser	Ala	Ile	Asp			580		585		590
35	Ile	Asp	Tyr	His	Thr	Ala	Val	Asp	Ser	Glu	Ala	Gly	His	Val	Gly	Gly			595		600		605
40	Tyr	Thr	Glu	Ser	Ser	Glu	Glu	Ser	Asn	Pro	Ile	Asp	Phe	Glu	Glu	Ser			610		615		620
	Thr	His	Glu	Asn	Ser	Lys	His	His	Ala	Asp	Val	Val	Glu	Tyr	Glu	Glu			625		630		635
45	Asp	Thr	Asn	Pro	Gly	Gly	Gly	Gln	Val	Thr	Thr	Glu	Ser	Asn	Leu	Val			645		650		655
	Glu	Phe	Asp	Glu	Glu	Ser	Thr	Lys	Gly	Ile	Val	Thr	Gly	Ala	Val	Ser			660		665		670
50	Asp	His	Thr	Thr	Val	Glu	Asp	Thr	Lys	Glu	Tyr	Thr	Thr	Glu	Ser	Asn			675		680		685
	Leu	Ile	Glu	Leu	Val	Asp	Glu	Leu	Pro	Glu	Glu	His	Gly	Gln	Ala	Gln			690		695		700
55																							

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	Gly	Pro	Val	Glu	Glu	Ile	Thr	Lys	Asn	Asn	His	His	Ile	Ser	His	Ser	705	710	715	720
5	Gly	Leu	Gly	Thr	Glu	Asn	Gly	His	Gly	Asn	Tyr	Asp	Val	Ile	Glu	Glu	725	730	735	
	Ile	Glu	Glu	Asn	Ser	His	Val	Asp	Ile	Lys	Ser	Glu	Leu	Gly	Tyr	Glu	740	745	750	
10	Gly	Gly	Gln	Asn	Ser	Gly	Asn	Gln	Ser	Phe	Glu	Glu	Asp	Thr	Glu	Glu	755	760	765	
	Asp	Lys	Pro	Lys	Tyr	Glu	Gln	Gly	Gly	Asn	Ile	Val	Asp	Ile	Asp	Phe	770	775	780	
15	Asp	Ser	Val	Pro	Gln	Ile	His	Gly	Gln	Asn	Lys	Gly	Asn	Gln	Ser	Phe	785	790	795	800
	Glu	Glu	Asp	Thr	Glu	Lys	Asp	Lys	Pro	Lys	Tyr	Glu	His	Gly	Gly	Asn	805	810	815	
20	Ile	Ile	Asp	Ile	Asp	Phe	Asp	Ser	Val	Pro	His	Ile	His	Gly	Phe	Asn	820	825	830	
	Lys	His	Thr	Glu	Ile	Ile	Glu	Glu	Asp	Thr	Asn	Lys	Asp	Lys	Pro	Ser	835	840	845	
25	Tyr	Gln	Phe	Gly	Gly	His	Asn	Ser	Val	Asp	Phe	Glu	Glu	Asp	Thr	Leu	850	855	860	
	Pro	Lys	Val	Ser	Gly	Gln	Asn	Glu	Gly	Gln	Gln	Thr	Ile	Glu	Glu	Asp	865	870	875	880
30	Thr	Thr	Pro	Pro	Ile	Val	Pro	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	885	890	895	
	Ser	Glu	Pro	Glu	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ser	Glu	900	905	910	
35	Pro	Glu	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ser	Glu	Pro	Glu	915	920	925	
	Thr	Pro	Thr	Pro	Pro	Thr	Pro	Glu	Val	Pro	Ala	Glu	Pro	Gly	Lys	Pro	930	935	940	
40	Val	Pro	Pro	Ala	Lys	Glu	Glu	Pro	Lys	Lys	Pro	Ser	Lys	Pro	Val	Glu	945	950	955	960
45	Gln	Gly	Lys	Val	Val	Thr	Pro	Val	Ile	Glu	Ile	Asn	Glu	Lys	Val	Lys	965	970	975	
	Ala	Val	Ala	Pro	Thr	Lys	Lys	Pro	Gln	Ser	Lys	Lys	Ser	Glu	Leu	Pro	980	985	990	
50	Glu	Thr	Gly	Gly	Glu	Glu	Ser	Thr	Asn	Lys	Gly	Met	Leu	Phe	Gly	Gly	995	1000	1005	
	Leu	Phe	Ser	Ile	Leu	Gly	Leu	Ala	Leu	Leu	Arg	Arg	Asn	Lys	Lys	Asn	1010	1015	1020	
55																				

His Lys Ala
1025

5 (2) INFORMATION FOR SEQ ID NO:5255:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 amino acids
 (B) TYPE: amino acid
 10 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5255:

20 Gly Glu Lys Cys Met Phe Leu Ala Trp Asn Glu Ile Arg Arg Asn Lys
 1 5 10 15
 Leu Lys Phe Gly Leu Ile Ile Gly Val Leu Thr Met Ile Ser Tyr Leu
 20 25 30
 25 Leu Phe Leu Leu Ser Gly Leu Ala Asn Gly Leu Ile Asn Met Asn Lys
 35 40 45
 Glu Gly Ile Asp Lys Trp Gln Ala Asp Ala Ile Val Leu Asn Lys Asp
 50 55 60
 30 Ala Asn Gln Thr Val Gln Gln Ser Val Phe Asn Lys Lys Asp Ile Glu
 65 70 75 80
 Asn Lys Tyr Lys Lys Gln Ala Thr Leu Lys Gln Thr Gly Glu Ile Val
 85 90 95
 Ser Asn Gly His Gln Lys Asp Asn Val Leu Val Phe Gly Val Glu Lys
 100 105 110
 40 Ser Ser Phe Leu Val Pro Ser Leu Ile Glu Gly His Lys Ala Thr Lys
 115 120 125
 Asp Asn Glu Val Leu Ala Asp Glu Thr Leu Lys Asn Lys Gly Leu Lys
 130 135 140
 45 Leu Gly Asp Thr Leu Ser Leu Ser Xaa Xaa Arg
 145 150 155

50

Claims

1. Computer readable medium having recorded thereon a nucleotide sequence of the Staphylococcus aureus ge-
 nome as depicted in SEQ ID NOS:1-5,191, a representative fragment thereof or a nucleotide sequence at least
 55 95 % identical to a nucleotide sequence depicted in SEQ ID NOS:1-5,191.
2. Computer readable medium having recorded thereon any one of the fragments of SEQ ID NOS:1-5,191 depicted
 in Tables 2 and 3 or a degenerate variant thereof.

3. The computer readable medium of claim 1, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
- 5 4. The computer readable medium of claim 3, wherein said medium is selected from the group consisting of a floppy disc, a hard disc, random access memory (RAM), read only memory (ROM), and CD-ROM.
5. A computer-based system for identifying fragments of the *Staphylococcus aureus* genome of commercial importance comprising the following elements:
 - 10 (a) a data storage means comprising the nucleotide sequence of SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191;
 - (b) search means for comparing a target sequence to the nucleotide sequence of the data storage means of step (a) to identify homologous sequence(s), and
 - 15 (c) retrieval means for obtaining said homologous sequence(s) of step (b).
6. A method for identifying commercially important nucleic acid fragments of the *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to a nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence is not randomly selected.
- 20 7. A method for identifying an expression modulating fragment of *Staphylococcus aureus* genome comprising the step of comparing a database comprising the nucleotide sequences depicted in SEQ ID NOS:1-5,191, a representative fragment thereof, or a nucleotide sequence at least 95% identical to the nucleotide sequence of SEQ ID NOS:1-5,191 with a target sequence to obtain a nucleic acid molecule comprised of a complementary nucleotide sequence to said target sequence, wherein said target sequence comprises sequences known to regulate gene expression.
- 25 8. A protein-encoding nucleic acid fragment of the *Staphylococcus aureus* genome, wherein said fragment comprises the nucleotide sequence of any one of the fragments of SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence, or a degenerate variant of any of the aforementioned sequences.
- 30 9. The nucleic acid fragment of claim 8 which is DNA.
10. The nucleic acid fragment of claim 8 which is RNA.
11. A vector comprising a fragment of claim 8.
- 40 12. A fragment of the *Staphylococcus aureus* genome, wherein said fragment modulates the expression of an operably linked open reading frame, wherein said fragment consists of the nucleotide sequence from about 10 to 200 bases in length which is 5' to any one of the open reading frames depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.
- 45 13. A vector comprising a fragment of claim 12.
14. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome of claim 8.
- 50 15. A method for producing a polypeptide in a host cell comprising the steps of:
 - 55 (a) incubating an organism of claim 14 under conditions where said fragment is expressed to produce said protein, and
 - (b) isolating said protein.
16. An organism which has been altered to contain any one of the fragments of the *Staphylococcus aureus* genome

of claim 12.

- 5 17. A method for regulating the expression of a nucleic acid molecule comprising the step of covalently attaching to said nucleic acid molecule a nucleic acid molecule consisting of the nucleotide sequence from about 30 to 300 bases 5' to any one of the fragments of the *Staphylococcus aureus* genome depicted in Seq ID Nos:1-5,191 and Tables 2 and 3 or a nucleotide sequence at least 95% identical to such a nucleotide sequence or a degenerate variant of any of the aforementioned sequences.
- 10 18. A nucleic acid molecule being a homolog of any of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:
 - (a) screening a genomic DNA library using as a probe a target sequence defined by any of SEQ ID NOS: 1-5,191 and Tables 2 and 3, including fragments thereof;
 - 15 (b) identifying members of said library which contain sequences that hybridize to said target sequence;
 - (c) isolating the nucleic acid molecules from said members identified in step (b).
- 20 19. A DNA molecule being a homolog of any one of the fragments of the *Staphylococcus aureus* genome of SEQ ID NOS:1-5,191 and Tables 2 and 3, wherein said nucleic acid molecule is produced by a process comprising the steps of:
 - (a) isolating mRNA, DNA, or cDNA produced from an organism;
 - (b) amplifying nucleic acid molecules whose nucleotide sequence is homologous to amplification primers derived from said fragment of said *Staphylococcus aureus* genome to prime said amplification;
 - 25 (c) isolating said amplified sequences produced in step (b).
20. A polypeptide encoded by a fragment of claim 8.
- 30 21. An antibody which selectively binds to any one of the polypeptides of claim 20.
22. A kit for analyzing samples for the presence of polynucleotides derived from *Staphylococcus aureus*, comprising at least one polynucleotide containing a nucleotide sequence of any one of the fragments SEQ ID NOS:1-5,191 depicted in Tables 2 and 3 or a nucleotide sequence at least 95% identical thereto or a degenerate variant of any of the aforementioned sequences, that will hybridize to a *staphylococcus aureus* polynucleotide under stringent hybridization conditions, and a suitable container.
- 35 23. A *Staphylococcus aureus* polypeptide comprising an amino acid sequence identical to an amino acid sequence selected from the group consisting of SEQ ID NOS:5,192 to 5,255 or comprising an amino acid sequence having at least 95% identity to such a sequence.
- 40 24. A *Staphylococcus aureus* polypeptide antigen comprising at least one epitope derived from a *Staphylococcus aureus* polypeptide selected from the group consisting of SEQ ID NOS:5,192 to 5,255.
25. A polypeptide comprising at least one epitope encoded by a *Staphylococcus aureus* amino acid sequence selected from the group consisting of the epitopic sequences listed in Table 4.
- 45 26. The polypeptide of claim 24 or 26, wherein said polypeptide is fixed to a solid phase.
27. A diagnostic kit for detecting *Staphylococcus aureus* infection comprising
 - 50 (a) an isolated polypeptide antigen of claim 24, and
 - (b) means for detecting the binding of an antibody contained in a biological fluid to said antigen.
28. A vaccine composition comprising a polypeptide of claim 24 present in a pharmaceutically acceptable carrier.
- 55 29. A method of vaccinating an individual against *Staphylococcus aureus* infection comprising, administering to an individual the vaccine composition of claim 28.

Figure 1

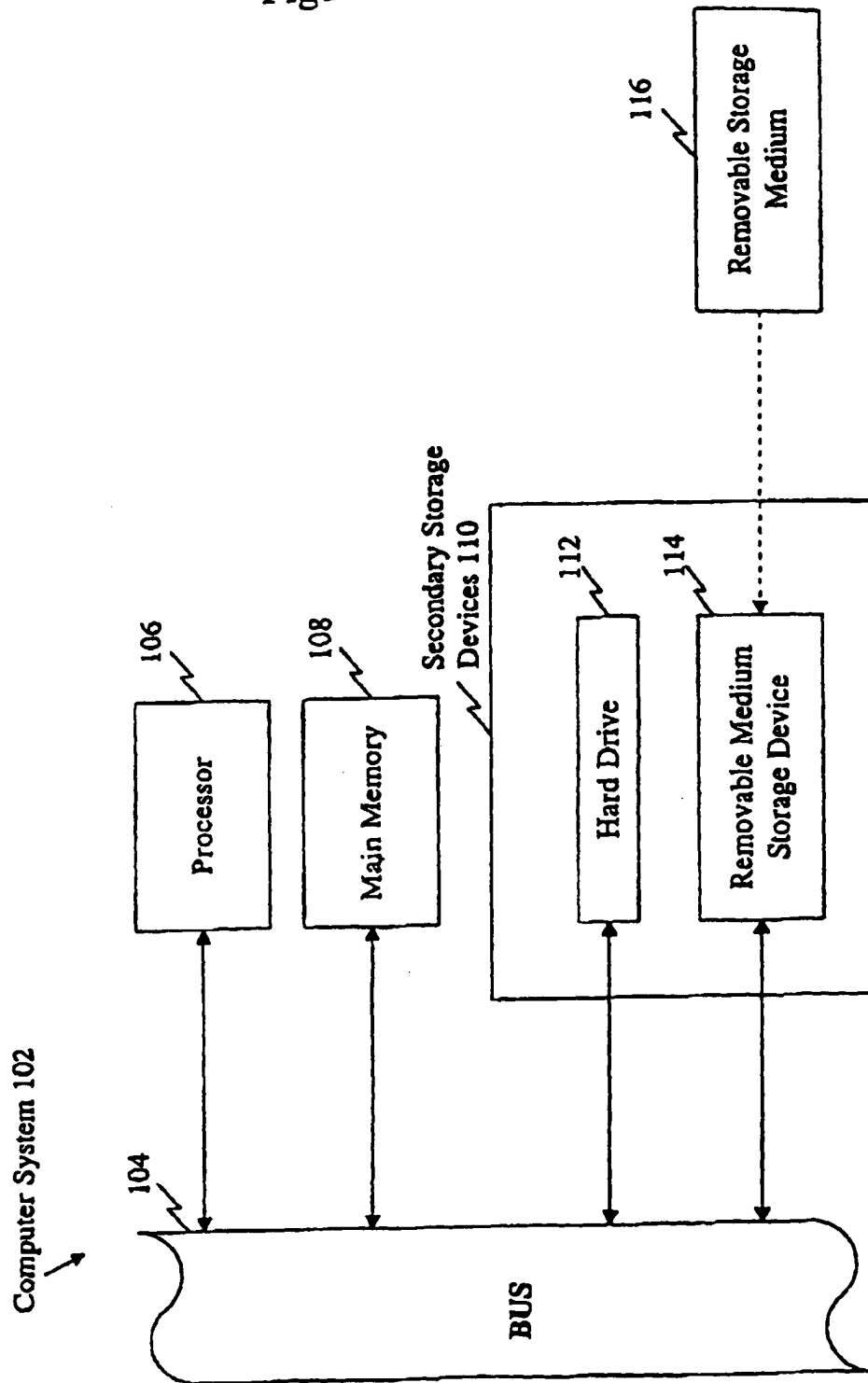


Figure 2

